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(54) Title: CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

(57) Abstract: The invention describes the use of nucleic acids and polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi for the preparation of a medicament for treating diseases associated with yeast or fungi or for the treatment of proliferative disorders or for preventing apoptosis in certain diseases. Methods are provided to identify compounds which selectively modulate the expression or functionality of said polypeptides in the same or a parallel pathway. Also provided are compounds as well as pharmaceutical compositions, medicaments and vaccines. The invention also comprises new nucleic acid sequences, probes and primers derived thereof, expression vectors and host cells transformed with said vectors, polypeptides and antibodies raised against said polypeptides.

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CELL DEATH RELATED DRUG TARGETS IN YEAST AND FUNGI

The present invention relates to the identification of genes and proteins encoded thereof from yeast and fungi whose expression is modulated upon programmed cell death and which genes, proteins or functional fragments and equivalents thereof may be used as selective targets for drugs to treat infections caused by or associated with yeast and fungi or for the treatment of proliferative disorders or for the prevention of apoptosis in certain diseases.

Invasive fungal infections (e.g. *Candida* spp, *Aspergillus* spp., *Fusarium* spp., *Zygomycetes* spp.) (Walsh, 1992) have emerged during the past two decades as important pathogens causing formidable morbidity and mortality in an increasingly diverse and progressively expanding population of immunocompromised patients. Those with the acquired immune deficiency syndrome (AIDS) constitute the most rapidly growing group of patients at risk for life-threatening mycosis. But fungal infections have also increased in frequency in several populations of other susceptible hosts, including very-low-birth-weight infants, cancer patients receiving chemotherapy, organ transplant recipients, burn patients and surgical patients with complications.

These fungal infections are not limited to humans and other mammals, but are also important in plants where they can cause diseases or cause the production of unwanted compounds. (e.g. *Fusarium* spp., *Aspergillus* spp., *Botrytis* spp., *Cladosporium* spp.).

Although recent advances in antifungal chemotherapy have had an impact on these mycoses, expanding populations of immunocompromised patients will require newer approaches to antifungal therapy. The discovery of novel antifungal agents is thus an essential element of any new antifungal therapy.

Classical approaches for identifying anti-fungal compounds have relied almost exclusively on inhibition of fungal or yeast growth as an endpoint. Libraries of natural products, semi-synthetic, or synthetic chemicals are screened for their ability to kill or arrest growth of the target pathogen or a related nonpathogenic model organism. These tests are cumbersome and provide no information about a compound's mechanism of action. The promising lead compounds that emerge from such screens must then be tested for possible host-toxicity and detailed mechanism of action studies must subsequently be conducted to identify the affected molecular target.

Cells from multicellular organisms can commit suicide in response to specific signals or injury by an intrinsic program of cell death. Apoptosis is a form of programmed cell death which leads to elimination of unnecessary or damaged cells. To

survive, all cells from multicellular organisms depend on the constant repression of this suicide program by signals from other cells (Raff, 1992). It has been assumed that such an altruistic form of cell survival arose with multicellularity and would have been counterselected in unicellular organisms. Recent findings indicate, however, that a
5 similar process of cell survival also operates in single-celled eukaryotes.

It has been found that expression of the mammalian *Bax* gene triggers cell death in *Saccharomyces cerevisiae* and the fission yeast *Schizosaccharomyces pombe* with morphological changes similar to apoptosis (Jürgensmeier *et al.*, 1997). However, the mechanism of *Bax* lethality in *S. cerevisiae* remains unclear.

10 Since it has been discovered that the mammalian *Bax* gene triggers apoptotic changes in yeast (Ligr *et al.*, 1998), this can be an indication that the molecular pathways eventually leading to programmed cell death may also be partially present in yeast cells and other unicellular eukaryotes.

It is an aim of the present invention to provide nucleic acid as well as
15 polypeptide sequences which represent potential molecular targets for the identification of new compounds which can be used in alleviating diseases or conditions associated with yeast or fungi infections.

It is a further aim of the present invention to provide uses of these nucleic acid and amino acid molecules for the preparation of a medicament for treating diseases
20 associated with yeast or fungi.

It is also an aim of the invention to provide pharmaceutical compositions and vaccines comprising these nucleic acids or polypeptides.

It is also an aim of the present invention to provide vectors comprising these nucleic acids, as well as host cells transfected or transformed with said vectors.

25 It is also an aim of the invention to provide antibodies against these polypeptides, which can be used as such, or in a composition as a medicine for treating diseases associated with yeast and fungi.

It is another aim of the invention to provide methods to selectively identify compounds capable of inhibiting or activating expression of such polypeptides in yeast
30 or fungi infections. The nucleic acid and polypeptide molecules alternatively can be incorporated into an assay or kit to identify these compounds.

It is also an aim of the invention to provide a method of preventing infection with yeast or fungi.

It is also an aim of the invention to provide probes and primers deriv d from the
35 nucleic acid sequenc s of the invention.

All the aims of the present invention have been met by the embodiments as set out below.

The present inventors identified a range of specific nucleotide sequences which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. As explained in Example 2, genes showing a difference of a factor 5 or more in expression as a result of *Bax*-induced cell death, were identified as differentially expressed candidate genes. Some of these genes are clearly down-regulated in a *Bax*-expressing strain, while other genes show an upregulated expression (Table 1). Example 3 describes a further experiment wherein the results of differential expression were analysed using the Pathways™ software and differentially expressed nucleic acid sequence were identified.

According to a first embodiment, the invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more

- preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e); and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using
5 BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide
10 or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to
15 determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine
20 identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15,
25 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
30 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 457, 459, 461, 463, 465, 467, 469, 471 and 473.

The invention also relates to nucleic acid sequences from *Candida albicans*, as represented by the SEQ ID NOs 285, 287, 289, 291, 293, 295, 297, 299, 301, 303,
35 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371,

373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481, and 483.

5 The expression "a pathway eventually leading to programmed cell death" refers to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

10 The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi" not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are
15 commonly known as "non-pathogenic".

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,
20 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295,
25 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465,
30 467, 469, 471, 473, 475, 477, 479, 481 or 483 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death.

According to the invention, these sequences and their homologues in other yeast and fungi as well as the polypeptides which they encode represent novel
35 molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides.

Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporium* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp.,
 5 *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

According to another embodiment, the invention also relates to a nucleic acid sequence encoding a polypeptide which is involved in a pathway eventually leading to
 10 programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386,
 15 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which
 20 is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366,
 25 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which
 30 is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402,
 35 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483; and,
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f).

According to a more specific embodiment, these nucleic acid sequences are derived from *Saccharomyces cerevisiae*, *Candida albicans* or *Aspergillus fumigatus*.

A nucleic acid sequence according to the invention may comprise an mRNA sequence or alternatively a DNA sequence and preferably a cDNA sequence. A nucleic acid sequence according to the invention may also comprise any modified nucleotide known in the art.

The present invention further relates to a nucleic acid molecule capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook et al., 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The term "nucleic acid sequence" also includes the complementary sequence
5 to any single stranded sequence given, or the antisense version thereof.

The invention also relates to mRNA, DNA or cDNA versions of the nucleic acid molecules of the invention.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid sequence capable of hybridizing to any of the above defined
10 nucleic acid sequences.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid sequences of
15 at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically
20 with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under
25 hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto
30 the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR
35 cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be

cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined
5 herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzyme
10 labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a
15 suitable expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to a control sequence, such as a suitable inducible promoter, or the like, to ensure expression of the proteins according to the invention in a suitable host cell. The expression vector may also comprise a reporter molecule. The expression vector may advantageously be
20 a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Preferably the host cell is a lower eukaryotic cell such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the
25 invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

The invention further relates to any nucleic acid as defined above for use as a medicament.

30 Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides, leading to impaired growth or death of yeast and
35 fungi with reductions of associated illnesses or diseases.

According to another embodiment, the invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2,
5 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48,
50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92,
94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126,
128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158,
160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,
10 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222,
224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254,
256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286,
288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318,
320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350,
15 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382,
384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414,
416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446,
448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478,
480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of
20 said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar,
preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
95% similar and most preferably more than 97% similar to any of the amino acid
sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28,
25 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72,
74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112,
114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144,
146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176,
178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,
30 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240,
242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272,
274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304,
306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336,
338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368,
35 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400,
402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c), for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide scanning techniques as described in Geysen *et al.* (1996). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75,
5 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to this aspect of the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106,
10 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276,
15 278, 280, 282, 284, 458, 460, 462, 464, 466, 468, 470, 472 and 474. Also according to the invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378,
20 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 476, 478, 480, 482 and 484.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative
25 amino acid changes.

The nucleic acid molecules or the polypeptides of the invention may be provided in a pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention also relates to a vaccine for immunizing a mammal against infections caused by yeast and fungi comprising at least one (recombinant)
30 nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as
35 proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids,

amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete. A vaccine may also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions.

The term "therapeutic" refers to a composition capable of treating infections caused by yeast or fungi.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

According to another embodiment, the present invention provides a method of identifying compounds which selectively inhibit, induce or interfere with the expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds may carry agonistic or antagonistic properties. The compounds to be screened may be of extracellular, intracellular, biologic or chemical origin.

Such a screening method may comprise the following steps (a) contacting a compound to be tested with cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound, (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

The term "cells" as used above relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells.

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

The invention also relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein

differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

Alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2, (b) detecting the complex formed between the compound to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps:

incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence

according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the GAL4 protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of GAL4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose

will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant process in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively, compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, and even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughput assays or in cases where none of the binding partners are labeled. Other techniques which can be used to study interactions are : overlay, ligand blotting, band-shift, co-

immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein trageting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Yersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for
5 altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing
10 and protein translocation. All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughput assays.

In cases compounds need to be found to target tumor cells, screening assays
15 will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to in vitro and in vivo model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. In vivo modelsystems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds
20 identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

25 According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

The invention also relates to a compound identified using any of the methods of the invention.

30 Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmac utically acceptable carrier.

35 Th compounds of the invention can be used for th preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections,

for instance *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
 5 and *Sporothrix schenckii* infections.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

10 A medicament according to the invention not only relates to fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

The invention also relates to genetically modified yeast or fungi in which modification results in the overexpression or underexpression of at least one of the nucleic acids or polypeptides of the invention, which overexpression or
 15 underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungi. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

20 Also according to the invention is the use of a compound obtainable by a method of the invention for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention also relates to an isolated protein which is involved in a pathway for programmed cell death of yeast or fungi
 25 selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394,
 30 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484 or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90 or
 35 95% similar and most preferably more than 90% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,

306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344,
346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380,
382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452
5 454, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical,
preferably more than 75% or 80% identical, more preferably more than 85%, 90%
or 95% identical and most preferably more than 97% identical to any of the amino
acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302,
10 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342,
344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376,
380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416,
418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450,
452, 454, 476, 478, 480, 482, or 484; and,

15 (d) a functional fragment of any of said proteins as defined in a) to c).

According to the invention, the polypeptides as defined above may be used as
a medicament.

Also encompassed within the present invention are antibodies, monoclonal or
polyclonal, capable of specifically binding to one or more epitopes of the proteins of the
20 invention. The term "specific binding" implies that there is substantially no cross-
reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to
techniques which are known to those skilled in the art. Monoclonal antibodies may be
prepared using conventional hybridoma technology as described by Kohler and
25 Milstein (1979). Polyclonal antibodies may also be prepared using conventional
technology well known to those skilled in the art, and which comprises inoculating a
host animal, such as a mouse, with a protein or epitope according to the invention and
recovering the immune serum. The present invention also includes fragments of whole
antibodies which maintain their binding activity, such as for example, Fv, F(ab') and
30 F(ab')₂ fragments as well as single chain antibodies.

Antibodies according to the invention may also be used in a method of
detecting the presence of a polypeptide according to the invention, which method
comprises reacting the antibody with a sample and identifying any protein bound to
said antibody. A kit may also be provided for performing said method which comprises
35 an antibody according to the invention and means for reacting the antibody with said
sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi such as, but not restricted to,
5 *Candida albicans*, *Aspergillus* spp., *Fusarium* spp., *Botritis*, spp., *Cladosporium* spp.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

10 According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic
15 acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art
20 (Sambrook et al., 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides
25 of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

The invention further relates to the compounds identifiable according to the above-described method and its use as a medicament.

The invention further relates to a method for preparing a pharmaceutical
30 composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate
35 due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal

benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

5 The expression "apoptosis" or "apoptosis-related diseases" includes diseases such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

10 According to another embodiment, the invention relates to the use of a nucleic acid molecule or a polypeptide described in the invention or human homologues thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

15 The invention also relates to a pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

20 The invention also relates to a vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule of the invention or a human homologue thereof or at least one polypeptide of the invention or a human analogue thereof in a pharmaceutically acceptable carrier.

25 The invention also relates to the use of an antibody of the invention capable of binding to at least one of the polypeptides of the invention or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

30 According to yet another embodiment, the invention relates to an expression vector comprising a human homologue of a nucleic acid sequence of the invention. Said expression vector may comprise an inducible promoter and may further comprise a sequence encoding a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

35 According to another embodiment the invention relates to a nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences described in the invention.

The invention also relates to an antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to a nucleic acid molecule which is a human analogue of the invention.

5 The invention also relates to a polypeptide encoded by the nucleic acid molecule comprising said human homologues of the nucleic acids described in the invention.

10 The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

- Figur 1.** *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID Nos 1 to 284)
- Figure 2.** *Candida albicans* sequences (SEQ ID Nos 285 to 456).
- 5 **Figure 3.** Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters. The filters are cut in the upper right corner for orientation and the DNA is on the labelled side of the filter. Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.
- 10 The spots represent the genome wide expression profile without (A) and with (B) *Bax* modulated expression (Example 2).
- Figure 4.** Results from a second experiment analogous and analysed as described in the examples section (Example 3).
- 15 **Table 1.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed more than fivefold in a first experiment (see Example 2). The factor by which the transcript level was affected, is expressed as the Qt value. A Qt value higher than 1 indicates upregulation while a Qt value lower than 1 indicates a
- 20 downregulation. For instance, a Qt of 0.5 indicates a two-fold lower transcript level of a particular mRNA due to *Bax* expression in *S. cerevisiae*. Upregulation or downregulation of a specific mRNA is stated when Qt had a value of at least five or at most 0.21, respectively.
- 25 **Table 2.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly in a second experiment (see Example 3). In this experiment, the Qt values were calculated using the Pathways Software (Research Genetics).

EXAMPLES**Exempl 1. Differential gene expression analysis upon Bax-induced cell death****Materials and media**

Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was
 5 used for the construction and the amplification of plasmids. Yeast strains were grown
 under normal conditions on standard media (Sherman *et al.*, 1979). The
Saccharomyces cerevisiae strain INVSc1 (Invitrogen®) was transformed by means of
 the lithium acetate method (Schiestl and Gietz, 1989) with YIpUTyL or YIpUTyLMuBax,
 after linearisation in the Ty δ element (Zhu, 1986).

10

Cloning of mouse BAX cDNA

Mouse *Bax* cDNA, encoding the mouse Bax- α protein, was cloned by Pfu DNA
 polymerase (Stratagene®) chain reaction amplification (PCR) from an EL4/13.18
 thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

15

5'-ATGGACGGGTCCGGGAGCAG-3' and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3'.

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to
 standard procedures (Sambrook J. *et al.*, 1989).

20 **Plasmid constructions**

The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *ClaI* and *BglII*. A *BamHI-HindIII* GAL1
 promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI* FLP
 terminator fragment was inserted into this *XbaI-HindIII*(blunted)-opened plasmid so that
 25 the plasmid YIpUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in
 the *KpnI-AatII*-opened and blunted YIpUT resulted in the plasmid YIpUTy. Subsequent
 insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-
 openend and blunted YIpUTy resulted in the plasmid YIpUTyL.

30 Mouse *Bax* cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII*
 and subcloned into the *XbaI-HindIII*-opened plasmid YIpUTyL, obtaining the final
 expression plasmid YIpUTyLMuBax.

The plasmid YIpUTyLMuBax has been deposited in the BCCM™/LMBP culture
 collection as p5CTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

5 The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

10 Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

15 The yeast filters consist of over 6000 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains
20 the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

25

Results**Induction of Bax-expression in yeast cells**

30 *S. cerevisiae* cells (strain INVSc1) were transformed with the expression plasmid YIpUTyLMuBax or the parental plasmid YIpUTyL as a negative control. Alternative yeast strains (such as W303-1A (Thomas and Rothstein, 1989)) with equivalent properties are known in the art and can also be used.

35 The Ty δ element of both plasmids allowed a stable multi-copy integration in the genome of the yeast cell. Southern analysis of the cells containing YIpUTyLMuBax revealed the integration of 5 GAL1-controlled Bax-cassettes near Ty elements.

The yeast cells containing YlpUTyLMuBax and the yeast cells containing YlpUTyL were grown overnight in 10 ml minimal glucose-containing medium. The precultures were then further diluted to an OD₆₀₀ of 0,2 in 100 ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells containing YlpUTyL were washed and a dilution thereof was transferred into 100 ml galactose-containing medium and incubated for 15 hours. After this additional period the cultures reached an OD₆₀₀ of 1. The yeast cells containing YlpUTyLMuBax were also washed and transferred into 100 ml galactose-containing medium and incubated for 15 hours.

10

RNA isolation

Total RNA was isolated using RNAPure™ Reagent (Genhunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 10⁹ cells were concentrated in a microcentrifuge tube and 1ml RNAPure™ Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA digestion. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 µl RNase free dH₂O.

20

First strand cDNA synthesis in the presence of α-³³P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YlpUTyLMuBax or INVSc1 YlpUTyL yeast cells and incorporation of α-³³P dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH₂O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

30

6 µl 5x concentrated First Strand Buffer (GIBCO-BRL)

1 µl 0,1 M DTT

1 µl RNase Block (40 units/µl) (Stratagene)

1,5 µl 20 mM dXTP-solution (X = A, G and T) (Pharmacia)

1,5 µl SuperScript™ Revers Transcriptase (200 units/µl) (GIBCO-BRL)

35

10 µl α-³³P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham)

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Pharmacia). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 3 or 5 10^8 cpm/ μ g for both the INVSc1YIpUTyL and the INVSc1YIpUTyLMuBax probe.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α - 32 P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 or 10 ml MicroHyb™ solution (42°C) containing 5 μ l polydA (0,5 or 1 μ g/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette with storage phosphorscreen. After 4 days of development the screen was developed and scanned using the PhosphorImager™ 455 SI from Molecular Dynamics. The results of these can be seen in Figure 3.

In-between the hybridisation experiments, the filters were stripped off by incubation in 500 ml of a 0,5% SDS solution (prewarmed to near boiling temperature) during at least 1 hour at room temperature.

Example 2. Quantification of Hybridisation Signals

Quantification of the hybridisation signals was done using the ImageQuant™ 4.1 software tool from Molecular Dynamics (Sunnyvale, CA). The quantification was performed per grid of the Yeast GeneFilters™, and by drawing a roster of 24 columns and 8 rows onto each grid of each filter. As such, each rectangle of the roster corresponds to a spot on the Yeast GeneFilters™. Subsequently, from each grid a volume-report (quantification) was drawn up and the data were transferred to a Microsoft™ Excel sheet. Also for each grid a correction factor was calculated. Signals neighboring big and dark spots were separately quantified. For each grid, a background level was calculated.

Statistical processing of quantification results

The statistical processing of the results was accomplished in Microsoft™ Excel. For each grid, the following statistical functions were separately defined:

1. The frequency of occurrence of the values in a precisely defined intensity range(data range), established between 1000 and 61000, split up in intervals of 5000.
2. The frequency in terms of percentage.
3. The cumulated frequency in terms of percentage.

These numeric values were used for the graphical display of the cumulated frequency in terms of percentage.

Subsequently, the results of the two experiments (hybridization with cDNA from YlpUTyL containing INVSc1 cells and hybridization with cDNA from YlpUTyLMuBax containing INVSc1 cells) were integrated by determination of a second range of statistical functions:

1. The average of the values of the two experiments for each spot on the filter.
2. The standard deviation on this average. This is a measure for the distribution of the values around this average.
3. The standard deviation in terms of percentage.

The quotient of the values of the second experiment (Bax expression) against the values from the first experiment (control) was determined. This immediately gave the factor by which the expression of a specific gene is changed upon Bax induction.

In order to process all these data and to be able to discriminate between differences in gene expression, a gene showing a standard deviation in terms of percentage of at least 90% and a difference of a factor 5 in expression as a result of Bax induction, was identified as a differentially expressed candidate gene. (Table 1). Requantification of these candidates confirmed their selection.

When the expression pattern of all 6144 genes is compared in the two experiments, it could be concluded that the expression profile of 142 genes (this is 2,3 %) has been changed with at least of factor 5. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 1. The sequences of these genes and the amino acid sequences which they encode are shown in Figure 1.

Example 3 . Quantification of Hybridisation Signals using the Pathways™ software

Quantification of the hybridisation signals was done using the Pathways™ Software (Research Genetics) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 2.

Surprisingly, using this Software package for analysing the results in this example and when compared to the results of example 2, some additional genes were found which expression are up-or down-regulated upon *Bax* expression in *S. cerevisiae*.

The sequences of up- and down regulated genes and the corresponding amino acid sequences from Examples 2 and 3 are shown in Figure 1.

Example 4 Search for homologues in *Candida albicans*

Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minnesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.

Example 5 . Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; 5 Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to 10 the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally 15 sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test 20 compound.

The assay to be set up involves measurement of growth or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti- 25 sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

30 **Example 6. Assay for High Throughput screening for drugs**

35 35 µl minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers 2.5 µl of R-compound at 10^{-3} M in DMSO from a stock plate into the assay plate.

The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with $20\text{ }\mu\text{g/ml}$ uridine. A single colony is scooped
5 up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml.
10 Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (+/- 0.04) is reached.

$200\text{ }\mu\text{l}$ of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a $450\text{ }\mu\text{l}$ total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

15 Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Tabl 1.

ORF	Qt	Sequence ID Number
YAR061W	7.80	SEQ ID NO 1
YAR073W	11.19	SEQ ID NO 3
YBL048W	5.07	SEQ ID NO 5
YBL051C	5.22	SEQ ID NO 7
YBL066C	6.04	SEQ ID NO 9
YBL078C	6.94	SEQ ID NO 11
YBR072W	26.56	SEQ ID NO 13
YBR073W	5.46	SEQ ID NO 15
YBR086C	7.14	SEQ ID NO 17
YBR093C	11.05	SEQ ID NO 19
YBR181C	0.15	SEQ ID NO 21
YCL007C	20.99	SEQ ID NO 23
YCL016C	23767.57	SEQ ID NO 25
YCR052W	10.51	SEQ ID NO 27
YCR064C	14.91	SEQ ID NO 29
YCR073WA	5.92	SEQ ID NO 31
YDL010W	5.31	SEQ ID NO 33
YDL036C	5.34	SEQ ID NO 35
YDL083C	0.16	SEQ ID NO 37
YDL125C	6.80	SEQ ID NO 39
YDL133CA	0.21	SEQ ID NO 41
YDL136W	0.20	SEQ ID NO 43
YDL167C	6.37	SEQ ID NO 45
YDL184C	0.21	SEQ ID NO 47
YDL191W	0.17	SEQ ID NO 49
YDR103W	6.26	SEQ ID NO 51
YDR238C	5.75	SEQ ID NO 53
YDR259C	9.68	SEQ ID NO 55
YDR294C	8.38	SEQ ID NO 57
YDR430C	5.66	SEQ ID NO 59
YDR438W	6.47	SEQ ID NO 61
YDR450W	0.16	SEQ ID NO 63
YDR471W	0.11	SEQ ID NO 65
YDR486C	5.27	SEQ ID NO 67
YDR499W	6.14	SEQ ID NO 69
YDR507C	6.34	SEQ ID NO 71
YDR515W	5.42	SEQ ID NO 73
YDR518W	6.15	SEQ ID NO 75
YDR519W	5.57	SEQ ID NO 77
YER102W	0.19	SEQ ID NO 79
YER153C	5.63	SEQ ID NO 83
YFL014W	41.08	SEQ ID NO 85
YFL015C	5.62	SEQ ID NO 87
YFR022W	9.44	SEQ ID NO 89
YGL011C	6.14	SEQ ID NO 91
YGL031C	0.11	SEQ ID NO 93
YGL032C	0.14	SEQ ID NO 95
YGL043W	10.74	SEQ ID NO 97
YGL102C	0.15	SEQ ID NO 99
YGL103W	0.17	SEQ ID NO 101
YGL130W	8.35	SEQ ID NO 103

YGL147C	0.08	SEQ ID NO 105
YGL213C	6.02	SEQ ID NO 107
YGL235W	6.23	SEQ ID NO 109
YGL260W	6.61	SEQ ID NO 111
YGR085C	0.16	SEQ ID NO 113
YGR118W	0.17	SEQ ID NO 115
YGR142W	8.91	SEQ ID NO 117
YGR236C	12.72	SEQ ID NO 119
YGR277C	6.27	SEQ ID NO 121
YGR284C	5.95	SEQ ID NO 123
YGR285C	5.84	SEQ ID NO 125
YHR010W	0.20	SEQ ID NO 127
YHR021C	0.16	SEQ ID NO 129
YHR141C	0.10	SEQ ID NO 131
YHR217C	7.6	SEQ ID NO 133
YIL112W	11.15	SEQ ID NO 135
YIL115C	7.67	SEQ ID NO 137
YIL148W	0.13	SEQ ID NO 139
YIL150C	6.83	SEQ ID NO 141
YIL167W	6.66	SEQ ID NO 143
YJL034W	11.61	SEQ ID NO 145
YJL035C	14.48	SEQ ID NO 147
YJL070C	5.29	SEQ ID NO 149
YJL078C	5.16	SEQ ID NO 151
YJL179W	0.19	SEQ ID NO 153
YJL180C	0.14	SEQ ID NO 155
YJL181W	0.21	SEQ ID NO 157
YJL187C	0.17	SEQ ID NO 159
YJL188C	0.1	SEQ ID NO 161
YJL189W	0.08	SEQ ID NO 163
YJL190C	0.09	SEQ ID NO 165
YJL197W	0.13	SEQ ID NO 167
YJL198W	0.2	SEQ ID NO 169
YJR049C	0.17	SEQ ID NO 171
YKR094C	0.14	SEQ ID NO 173
YLR040C	10.13	SEQ ID NO 175
YLR048W	8.55	SEQ ID NO 177
YLR088W	6.09	SEQ ID NO 179
YLR159W	0.18	SEQ ID NO 181
YLR167W	0.06	SEQ ID NO 183
YLR232W	7.4	SEQ ID NO 185
YLR233C	7.63	SEQ ID NO 187
YLR234W	5.68	SEQ ID NO 189
YLR238W	6.74	SEQ ID NO 191
YLR241W	6.48	SEQ ID NO 193
YLR321C	12.17	SEQ ID NO 195
YLR322W	5.54	SEQ ID NO 197
YLR325C	0.06	SEQ ID NO 199
YLR344W	0.12	SEQ ID NO 201
YLR367W	0.19	SEQ ID NO 203
YLR393W	7.05	SEQ ID NO 205
YLR423C	8.61	SEQ ID NO 207
YML026C	0.11	SEQ ID NO 209
YML063W	0.16	SEQ ID NO 211

YML128C	5.1	SEQ ID NO 213
YML130C	5.41	SEQ ID NO 215
YMR022W	6.45	SEQ ID NO 217
YMR118C	5.13	SEQ ID NO 219
YMR143W	0.08	SEQ ID NO 221
YMR174C	6.75	SEQ ID NO 223
YMR191W	9.56	SEQ ID NO 225
YMR230W	0.13	SEQ ID NO 227
YNL054W	5.19	SEQ ID NO 229
YNL067W	0.12	SEQ ID NO 231
YNL075W	0.16	SEQ ID NO 233
YNL096C	0.14	SEQ ID NO 235
YNL162W	0.07	SEQ ID NO 237
YNL178W	0.11	SEQ ID NO 239
YNL182C	0.18	SEQ ID NO 241
YNL190W	0.07	SEQ ID NO 243
YNL208W	5.87	SEQ ID NO 245
YNL210W	0.02	SEQ ID NO 247
YOL031C	5.32	SEQ ID NO 249
YOL048C	14.34	SEQ ID NO 251
YOR010C	7.27	SEQ ID NO 253
YOR019W	5.19	SEQ ID NO 255
YOR027W	6.03	SEQ ID NO 257
YOR031W	5.35	SEQ ID NO 259
YOR096W	0.12	SEQ ID NO 261
YOR248W	0.18	SEQ ID NO 263
YOR293W	0.11	SEQ ID NO 265
YOR312C	0.12	SEQ ID NO 267
YOR369C	0.21	SEQ ID NO 269
YPL047W	5.09	SEQ ID NO 271
YPL090C	0.1	SEQ ID NO 273
YPL137C	10.41	SEQ ID NO 275
YPL159C	5.61	SEQ ID NO 277
YPL175W	5.95	SEQ ID NO 279
YPL180W	7.68	SEQ ID NO 281
YPL218W	6.26	SEQ ID NO 283
YPR102C	0.17	SEQ ID NO 285

Tabl 2.

ORF	Qt	Sequence ID Number
YGR236C	7.25	SEQ ID NO 119
YDR442W	0.049	SEQ ID NO 459
YGR182C	0.602	SEQ ID NO 467
YGR106C	0.478	SEQ ID NO 465
YKR040C	2.23	SEQ ID NO 471
YJL188C	0.075	SEQ ID NO 161
YOR096W	0.067	SEQ ID NO 261
YOR293W	0.107	SEQ ID NO 265
YDR450W	0.056	SEQ ID NO 63
YML026C	0.051	SEQ ID NO 209
YHR021C	0.114	SEQ ID NO 129
YLR167W	0.033	SEQ ID NO 183
YGL147C	0.061	SEQ ID NO 105
YGR085C	0.107	SEQ ID NO 463
YOR312C	0.083	SEQ ID NO 267
YOL127W	0.101	SEQ ID NO 473
YHR010W	0.077	SEQ ID NO 127
YDR471W	0.046	SEQ ID NO 65
YDL191W	0.128	SEQ ID NO 49
YDL136W	0.125	SEQ ID NO 43
YLR325C	0.061	SEQ ID NO 199
YJL189W	0.07	SEQ ID NO 163
YIL148W	0.145	SEQ ID NO 139
YHR141C	0.069	SEQ ID NO 131
YBL003C	0.119	SEQ ID NO 457
YDR529C	0.352	SEQ ID NO 461
YGR183C	0.781	SEQ ID NO 469

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CLAIMS

1. Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which
5 nucleic acid sequence is selected from:
- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300,

- 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- 5
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
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- 25
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261,
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- 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483;
- 5 (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483; and
- 10 (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- 15 (g) the complement of any of the nucleic acid sequences as specified in a) to f), for the preparation of a medicament for treating diseases associated with yeast or fungi.
- 20
- 25
- 30
- 35 2. Use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

25

3. A pharmaceutical or fungicidal composition comprising a nucleic acid molecule as defined in claim 1 or a polypeptide as defined in claim 2 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

30

4. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid molecule as defined in claim 1 or at least one polypeptide as defined in claim 2 in a pharmaceutically acceptable carrier.

35

5. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or the polypeptides as defined in claim 2, which overexpression or

underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungus.

5 6. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 10 (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound,
- 15 (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 20 (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

25 7. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 30 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting on or more wild type cells with said compound,
- 35 (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is

indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

- 5 (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 10 (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

8. A method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

15

- (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2,
- (b) detecting the complex formed between the compound to be tested and said polypeptide,
- 20 (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound being tested.
- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

25

9. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene,
- 30 (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested.

10. A method according to any of claims 6 to 9 where in said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.
- 5 11. A compound identifiable according to the method of any of claims 6 to 9.
12. A compound according to claim 11 for use as a medicament.
- 10 13. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound according to claim 12 with a suitable pharmaceutically acceptable carrier.
- 15 14. Use of a compound according to claim 11 or 12 for the preparation of a medicament for treating diseases associated with yeast and fungi.
- 15 15. Use of a compound according to claim 11 or 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
- 20 16. Use of a compound according to claim 12 where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
25 and *Sporothrix schenckii*.
17. A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:
- 30 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
35 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,

454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- 5 (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 10 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 15 (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 20 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 25 (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;
- 30 (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 35 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; and,

- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to e).

5 18. A nucleic acid according to claim 16 characterized in that it is derived from *Candida albicans*.

 19. A nucleic acid molecule capable of selectively hybridizing to a nucleic acid sequence as defined in claim 1 or the complement thereof.

10

 20. A nucleic acid sequence according to any of claim 17 to 19 which is mRNA

 21. A nucleic acid sequence according to any of claims 17 to 19 which is
15 DNA.

 22. A nucleic acid sequence according to any of claims 17 to 19 which is cDNA.

20 23. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to any of claims 17 to 22.

 24. An isolated protein which is involved in a pathway for programmed cell
25 death of yeast or fungi selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394,
30 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and
35 most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308,

- 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348,
352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384,
386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424,
426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476,
5 478, 480, 482 or 484;
- (c) a protein having an amino acid sequence which is more than 70% identical,
preferably more than 80% identical, more preferably more than 90% identical
and most preferably more than 97% identical to any of the amino acid
sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,
10 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344,
346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380,
382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,
454, 476, 478, 480, 482 or 484; and,
- 15 (d) a functional fragment of any of said proteins as defined in a) to c)

25. An expression vector comprising a nucleic acid sequence according to
any of claims 17 to 23.
- 20 26. An expression vector according to claim 25 which comprises an
inducible promoter.
27. An expression vector according to claim 25 or 26 which comprises a
sequence encoding a reporter molecule.
- 25 28. A host cell transformed, transfected or infected with the vector of any of
claims 25 to 27.
29. A nucleic acid molecule according to any of claims 17 to 23 for use as a
30 medicament.
30. A polypeptide according to claim 24 for use as a medicament.
31. An antibody capable of specifically binding to a polypeptide according to
35 claim 24.

32. An antibody according to claim 31 for use as a medicament.
33. A pharmaceutical composition comprising an antibody according to claim 31 or 32.
- 5 34. Use of an antibody according to claim 31 or 32, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2, for the preparation of a medicament for treating diseases associated with yeast and fungi.
- 10 35. Use of an antibody according to claim 34 where the fungus is *Candida albicans*.
- 15 36. A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively hybridises with any of said nucleic acid molecules.
- 20 37. A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively amplifies any of said nucleic acid molecules.
- 25 38. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or a human homologue thereof or at least one of the polypeptides as defined in claim 2 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.
- 30 39. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences as defined in claim 1 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.
- 35 40. A compound identifiable according to the method of claim 39.

41. A compound according to claim 40 for use as a medicament.

42. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising
5 admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

43. Use of a compound according to claim 40 or 41 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain
10 disorders.

44. Use of a nucleic acid molecule selected from any of the nucleic acid molecules as defined in claim 1 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
15

45. Use of a polypeptide selected from any of the polypeptides as defined in claim 2 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

46. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.
20

47. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule as defined in claim 1 or a human homologue thereof or at least one polypeptide as defined in claim 2 or a human analogue thereof in a pharmaceutically acceptable carrier.
25

48. Use of an antibody according to claim 31 or 32 or an antibody capable of binding to at least one of the polypeptides as defined in claim 2 or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
30

35

55

49. An expression vector comprising a human homologue of a nucleic acid sequence as defined in claim 1.

50. An expression vector according to claim 49 which comprises an inducible promoter.

5

51. An expression vector according to claim 49 or 50 which comprises a sequence encoding a reporter molecule.

52. A host cell transformed, transfected or infected with the vector of any of claims 49 to 51.

10

53. A nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences as defined in claim 1.

54. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 53.

15

55. A polypeptide encoded by a nucleic acid molecule according to claim 53.

20

FIG. 1:

YAR061W, 704 bp, CDS: 501-704 (SEQ ID NO 1)

AAAATTTGGCACTTCAGAGCTTATCGTATCTTCTCCCGGAGTTCTCAAGACTTATACTT
CAGCCCGTTTAGGAATGCATAAAAGCAAATAGGATTCGTTACAACGCTGCAGGACTCTT
TAGGACTGCATCAAGGTAAGCCTCGCTGCACCTAAACGCAAAATGTGGTTGTAACCTTTT
TAATTTTTTCTTGAACCTGTTGAGTCGTAATAAATCGTTTCTGGGAAGTGAAGGTAAT
AATGTAATGGAATCGGCGTTACTCGCATGTGCAGATATCAGCGACAAAAGTGTGTAGG
GACGTTTCGATACCAAAATTTCTTAAATACAGCGCAGGAACATCACTACGCTAAACAAAT
CGTAGCGCATACATCTGATCGAAAAAGACAGTTCCCAAAACAATGACATATGAAGAGAC
CAGCATCAAAATTTTCATCATTAACAGCATGGCTAAAAGTTATTGTTTAATATACCCATA
CCTGATTGACGAACCAAGAAATGCCTTATCACTATTTATTTTGGCACTCTTCACCTACC
TGGCCACGTCCAATGTTGTTTCAGGAAGTACACAAGCATGCCTGCCAGTGGGCCCCGAGGA
AAAATGGGATGAATGTCAACTTTTATAAATACTCATTACTGGATTCAACAACGTATTCCT
ACCCGCAATATATGACTTCTGGATATGCCTCGAATTGGAATTAG

YAR061W, 67 aa (SEQ ID NO 2)

MPYHYLFLALFTYLATSNVVSSTQACLPGVPRKNGMNVNFYKYSLLDSTTYSYPQYMTS
GYASNWN

YAR073W, 1712 bp, CDS: 501-1712 (SEQ ID NO 3)

AGTGGCTCATGATCTGTAAATGATCGGTTGACCGCAGTATTATATAATAACATCCGTATA
AGTACATATACTACCATGTCTGTTCTCTACATTGCTTTTTTATTCAAGATTATTGGTTTTTC
CTAACC GCCGCGCGCGCAGGTACCCGCGCATCTCTTCTTCTCGAAGAAAGCGGAAAAA
ACAAAAAAGATATAAATAGTGGAGTCTTTTCCATTAAACATTTAGAAAAAATTCG
AATGGAAATTTCTTGCCGAACATTTAACCGGAGACCCTTGGCGGCTTTTTCTCAGTTTCG
TGGGCTAGTACATTTTACCTAGTATGCTGGGAACTTTTTTTCCGTATTCTATTCTATTCC
TTGCCTTACTTTTTCTTATCATTTTTTTATATAACCAATTTCAAAAATACTTTTTAACTGTC
ATAGACGCATTTTGTATTATACAAATTAAGAAGTCAAATATAATATGTGCAATTAATAA
CTCCACAAGTAGCGAAAGCAATGGCCGCCATTAGAGACTACAAGACCGCACTAGATCTTA
CCAAGAGCCTACCAAGACCGGATGGTTTGTGTCAGTGCAGGAAGTATGGACTCCAAGATCA
GAGGTGGGTGGCTTATAACGATTTTTTTAATCTTACCAGGTTTAGTCGATTTTGGCGTCCT
CTGAAGTTAGCCTACAGACCAAGCTAACAGGAATATTACTTTAAACATTCCATTAGTAT
CCTCTCCAATGGACACTGTGACGGAATCTGAAATGGCCACTTTTATGGCTCTGTTGGATG
GTATCGGTTTCATTACCATTAACCTGTACTCCAGAGGACCAAGCTGACATGGTCAGAAGAG
TCAAGAACTATGAAAATGGGTTTATTAACAACCCTATAGTGATTTCTCCAACCTACGACCG
TTGGTGAAGCTAAGAGCATGAAGGAAAAGTATGGATTGTCAGGCTTCCCTGTCACGGCAG
ATGGAAAGAGAAATGCAAAGTTGGTGGGTGCCATCACCTCTCGTGATATACAAATTCGTTG
AGGACAACCTCTTACTCGTTTCAGGATGTATGACCAAAAACCCTGTTACCGGCGCACAAAG
GTATCACATTATCAGAAGGTAACGAAATCTTAAAGAAAATCAAAAAGGGTAGGCTACTGG
TTGTTGATGAAAAGGGTAACCTTAGTTTCTATGCTTTCCCGAAGTATTTAATGAAAATC
AGAAGTACCCATTAGCGTCCAAATCTGCCAACACCAAGCAACTGTTATGGGGTGCTTCTA
TTGGGACTATGGACGCTGATAAAGAAAGACTAAGATTATTGGTAAAAGCTGGCTTGGATG
TCGTCATATTGGATTCCCTCTCAAGGTAACCTATTTTCCAATTGAACATGATCAAATGGA
TTAAAGAACTTTCCAGATTTGGAAATCATGTGCTGGTAACGTTGTCACCAAGGAACAAG
CTGCCAATTTGATTGCTGCCGGTGCGGACGGTTTGAGAATTGGTATGGGAAGTGGCTCTA
TTTGATATTACCCAAAAAGTTATGGCTTGTGGTAGGCCACAAGGTACAGCCGTCTACAACG
TGTGTGAATTTGCTAACCAATTCGGTGTTCATGTATGGCTGATGGTGGTGTTCAAAAAC
ATTGGTCATATTATTACCAAGCTTTGGCTCTTGGTTCTTCTACTGTTATGATGGGTGGT
ATGTTGGCCGGTACTACCGAATCACCAGGTGA

YAR073W, 403 aa (SEQ ID NO 4)

MAAIRDYKTALDLTKSLPRPDGLSVQELMDSKIRGGLAYNDFLILPGLVDFASSEVSLQT
KLTRNITLNIPLVSSPMDTVTESEMATFMALLDGIGFIHNCPTPEDQADMVRRVKNYENG
FINNPVIVISPTTVGEAKSMKEYGFAGFPVTADGKRNAKLVGAITSRDIQFVEDNSLLV
QDVMTPKNPVTGAQGITLSEGNEILKKIKKGRLLVDEKGNLVSMLSRDLMKNQKYPAS
KSANTKQLLWGASIGTMDADKERLRLLVKAGLDVVILDSSQNSIFQLNMIKWIKETFPD
LEIIAGNVVTKQAANLIAAGADGLRIGMTGSICITQKVMACGRPQGTAVYNVCEFANQ
FGVPCMADGGVQKHWSYYYQSFQSWFFCYDQWYVGRYYRITR

YBL048W, 812 bp, CDS: 501-812 (SEQ ID NO 5)

GGGAGAAGCTTATCTTACTGTAGAAAGAAAATGGGATTGCGTTACTCCATATATATTGAAA
ATCCGTTATCTTCCCCATCATCATCGTATAAATCAATAAACGACCCGTTATTCCACTCTC
AGCATCGATCGCAAAAAACGTGAGCTTCATCACCTACGGTTGTAGACATTGCAAGACAC
ATCTTTCCAGTTCCTTCCAGATTATTTCTAGAGATTATAGGGGTAGGACCGGAACGCTT
ATTTAATGAACAAAGTTGTTAATGTCGTTGAAGGAAAGGTCGAGCAACGAAGAATGTTGA
CTGGCGACTACTTAGTCTGTGATATTCCTTTGTCATTGGTGCAAGAGGAACGTAGGTTGGA
AATACTTGCAGAGCAGCAATGATGATCAGCAGTATAAGGAAGGAAAGTTTATCTTAGAGC
TGAAAAACATTTGTAAATGTACTTGATGTCTTCCTTTGTCTGCTATCTAGCACCTCTCGT
CTTTTAGTGCTTTTTAGCGTATGATTCTTTTTAAGAATCTGGTCTTTCTTCCTTCTATTT
TGATTGGGTATATTTCTATTTCGTGTTTCATTACTGGTCTGGGTTAATTGGGTTTTGGTTT
GGTCCAGTTGTTTTCAAGTAGCCTTTATTTTTTCATTGTGGTATTTTATCTTATCGATTT
ATACTTTTTTTTATTCAAAGAAAATTAACAGATAATCTCTTATGAGCCTAGCTACTTTG
TTTTTCTTACAGGGCCATTGACTTATGCCCTGAACGAGTCTTACTTTACTTTTTTTGTA
TTTTCAATAATGTCGTGTTCCCATGTTGTAA

YBL048W, 103 aa (SEQ ID NO 6)

MILFKNLVFLPSILIGYISIRVSLLVWNWLVWSSCFQVAFIFSLWYFILSIYTFYFSK
KIKQIISYEPSYFVFSYRAIDLCPERVLLYFFCIFNNVFPML

YBL051C, 2507 bp, CDS: 501-2507 (SEQ ID NO 7)

GGGAAATATCAATTCCCGTATTTCAATGTTAGTAATTTGCCTTCGTAAATTACGGAATCA
CATAGCTTTTCATTTTGTTCCTTTGATATATTTCCCTACTACATACTCTTTTCAATAACTC
TACAGGGTCTGACATTTTAACTTTTCAGGTTAATGATGGTGTCTTACTATATCTCGAG
TCGTACAGAAGTTAGTTCAGATAAACTGCTTCGGTGCTGCCCACTTCTTATCATTACTTC
AACTTTACCTTCCCTATACCTGTGTGTCCTTATTAATTCAAGTTAATCCGAGGTAATAGA
TTAGGGTAACCTTCAATGATGTCACGAAACACGGATGCTGCAACTTTGCGATTTTTTCCT
GGAAAAGAATAACAATTAAAGGCAGCCTTTCAGCTGAGATTACCAGCAGGTCTTTGGAGA
TTAGCGCAAGAAGAAGTGTGATATAGTACTCATAGAGGCAGGCTACAGACTAGGGAAAGC
GTGTTCAACAACAATAAGAAATGGAGACCAGTTCTTTTGAGAATGCTCCTCTGCAGCCA
TCAATGATGCTCAGGATAATAATATAAATACGGAGACTAATGACCAGGAAACAAATCAGC
AATCTATCGAAACTAGAGATGCAATTGACAAAGAAAACGGTGTGCAAACGGAAACTGGTG
AGAACTCTGCAAAAAATGCCGAACAAAACGTTTCTTCTACAAATTTGAATAATGCCCCCA
CCAATGGTGCTTTGGACGATGATGTTATCCCAAATGCTATTGTTATTAATAAACATTCCGT
TTGCTATTAAAAAAGAGCAATTGTTAGACATTATTGAAGAAATGGATCTTCCCCTTCCTT
ATGCCCTTCAATTACCACTTTGATAACGGTATTTTTTCAGAGGACTAGCCTTTGCGAATTTCA
CCACTCCTGAAGAACTACTCAAGTGATACTTCTTTGAATGGAAAGGAAATCAGCGGGA
GGAAATTGAAAGTGGAATATAAAAAATGCTTCCCCAAGCTGAAAGAGAAAGAATCGAGA
GGGAGAAGAGAGAGAAAAGAGGACAATTAGAAGAACAACACAGATCGTCATCTAATCTTT
CTTTGGATTCTTTATCTAAAATGAGTGGAAGCGGAAACAATAACTTCTAACAATCAAT
TATTCTCGACTCTAATGAACGGCATTAAATGCTAATAGCATGATGAACAGTCCAATGAATA
ATACCATTAAACAATAACAGTTCTAATAACAACAATAGTGGTAACATCATTCTGAACCAAC
CTTCACCTTCTGCCCAACATACTTCTTCATCGTTGTACCAAACAAACGTTAATAATCAAG
CCCAGATGTCCACTGAGAGATTTTATGCGCCTTTACCATCAACTTCCACTTTGCCTCTCC
CACCCCAACAACCTGGACTTCAATGACCCTGACACTTTGGAAATTTATTCCCAATTATTGT
TATTTAAGGATAGAGAAAAGTATTATTACGAGTTGGCTTATCCCATGGGTATATCCGCTT
CCCACAAGAGAATTATCAATGTTTGTGCTCGTACTTAGGGCTAGTAGAAGTATATGATC
CAAGATTTATTATTATCAGAAGAAAGATTCTGGATCATGCTAATTTACAATCTCATTTGC
AACAACAAGGTCAATGACATCTGCTCATCCTTTGCAGCCAACTCCACTGGCGGCTCCA
TGAATAGGTCACAATCTTATACAAGTTTGTACAGGCCCATGCAGCAGCTGCAGCGAATA
GTATTAGCAATCAGGCCGTTAACAATTCTTCCAACAGCAATACTATTAACAGTAATAACG
GTAACGGTAACAATGTCATCATTAATAACAATAGCGCCAGCTCAACACCAAAAAATTTCTT
CACAGGGACAATTCTCCATGCAACCAACACTAACCTCACCTAAAATGAACATACACCAATA
GTTCTCAATAAATTCGCGAGACCAACCGCAACCACTCAACCACAAACACAGCAAAAATG
TTCAGTCAGCTGCGCAACAACAACAATCTTTTTTAAGACAACAAGCTACTTTAACCAT
CCTCAAGAATTCCATCCGGTTATTCTGCCAACCATTATCAAATCAATTCCGTTAATCCCT
TACTGAGAAATTCTCAAATTTACCTCCAAATTCACAAATCCCAATCAACAGCCAAACCC

TATCCCAAGCGCAACCACCAGCACAGTCCCAAACCTCAACAACGGGTACCAGTGGCATACC
AAAATGCTTCATTGTCTTCCAGCAGTTGTACAACCTTAACGGCCCATCTTCAGCAAACCT
CACAGTCCCAACTGCTTCCACAGCACACAAATGGCTCAGTACATTCTAATTTCTCATATC
AGTCTTATCACGATGAGTCCATGTTGTCCGCACACAATTTGAATAGTGGCGACTTGATCT
ATAAATCTTTGAGTCACTCTGGACTAGATGATGGCTTGGAACAGGGCTTGAATCGTTCTT
TAAGCGGACTGGATTTACAAAACCAAAACAAGAAGATCTATGGTAA

YBL051C, 668 aa (SEQ ID NO 8)

METSSFENAPPAAINDAQDNNINTETNDQETNQSSIETRDAIDKENGVTETGENSAKNA
EQNVSSSTNLNNAPTNGALDDVIPNAIVIKNIPFAIKKEQLLDIIEMDLPLPYAFNYHF
DNGIFRGLAFANFTTPEETTQVITSLNGKEISGRKLKVEYKMLPQAEERIEREKREKR
GQLEEQRSSNLSLDSLKMSGSGNNNTSNNQLFSTLMNGINANSMMNSPMNNTINNNS
SNNNSNGNIILNQPSLSAQHTSSSLYQTNVNNQAQMSTERFYAPLPSTSTLPLPPQQLDF
NDPDTLEIYSQLLLFDREKYYEYELAYPMGISASHKRIINVLC SYLGLVEVYDPRFIIIR
RKILDHANLQSHLQQQGMSTSAHPLQPNSTGSGMNRSSQSYTSLLOAHAAAAANSISNQAV
NNSSNSNTINSNNGNGNNVIINNNSASSTPKISSQGQFSMQPTLTSPKMNIHSSQYNSA
DQPQQPQPQTQQNVQSAAQQQSFRLRQATLTSSRIPSGYSANHYQINSVNPLLRNSQI
SPPNSQIPINSQTLQAQPPAQSQTOQRVPVAYQNASLSSQQLYNLNGPSSANSQSQQLLP
QHTNGSVHSNFSYQSYHDESMLSAHNLNSADLIYKSLSHSGLDDGLEQGLNRSLSGLDLQ
NQKKKNLW

YBL066C, 3674 bp, CDS: 501-3674 (SEQ ID NO 9)

ATCCCAAGAAGAAGATTAGACTGATTTTTACCTACCCCTCCACCGTCGGAAGAAACACTT
CTGAAGTGTTAAGGGTAATCGACGCCCTTGCAATTGACTGACAAGGAGGGCGTAGTAATC
CAATTAATTGGCAGCCAGCTGACGATGTCAATTATCTCCCTCTGTCTCCAATGATGAGG
CGAAGGCTAAAATTTGGTCAATTTAATGAAATTAACCCCTATTTAAGATTCCACCAAGTCGA
AATAAGCTTTGAAATAAACGACTTTACTATATACAGGTATATGAAGTATCTCTAACTAAA
ACTTTTATCTATCTTTTCAATCTTATTATATCTCATCTCGTACGAAGGGCCGCTCATTGGA
TCATTTTCTCTTTACATACCGTAAAGGAATGGCGTTAAAAATATATATGAAAATGCATG
TAATAAACTCTCTGCAGAAACCTTAATGTCAAAGGTCCCGTATACAGATTATATTGGCTC
TGCGTATACGCATTCTCGTCATGGTGAAGGATAATCGAGATTCTGACCAAGACCAAGATT
TTAGTTCTGCTCACATGAAAAGACAACCGGAGCAGCAACAGTTGCAACAGCACCAGTTCC
CAAGTAAGAAACAACGAATATCTCACCATGATGACAGTCATCAAATCAACCATAGACCAG
TTACCTCATGTACACATTGTAGACAGCACAAAATCAAATGCGATGCTAGTCAAATTTCC
CTCATCTCTTGCTCCAGATGCGAAAAAATTTGGTCTCCACTGTGAAATCAATCTCAATTCA
GGCCTAAGAAGGGCTCACAGTTGCAACTACTGAGACAAGATGTGGATGAAATCAAATCTA
AACTCGATACTCTTCTGGCCAATGACAGCGTTTTCGTTCATCTTTTACAACAGATTCCCA
TGGGCAATAGCCCTTTTGAATAAGCTCAATCTGCATCCAACCTCCAACCTCCGGGTACTATTA
TCCCTAACCAGATTCTTCTCTCTCAGGTCTCCAACCTCTTCCGCGGCTCAACGAG
ATTCTAAGGTTTCAGTTCAAACCTTATTTGTCCAGGGAACCCCAACTCTTACAAGCAAATC
AGGGCAGCAATACGAATAAATTTAAAGCAAATAATGAAGCATCTTCTCACATGACGTTGC
GCGCATCTTCTTTAGCGCAAGATTGCAAGGCTTGGTTGCAACAGAGCCAAATAAGCTGC
CCCCGCTGCTAAATGACTCAGCATTGCCTAATAATTCAAAGAATCTTTACCTCTGCTT
TGCAAAATGGCTTTTATAAGAACAACCTCTGCAGGTAACACTCCGAACGGCCCCCTTCTCTC
CAATTCAAAAAACATATTTCCCTCATACTACGTCGACCACCGTTACAACGACAACAAATC
AACCACCATTTGCAGCAACAAGCCACGTAGCAACAAATAACAATGCAGATAGGACGAAGA
CGCCGGTAGTAGCCACCACCAGACTATGCCATTATTGCCCTTCGCCGCATGCAAATGTAG
ATGAGTTTGTACTGGGCGATATTAGTATTTCCATTGAAAAAGCGAATAGATTACACCATA
TTTTCGTGACTAGGTATCTGCCGTATTTTCTATTATGTATTCCAATAACGCCACCGAAT
TATACTCCCAATCTCAGTTGCTTTTCTGGACCGTGATGTTGACGGCATGTCTGTCTGATC
CTGAACCGACGATGTATTGCAAGCTAAGCTCTTTGATCAAGCAACTTGCCATAGAGACCT
GCTGGATAAGAACACCTAGATCCACACATATTTGCAAGCTTTGTTAATATTGTGCATTT
GGCCTTTGCCTAACCAAAAAGTCTTAGATGATTGTTCTTACCGTTTGTAGGATTAGCAA
AGTCACTGTCTTATCAATTAGGTTTGCACAGAGGTGAATTCATTTCTGAATTCACAAGAA
CTCAAACATCAATGCCAAATGCAGAAAAGTGGAGAACTAGGACTTGGCTGGGAATATTTT
TGCCGAACCTTTGTTGGGCGAGTATCCTTGGTTTGGCCACCACTTCACAGACAGACTATT
TATTAGAAAAAGCCTTATCTGTGGTGACGAAGAATCAGAAGAAGATAACAATGACAGTA
TTGACAATAACAACAATGATAAAAGGAACAAGAAAGACGAGCCGACGTTGAAAGTAAAT
ACAAACTACCGGGCAGTTTGTAGAAGATTGCTCAGCCTGGCGAATTTCCAAGCAAAATTTGT
CTCATATCATTTGGTTCTTCCACTTCCAGTCTGATGGTTTATTGGAACCAAGTATCGTG

CTGAGACACTGTCCATCTTGGGAAAAGAGTTAGATTTATTAGCAAAAACCTTTAAATTTCC
AGAGTGACGATACTGTCAACATTTATTTTCTTTATGTTAAATTAAGTGTCTGTTGTTTTG
CATTCTACCCGAAACACCTCCTACCGATCAAATTCATATGTCACAGAGGCCTATCTAA
CAGCTACTAAAATTGTCACTCTATTGAATAATCTTTTAGAAAACACACCAATTAATTGAAC
TGCCTATTTATATTAGACAAGCTGCTACATTTTCTGCACTGATTCTCTTTAAATTGCAGT
TGACTCCTTTACTTCCTGACAAATATTTTGATTACAGCAAGGCAATCCGTGGTCACTATCC
ATAGACTTTATAGAAATCAGTTAACTGCGTGGGCCACTAGTGTGAGAATGATATTTTCCA
GAACTGCAAGTATGTTAGAAAACTGAACTTCGTACTGATCATGCATCCAGAAGTTTTTG
TGGAAGAAGACGGTATTATTTCTAGGATGAGATCACATTTAACAGGGTCTCTATTCTATG
ATTTGGTTTTGGTGTGTTACGAGGCGAGAAGAAGGGAAATGGATCCCGAATATAACAAGC
AAGCCTTAGAGAAAGCCGCTAAGAAAAGAAAATTTTCTCAAATGGTATCTACAATGGCA
CTTCGTTACGGGTGGCATAACGGACAGAAAACCTATATCCATTGCCACTATATAACCATA
TCTCCAGAGATGACTTTGAACTGTAACAAAAACAACACCAAGTGAACCACTGTTACCA
CTTTAGTTCCCTACTAAGAATGCCTTAAAGCAGGCAGAAAAGCTAGCCAAGACAAATAACG
GAGATTCTGACGGTTCTATAATGGAGATTAACGGGATACCTCTTTCCATGCTCGGGGAAA
CAGGCAGCGTAAAATTTCAAAGTTTATTCGCTAATACCTCGAATAGTAACGATTATAATA
ATAATAGGACGTTATTGGATGCGTCTAATGACATATCAATTCCTCTAATTCATTTATC
CAGTGGCTTCTGTCCCCGCTTCGAATAACAATCCACAAAGTACTAAGGTAGACTATTATA
GTAACGGACCTAGTGTAATTCCTGATCTCTCCATGAAAAGATCAGTAAGCACTCCCGTTA
ATCATTTTCTGCGTCCGTTCCAGGGTTAAGGAACCAACCCCGTTGGCAACTTATCTAATA
ATGTTACATTGGGAATAGACCACCTATTCCAAGGGAGCACAGTAATTTACAAAATGTCA
CCATGAATTATAATAATCAATTCAGCAACGCCAACGCGATTGGAAGATCACAAAGTAGTA
TGTCCTTACGTCACCTTTGTTTCCGTCAATATATGACAGTTGGATTCCGCGTCCGA
CCCCGTCCTCTAA

YBL066C, 1057 aa (SEQ ID NO 10)

MVKDNRSDQDQDFSSAHMKRQPEQQQLQHQFSPKKQRISHHDDSHQINHRPVTSTHCH
RQHKIKCDASQNFPHPCSRCEKIGLHCEINPQFRPKKGSQQLLRQDVDEIKSKLDTLLA
NDSVFVHLLQQIPMGNSLLNKLNLHPTPTPGTIIIPNDSSPSSGSPSSAAQRDSKVSQ
TYLSREPQLLQANQGSNTNKFKANNEASSHMTLRASSLAQDSKGLVATEPNKLPPLNDS
ALPNNSESLEPPALQMAFYKNNAGNTPNGPFSPIQKTYSPHTTSTTVTTTTNQPFAAT
SHVATNNNADRTKTPVVATTTTTPPLPSPHANVDEFVLGDISISIEKANRLHHIFVTRYL
PYFPIMYSNNATELYSQSQLFWTVMLTACLSDEPTMYCKLSSLIKQLAIETCWIRTPR
STHISQALLILCIWPLPNQKVLDDCSYRFVGLAKSLSYQLGLHRGEFISEFTRTQTSMPN
AEKWRTTWLGIFFAELCWASILGLPPTSQTDYLLEKALSCGDEESEEDNNDNNDNNDNND
KRNNKDEPHVESKYKLPGSFRLLSLANFQAKLSHIIGSSSTSSPDGLLEPKYRAETLSIL
GKELDLLAKTLNFQSDDTVNIYFLYVKLTVCFFAFLPETPPTDQIPYVTEAYLTATKIVT
LLNNLLETHQLIELPIYIRQAATFSALILFKLQLTPLLDPKYFDSARQSVVTIHRLYRNO
LTAWATSVENDISRTASMLEKLNFLVIMHPEVFVEEDGIIISMRSHLTGSLFYDLVWCVH
EARRREMDPEYNKQALEKAAKKRKFSSNGIYNGTSSTGGITDRKLYPLPLYNHISRDDFE
TVTKTTPSGTTVTTLVPTKNALKQAEKLAKTNNGSDSGSIMEINGIPLSMLGETGSVKFQ
SLFANTSNSNDYNNNRTLLDASNDISIPNSIYPVASVPASNPNPQSTKVDYYSNGPSVI
PDLMSKRSVSTPVNHFASVPGLRNHPVGNLSNNVTLGIDHPIPREHSNLQNVMTMNNQ
FSNANAIGRSQSSMSHSRTPLFRSIYDSWIPRPTPVL

YBL078C, 854 bp, CDS: 501-854 (SEQ ID NO 11)

TAGTGGAGTACGAATTAGTTAAAGATACTATCGACTTTGAAGCCATTGTCAAAGAACATT
TTGATATGTTAAGCAAGACCTGTAGATCCGACATTGCCAAATATGACGGCTCAAAGACAG
ACCAATTGGTGATGAAGAACAATCTATTAATGACACCAATTTCAAATTAAGTGTTCA
AATTATGAAAACAACCTCATATAAATACGTACAAATTTTCTCTACTCGAAGTGATATAGA
TGTATATGTGTAAGTTTACGTTTAAAGTTAGAGTCATGTAATGCTAACTGTCTCCACCGAT
AATGTTGTATAATACCCGTGAAATCATAGCACATGATATATCATCACCCGGAGGCCGTT
ATTTTCGGCGCGCGCAAAAATATTTGGTATAATTATGGAATACAAAAAGGGGAACCAAT
AAAGTTGAGGAGGGGATTGATAAGAGAATCTAATAATTGTAAAGTTGAGAAAATCATAA
TAAAAATAATTACTAGAGACATGAAGTCTACATTTAAGTCTGAATATCCATTGTAAAAA
GGAAGGCGGAGTCGGAGAGGATTGCTGACAGGTTCAAGAATAGGATACCTGTGATTGCG
AAAAAGCTGAAAAGTCAGATATTCCAGAGATTGATAAGCGTAAATATCTAGTTCCCTGCTG
ACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAGAGAATTATGCTACCCCTGAGA
AGGCCATCTTCATTTTTGTCAATGATACTTTGCCACCTACTGCGCGTTGATGTCTGCCA
TATATCAAGAACACAAGGATAAGGACGGTTTTTGTATGTCACCTTACTCAGGAGAAAATA

CATTTGGCAGGTAG

YBL078C, 117 aa (SEQ ID NO 12)

MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF
VYVIRKRIMLPPEKAIFIFVNDTLPPPTAALMSAIYQEHKDKDGLYVVTYSGENTFGR

YBR072W, 1145 bp, CDS: 501-1145 (SEQ ID NO 13)

GCAGCAGCAACTCCGTGTGTACCCCTAACTCCGTGTGTACCCCTAAAGAACCTTGCCCTGT
CAAGGTGCATTGTTGGATCGGAATAGTAACCGTCTTTACATGAACATCCACAACCAACGA
AAGTGCTTTTTCAAGCATTGCTTGATTTCTAGAAAGATCGATGGTTATTCCCTCCCCCTT
ATGCGTCCAAAAATATAGGGTGCTCGTAACAGTAAGGTATTTCGCACTTAGCGTGCTCGCA
ACACAAAATTAAGTAATATGCGAGTTTTAGATGTCCTTGCGGATCTATGCACGTTCTTGA
GTGGTATTTTATAACAACGGTTCTTTTTTACCCTTATTCTTAAACATATAAATAGGACCT
CCATTAGTTAGAGATCTGTTTTTAATCCATTACCTTTTATTCTACTCTCTTATACTAAT
AAAACCACCGATAAAGATATATCAGATCTCTATTAAAAACAGGTATCCAAAAAAGCAAACA
AACAACTAAACAAATTAACATGTCAATTAACAGTCCATTTTTTGATTTCTTTGACAACA
TCAACAACGAAGTTGATGCCTTTAACAGATTGCTGGGTGAAGGCGGCTTAAGAGGCTACG
CACCAAGACGTCAGTTAGCAAAACACACCCGCAAAGGATTCTACTGGCAAGGAAGTTGCTA
GACCAATAACTATGCTGGCGCTCTTTATGATCCCAGAGATGAAACCTTAGATGATTGGT
TCGACAATGACTTGTCCTGTTCCTCATCTGGTTTTCGGTTTCCCTAGAAGTGTGCGAGTTT
CAGTTGATATTTTGGACCATGACAACAACACGAGTTGAAAGTCGTGGTTTCTGGTGTCA
AAAGCAAGAAGGACATTGATATTGAGTACCATCAAAACAAGAACCAAATTTTGGTTTCTG
GTGAAATTCCATCTACCTTGAATGAAGAGAGTAAAGACAAGGTCAAGGTCAAGGAGAGCA
GCTCTGGTAAGTTCAAGAGAGTCATCACTTTGCCAGACTACCCAGGTGTGGATGCAGACA
ACATTAAAGCAGACTACGCAAATGGTGTTTTGACATTAACAGTTCCAAAATTGAAGCCTC
AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAA

YBR072W, 214 aa (SEQ ID NO 14)

MSFNSPFFDFFDNINNEVDAFNRLLEGGLRGYAPRRQLANTPAKDSTGKEVARPNNYAG
ALYDPRDETLDWFDNDLSLFPSPGFGFPRSVAVPVDILDHDNNYELKVVPVGVKSKDID
IEYHQNKILVSGEIPSTLNEESKDKVKVKESSSGKFKRVITLPDYPGVDADNIKADYA
NGVLTTLTPKLKPQKDGKNHVKKIEVSSQESWGN

YBR073W, 3377 bp, CDS: 501-3377 (SEQ ID NO 15)

AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAAAGTGACCTGGCTCTATAGTGTGTCCCTCTCGCGAGGACCATTGTTGCTTGATA
TGGCTTGAAACATATGTCATCACATCTGAGCGATTTTACCCTTGAATTAGTTTGAATA
TATATGAGTTGATGAATAAATAGTTATAAAAACTTGCTTTGGCTTCGATATATGACCGTT
ATTTTTGACTAAGTTTAAACGAAGGAATCTAACCTCGTTCCTTGTAATTACCAAAATCTTC
AACAAACGCGCTGTTGGAGGTATCTCTATGGATGTGGCTTGAAATATGGATGTCTTGCCTA
CTTCTACTTCTGGGAAAGGCATTTTTACTCGATCGCGTTAATATATGCATCAAGAAAATA
AAAAATAAAACGCGAAGAGCTAAAAAAGAAAACCTACTATAAATAACCGATTAG
AATCGAGTTTTTGTATTGAAATGGCGGTAATAAGCGTTAAACCTCGACGAAGAGAGAAGA
TCCTACAGGAGGTAAAAACAGCTCGGTATATCAAACGGTATTTGATTCCGGTACTACTC
AAATGCAGATACCGAAATATGAGAACAAGCCATTCAAGCCTCCAAGAAGGGTTGGATCAA
ATAAGTACACACAACCTCAAACCAACCGCCACTGCAGTCACAACAGCCCCATATCTAAAG
CCAAAGTTACTGTCAACTTGAAAAGAAGCATTTTCGGCGGGACCTACTTTAAATCTTGCCA
AGAAGCCGAATAATCTGTCTCAAATGAAAACACTAGATATTTTACTATCATGTACAGGA
AGCCTACTACCAAAAAGCACAAGACTTGGAGTGGTGATGGCTACGCTACCTTAAAAGCCA
GTAGCGATAAGTTATGCTTTTATAACGAAGCAGGGAAATTTCTTGGGTCAAGTATGCTAC
CAAGTGATTCAAGTCTCTCTTTCGAAACTCTTTTCAAAGCAGGCTCCAATGAAGTACAAT
TGGATTACGAATTGAAGGAAAATGCAGAAATACGTAGCGCCAAAGAAGCCTTATCACAAA
ACATGGGAAATCCCAGCCCACCGACCACAAGCACAACAGAAACAGTGCCCTTCTACGAAGA
ATGACGGTGGCAAATACCAAATGCCCTCTGTCTCAGCTGTTTTCACTAAACACTGTGAAAA
GATTCAAATCAGTAACAAAGCAAACAAATGAACACATGACCACAGTACCTAAAACAGTCA
AAAATTCCAAAGCCAAAAAATATTATCCAGTATTTGATGTCAACAAAATCGATAATCCTA
TAGTAATGAACAAAATGCAGCCGCTGAAGTTGACGTAATTGTTGATCCATTACTGGGCA
AATTCCTTGCGCCCTCATCAGAGGGAAGGGGTGAAGTTCATGTATGATTGCTTAATGGGCT
TGCAAGACCAACTATTGAAAATCCGGATATCGATTGTACTACTAAAAGTTTAGTGTTAG

AAAATGACTCAGATATTAGTGGATGCCTTTTGGCTGATGATATGGGTTTAGGTAAAAACAC
TAATGAGTATAACTTTGATTTGGACATTAATTAGGCAAACCTCTTTTGCATCAAAAGTTT
CATGTTTCGCAATCAGGCATACCATTAACTGGACTTTGTAAGAAGATTTTAGTCGTTTGTC
CCGTTACTTTAATAGGAAATTGGAAAAGAGAATTTGGAAAATGGTTAAATTTGTCAAGAA
TAGGTGTTTTGACATTAAGCTCAAGGAATTCCTCGATATGGATAAAATGGCTGTCAGAA
ATTTTTTAAAGTGCAACGAACTTATCAAGTCTTGATTATTGGCTACGAAAAACTCTTGA
GTGTTTCTGAAGAATTAGAGAAAAATAAACATTTGATTGACATGCTGGTGTGTGACGAAG
GCCATCGACTAAAAAACGGGGCTTCTAAAATTTTAAATACGCTGAAGAGTTTAGACATAA
GAAGGAAGCTTTTGCTTACGGGAACCTTATACAAAATGATCTTAATGAGTTTTTCACTA
TTATAGATTTTCATAAACCCAGGAATCCTTGGAAGCTTCGCTTCTTTCAAAAGAAGATTCA
TTATCCCTATAACTAGAGCCAGAGACACTGCAACAGATACAACGAAGAATTGTTGGAAA
AGGGGGAAGAAAGGTCAAAAGAGATGATAGAAATTACGAAAAGATTTATTTTGAGACGAA
CAAATGCGATTTTAGAAAAAGTACCTTCTCCAAAGACGGATATAATTTTATTCTGTAAAC
CATACAGCCAACAGATATTGGCATTCAAAGATATTTTGCAGGGCGCACGTTTAGATTTTG
GACAATTGACGTTCAAGTTCTTCGCTAGGACTAATAACATTACTGAAAAAGGTTTGTAAC
CTCCTGGATTGGTTGGCTCAGATCCCTATTACAAATCACATATAAAGGATACCCAATCTC
AGGACAGCTATAGTCGTTCTTTGAACTCTGGTAAGTTAAAGGTATTAATGACATTACTAG
AAGGTATTAGGAAGGTACCAAGGAGAAGGTCGTCGTAAGTGTCTAACTACACTCAACAT
TGGATATAATTGAAAATTTGATGAATATGGCTGGGATGTCACATTGCAGACTCGACGGTT
CCATACCTGCTAAACAAAGGGACTCTATCGTCACATCTTTCAATCGGAATCCAGCCATAT
TTGGATTCTTTGTTGAGTGCAAAATCGGGAGGTGTAGGATTGAATCTAGTCGGTCGTTTCGC
GACTTATTTTATTTGATAATGATTGGAATCCTTCAGTAGATTGCAAGCGATGTCACGAA
TTCATAGAGATGGTCAAAAAAGCCGTGCTTCATATATAGACTTGTCACAACTGGGTGTA
TCGATGAGAAAAATATTGCAAGGCAATTAATGAAGAACAGTTTGAGCCAAAAATTTCTAG
GTGACTCGGAGATGAGAAAATAAAGAATCTTCTAATGATGATCTTTTCAATAAAGAGGACT
TGAAGGACCTGTTTTCTGTCCATACAGATACCAAGAGTAACACACATGACTTAATTTGTT
CTTGCGATGGTTTAGGTGAGGAAATTGAATATCCTGAAACAAATCAACAGCAGAACACCG
TAGAGCTGAGAAAGCGTAGCACTACGACATGGACAAGTGCCTGGATTACAAAAGAAAA
TGAATGAAGCAGCCACCAACGATGATGCCAAAAAGTCACAATACATTAGGCAATGTCTCG
TTCATTATAAGCATATCGATCCAGCAAGACAAGATGAATTATTTGATGAGGTTATCACAG
ATTCGTTACCGAATTGAAAGATAGTATTACCTTTGCGTTTGTAAGCCCGCGGAGATAT
GTCTCAGAGAACAATGA

YBR073W, 958 aa (SEQ ID NO 16)

MAVISVKPRRREKILQEVKNSSVYQTVFDSGTTQMQUIPKYENKPFKPPRRVGSNKYTQLK
PTATAVTTAPISKAKVTVNLKRSISAGPTLNLAKKPNNLSSNENTRYFTIMYRKPTTKKH
KTVSGDGYATLKASSDKLCFYNEAGKFLGSSMLPSDSDSLFETLFAKGSNEVQLDYELFV
NAEIRSAKEALSONMGNPSPPTTSTTETVPSTKNDGGKYQMPLSQLFSLNTVKRFKSVTK
QTNEHMTTVPKTSQNSKAKKYYPVFDVNKIDNPIVMNKNAAAEVDVIVDPLLKGFLRPHQ
REGVKFMYDCLMGLARPTIENPDIDCTTKSLVLENDSDISGCLLADDMGLGKTLMSITLI
WTLIRQTPFASKVSCSQSGIPLTGLCKKILVCPVTLIGNWKREFGKWLNLNRIGVLTLS
SRNSPDMDKMAVRNFLKVQRTYQVLIIGYEKLLSVSEELEKNKHLIDMLVCDGHRKLNK
ASKILNTLKSLEDIRKLLLTGTPIQNDLNEFFTIIIDFINPGILGSFASFRRFIIPITRA
RDTANRYNEELLEKEERSKEMIEITKRFILRRTNAILKYLPPKTDIILFCKPYSQOIL
AFKDILQGARLDFGQLTFSSSLGLITLLKKVCNSPGLVGSDDPYKSHIKDTQSQDSYSRS
LNSGKLKVLMTLLEGIRKGTKEKVVVVSNYTQTLDIENLMNMAGMSHCRLDGSIPAKQR
DSIVTSFNRNPAIFGFLLSAKSGGVGLNLVGRSRLILFDNDWNPSVDLQAMSRIHRDQK
KPCFIYRLVTTGCIDEKILQRQLMKNSLSQKFLGDSEMRNKESNDDLNFNKEDLKDLFSV
HTDTKSNTHDLICSDGLGEEIEYPETNQONTVELRKRSTTTWTSSALDLQKKMNEAATN
DDAKKSQYIRQCLVHYKHIDPARQDELFDVITDSFTELKDSITFAFVKPGEICLREQ

YBR086C, 3341 bp, CDS: 501-3341 (SEQ ID NO 17)

AGATCCTAAACAGCACGAAGCATATTATGCGCATAATTTGTTCTTGTAGGATCTTTTC
TTGACATTTTTTTTCTACTCTGCAGAACTTCTCTTTTTTTTCTCTAGGGACGAAAA
CAACAAGGGCACTTTTTTTTATCTTTTTTTTTTCTCTGTTGTTTTCAAAACAAAAAGAT
TCCACCACTACATCAGTGTGAAGACTGTAAAGCTTTCTGATAAATAAGCACTTTCCAT
ATTTTTCAACTGAAAAATAGTTTTCTTTTTTGACGCTATTATTGACTTCATTAAGAAATAT
CCCTTTTTTCCCGTTGCAATTATTTCTATAAGGGAAGCTGGAAATAGGGGGCTGGAAAA
GATATTTGAACAGTCGCTCCAATAACCGTTCTCACCATCATTAACTTTTTGAAGGTGAA
TACTGTTTCGGTCGATTTATGGCTAATTTGTCAAATACATTTGAAAAAGATTAAAAACAAG

CACAAGCGGTTGAGCATACTATGTCGAGACAATTACATCTCTAGATCCGAATTGTGTGTTA
TTGTATTCAATAAAACCTCGAGTGCAAACGAGAAGAGTTTGAATGTCGAATTCAAACGTT
TGAATATACATTCTATTATCGAACCTGGCCATGATCTGCAAACAAGCTATGCGTTTATTA
GAATCCATCAGGATAATGCGAAACCGCTTTTTTTCATTTTTCGAGAATCTGGACTTCATTG
AATCCATCATACCATATCATGATACTGAATTGTCCGATGATTTGCATAAACTGATTTCTA
TCAGCAAATCAAAAATCTGGAGGCTCCAAAACAGTATGAGTTGTACAACCTATCGAATT
TGACCAATAATCCCAAACAATCCTTATATTTTGCATTCTTACAGAACTATATAAAATGGT
TGATTCCCTTCTCCTTTTTTGGATTATCAATTAGATTTTTATCTAATTTTACGTATGAAT
TCAATTCCACATACTCGCTGTTCGCCATCCTATGGACATTGTCAATTTACAGCCTTTTTGGC
TTTATAAATATGAACCATTTTTGGTCTGATAGACTGAGTAAATACTCATCATTTTCTACCA
TTGAGTTTCTTCAAGATAAACAGAAAGCCCAAAAAAAGCTAGTTCCGGTTATCATGTTGA
AGAAATGTTGTTTTATTCTGTGGCTTTGTTGTTTGGCGCAATATTACTATCATTTCCAGC
TATATTGTTTTGCGTTGGAAATTTTCTACAAGCAAATTTATAACGGCCCAATGATTTCCA
TCTTGTCTTTTTTGCCCTACTATACTTATTTGACAGTTTACTCCGGTTTTAACTGTGATTT
ACAACAAATATTTCTGAGAACCAATGACAAAGTGGGAAAATCATAGCAGTGTGTGAATG
CAAAGAAATCTAAAGAAGCTAAGAACTTTGTTATTATTTTTCTATCCAGTTACGTTCCCC
TATTAATTACACTATTTCTTTATCTGCCAATGGGGCATTTGTTGACCGCAGAAATAAGAA
CTAAGGTTTTCAATGCCTTTTCAATATTTGGCCCGTTTACCTACCCATGATTCAGATTTTA
TTATTGATACAAAGCGCTATGAAGATCAATTTTTCTACTTTATTGTTATCAACCAACTGA
TTCAATTTAGCATGGAAAACCTTTGTTCCAAGCCTTGTAGCATTTGCTCAGCAGAAAATTA
ATGGACCAAATCCTAACTTTGTCAAAGCTGAGAGTGAATTCGGTAAAGCTCAACTCAGCT
CATCAGATATGAAAATTTGGTCAAAGGTTAAGTCGTACCAAACAGACCCCTGGGGAGCAA
CATTTGATTTGGACGCCAACTTCAAAAAGCTTCTTCTACAATTCGGGTATCTTGTATGT
TTTCTACAATTTGGCCACTAGCTCCATTTATCTGTTTGATAGTCAATTTGATTGTTTACC
AAGTCGATTTGAGGAAAGCTGTGCTTTATAGTAAACCTGAGTATTTTCCATTTCCAATCT
ACGATAAGCCATCCTCTGTGTCTAATAACCAAAAACTGACGGTTGGTCTATGGAACCTG
TCTTAGTTATGTTCTCCATCTTAGGTTGTGTTATCACTGCTACTTTGACCTATATGTACC
AGAGCTGTAATATAACAGGTGTCCGGCGCTCATACTTCCATCCATACGAATAAAGCTTGGT
ACCTAGCAAATCCAATAAACCACTCGTGGATAAATATTGTACTATATGCTGTTTTTATTG
AGCATGTTAGTGTGTGCTATTTTCTTCTTCTCTAGTATTTTGAAATCTTCCCATGATG
ACGTGCAATTTGAGCAATGTGCCAAAGCATGTAGTTAACGTGCAAAACCCACCAAAACAAG
AAGTCTTTGAAAAAATTCCTCCCCCTGAATTTAATTCGAATAACGAAAAAGAAGTCTT
AAAGAAAAGGGTCTGCGAATGAGAAGTTGCACCAAGAACTCGGTGAGAAACAGCCTGCCCT
CTTCTGCCAATGGATATGAGGCACATGCTGCCACTCATGCCAACAATGATCCGTCTTCTT
TATCCTCAGCCTCCTCGCCTTCATTATCTTCTTCTTCTTAGCAGCAAAACCGGTGTAG
TCAAAGCTGTTGATAACGATACAGCCGGATCTGCTGGTAAAAAGCCATTGGCCACAGAAA
GTACTGAAAAAAGAAATCTTTGGTGAAGGTGCCTACCGTTGGCTCATATGGTGTGTCGG
GCGCCACTTTACCAGAAACAATTCACATCTAAAAATTAATAAGTTTGAAGTTTGAAGG
ACGGTAAATCCATTAGGGATGCGAAATCCAGTGCAGAATCTTCCAACGCCACCAATAACA
ACACCTTAGGCACGGAAAGTAAGCTTTTGCCAGATGGTGACGCCGTTGATGCACTAAGTA
GAAAAATTGATCAAATACCCAAAATTTGCTGTTACTGGTGGCGAAAAATAACGAAAAATACC
AGGCCAAAGACGATGCTGCCACTAAGACTCCACTCATTAAAGATGCAAAATTTAAGCCTG
TTGTCAACGCAGCTGTTAACGATAACCAATCGAAGGTTTCAAGTGGCTACTGAACAAACAA
AAAAGACTGAAGTAAGCACGAAAAATGGCCCATCAAGATCTATTTCCACGAAGGAACTA
AGGATTCTGCGAGACCATCTAATAACAATACTACTACTACTACTACTACAGATGCTACTC
AGCCCCACCATCATCATCACCACCACCGCCATCGTGATGCTGGAGTGAAGAATGTCACGA
ACAATTCTAAGACAACCGAATCCTCTTCTCTTCTCATCGGCGGCAAAGGAAAAACCAAAAC
ATAAAAAGGGGCTATTGCATAAGCTGAAAAAGAAGCTTTAA

YBR086C, 946 aa (SEQ ID NO 18)

MSQTITSLDPNCVIVFNKTSANEKSLNVEFKRLNIHSIIIEPGHDLQTSYAFIRIHQDNA
KPLFSFLQNLDFIESIIPYHDTLSDDLHLKLISISKSKILEAPKQYELYNLSNLTNNPKQ
SLYFAFLQNYIKWLIPFSFFGLSIRFLSNFTYEFNSTYSLFAILWTLSTAFWLYKYEPF
WSDRLSKYSSFSTIEFLQDKQKAQKKASSVIMLKKCCFIPVALLFGAILLSFQLYCFAL
IFYKQIYNGPMISILSFLPTILICTFTPVLTVIYNKYFVEPMTKWNHSSVNVNAKKSKEA
KNFVIIIFLSSYVPLLITLFLYLPMGHLLTAETRTKVFNAFSILARLPHDSDFIIDTKRY
EDQFFYFIVINQLIQFSMENFVPSLVSIAQQKINGPNPNFVKAESEIGKAQLSSSDMKIW
SKVKSQYQTDPGATFDLDANFKLLLLQFGYLVMFSTIWLAPFICLIVNLIVYQVDLRKA
VLYSKPEYFPPIYDKPSSVSNTQKLTVGLWNSVLVMSILGCVITATLTMYQSCNIPG
VGAHTSIHTNKAWYLANPINHWINIVLYAVFIEHVSVAIFFLSSILKSSHDDVANGIV

PKHVNVQNPVKQEVFEKIPSPFNSNNEKELVQRKGSANEKLHQELGEKQPASSANGYE
AHAATHANNDPSSLSSASSPSLSSSSSSSSKTVVKAVDNDTAGSAGKKPLATESTEKRN
LVKVPVGSYGVAGATLPETIPTSKNYLRFDEGKSIRDAKSSAESSNATNNNLGTES
KLLPDGDAVDALSRKIDQIPKIAVTGGENNENTQAKDDAATKTPLIKDANIKPVVNAAVN
DNQSKVSVATEQTKKTEVSTKNGPSRSISTKETKDSARPSNNNTTTTTTTTDTATQPHHHH
HHRHRDAGVKNVTNNSKTTESSSSSSAAKEPKHKKGLLHKLKKKL

YBR093C, 1904 bp, CDS: 501-1904 (SEQ ID NO 19)

ACGTATTTGGAAGTCATCTTATGTGCGCTGCTTTAATGTTTCTCATGTAAGCGGACGTC
GTCTATAAACTTCAAACGAAGGTAAAAGGTTTCATAGCGCTTTTTCTTTGTCTGCACAAAG
AAATATATATTAAATTAGCAGCTTTTCGCATAGAACGCAACTGCACAATGCCAAAAAAG
TAAAAGTGATTAAAAGAGTTAATTGAATAGGCAATCTCTAAATGAATCGATACAACCTTG
GCACTCACACGTGGGACTAGCACAGACTAAATTTATGATTCTGGTCCCTGTTTTCGAAGA
GATCGCACATGCCAAATTATCAAATTGGTCACCTTACTTGGCAAGGCATATACCCATTTG
GGATAAGGGTAAACATCTTTGAATTGTTCGAAATGAAACGTATATAAGCGCTGATGTTTG
CTAAGTCGAGGTTAGTATGGCTTCATCTCTCATGAGAATAAGAACAACAACAATAGAGC
AAGCAAATTCGAGATTACCAATGTTTAAATCTGTTGTTTATTCAATTTTAGCCGCTTCTT
TGGCCAATGCAGGTACCATTCCTTAGGCAAACTAGCCGATGTCGACAAGATTGGTACCC
AAAAAGATATCTTCCCATTTTTGGGTGGTGCCGGACCATACTACTCTTTCCTGGCGACT
ATGGTATTTCTCGTGATTTGCCTGAAGGTTGTGAAATGAAGCAACTGCAAATGGTTGGTA
GACATGGTGAAAGATACCCTACTGTCTAGTCTGGCTAAGACTATCAAGAGTACATGGTATA
AGTTGAGCAATTACACTCGTCAATTCACCGCTCATTGTCTATTCTGAACGATGATTACG
AGTTTTTCATCCGTGATGACGATGATTTGGAATGGAACCCTTTTGCCAACTCGGACG
ATGTTTTGAACCCATACACTGGTGAAATGAACGCCAAGAGACATGCTCGTGACTTCTTG
CTCAATACGGTTACATGGTCGAAAACCAACCAGTTTCGCCGTTTTTACCTCTAATTCTA
AGAGATGTCATGACACTGCTCAATATTTTATTGATGGTTTAGGTGACCAATTCAACATCA
CCTTGCAGACTGTCTAGTGAAGCTGAATCCGCTGGTGCCAACTTTGAGTGCTTGTAAC
CATGTCTCTGCTTGGGACTACGATGCCAATGATGACATTGTAAATGAATACGACACAACCT
ACTTGGATGACATTGCCAAGAGATTGAACAAGGAAAAACAAGGTTTGAACCTGACCTCAA
CTGACCTAGTACTTTTATTCTCGTGGTGTGCAATTTGAAGTGAACGCTAAAGGTTACAGTG
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ACACTTATTACCATGAGGGTCCAGGTTACGACATTATCAAGTCTGTGCGTTCCAACCTTGT
TCAATGCCTCAGTCAAATTATTAAAGCAAAGTGAGATTCAAGACCAAAAGGTTTGGTTGA
GTTTTACCCACGATACCGATATCCTAACTTTTTTGACCACCGCTGGTATAATTGACGACA
AAAACAACCTTAACGCGAATACGTTCCATTTCATGGGCAACACTTTCCACAGATCCTGGT
ACGTTTCTCAAGGTGCTCGTGTCTACACCGAAAAATTCGAATGTTCTAACGACACCTACG
TCAGATACGTCATTAACGATGCTGTTGTTCCAATTGAAACCTGTTCCACTGGTCCAGGGT
TCTCTTGTGAAATCAATGACTTCTACGACTATGCTGAAAAGAGAGTAGCCGGTACTGACT
TCCTAAAGGTCTGTAAACGTCAGCAGCGTCAGTAACTCTACTGAATTGACCTTCTACTGG
ACTGGAACACTACTCATTACAACGCCAGTCTATTGAGACAATAG

YBR093C, 467 aa (SEQ ID NO 20)

MFKSVVYSILAASLANAGTIPLGKLADVDKIGTQKDIFFPLGGAGPYYSFPGDYGISRDL
PEGCEMKQLQMVGRHGERYPTVSLAKTIKSTWYKLSNYTRQFNGSLSFLNDDYEFFIRDD
DDLEMETTFANSDDVLNPHYTGEMNAKRHARDFLAQYGYMVENQTSFAVFTSNSKRCHDTA
QYFIDGLGDQFNITLQTVSEAESAGANTLSACNSCPAWDYDANDDIVNEYDTTYLDDIAK
RLNKENKGLNLTSTDASTLFSWCAFEVNAKGYSVDCDIFTKDELVHYSYYQDLHTYYHEG
PGYDIKSVGSNLFNASVKLLKQSEIQDQKVLWSFTHDTHILNFLTLAGIIDDKNLTA
YVPFMGNTFHRSWYVPQGARVYTEKFQCSNDTYVRYVINDAVVPIETCSTGPGFSCEIND
FYDYAEKRVAGTDFLKVCSNVSSVSNSTELTFYWDWNTTHYNASLLRQ

YBR181C, 1563 bp, exon1: 501-506, intron1: 507-858, exon2:
859-1563 (SEQ ID NO 21)

TAACTTCTCAACATAATTATGTAAAAAATTATCTCATTAAAGCCAGATAGCAAATATATCA
CATATTGCATTGATTAATTTGAGAAAAATATACATGTATCTTTTCAGTTAATTTTATTAA
AAATAAATTATTTCTTACTTTTTTTTCTACAGTTTGCAACCTTAACCTTTTTCTTGCA
TCCATACATCTTTGAACTCCATACATCTTATTTTTTTGCTGTTTTTTTTCAGTGTCTCGG
GCATACAGGCCGCTTATCTTCATGCCGGCCCATCATCCTAGGAAACTCTTTCGGTATGGG
CCAAGGGCAGGCCGAAAATCCTATGTGCGTGGAGCTGATACAATCTCGGCTGGCTTGGTTT
GTAGGGCACGGTCAATGAATGCCTGATGGGAGAAAAATTCATCTTTATGAAAAGTGATCT

TAATTTGAATAGTGTGCCCTTCAAAACATTTGGAAGTCATTAATTGAAACTATCCAGTGT
GAATAGACGACTGAGCCATCATGAAGGTATGTAATATCACCCAAATCCTTAGAATTCTAA
TGAATCAGCACGCGCTAACCGGCTGTTTCTGACTGTTTGATAAACGTATACCCACAAATT
AGTGCACCTATAATAAAAATTCTCAAGAACAACGTTGTTTAAACGAGATAATTCCTCTAA
TATACACGTACCGACACTTAGGAAAATATCTCGCTAAGTTCAAATTAAGGAATGAAAAAG
GAATTACGAAAAGGGTTTAGAAATATCAATGAAAATAAGAAAAACCTGTAACGGAAGAA
AGGACAGCAGGGATTCTGTTGGAATTTGTCTGATATTGGCTTCGGACAACCTTACTAACAAA
TGGTATTATTTATAACAGTTGAACATTTCTTACCCAGTCAACGGGTCTCAAAAGACCTTC
GAAATTGATGATGAACACCGTATTCTGTTTCTTCGACAAGAGAATCGGTCAAGAAGTC
GATGGTGAAGCCGTTGGTGATGAATTCAAGGGCTACGTCTTCAAGATCTCTGGTGGTAAC
GACAAACAAGGTTTCCCAATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTG
TTGACCAAGAACGTTTCTTGTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCC
GTCAGAGGTGCCATTGTTGGTCCAGATTGGCTGTCTTGGCTTTGGTCATTGTCAAGAA
GGTGAACAAGAATTGGAAGGTCTAACTGACACTACTGTTTCAAAGAGATTGGGTCCAAAG
AGAGCTAACAACATCAGAAAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTCTGTGATTTT
GTCATCAGAAGAGAAGTCACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAA
AGATTGGTTACTCCTCAAAGATTGCAAAGAAAGAGACACCAAGAGCTTTGAAGGTGAGA
AACGCTCAAGCTCAAAGAGAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTG
TCTGAAAGAAAGGCTGAAAAGGCCGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCT
TAA

YBR181C, 236 aa (SEQ ID NO 22)

MKLNISYPVNGSQKTFEIDDEHRI RVFFDKRIGQEVDGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPD LAVLALVIVKKGEQE
LEGLD TTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVT KGEKTYTKAPKIQRLVT
PQRLQRKRHQRLKVRNAQAQREAAEYAQLLAKRLSERKAEKAEIRKRRASSLKA

YCL007C, 893 bp, CDS: 501-893 (SEQ ID NO 23)

ATTACTTTAAATTGTTTGTCTATTCCAACATAATCATTAGCAGCACATGTCGAGCAACAG
ATAAACACAGCAGCGGCACGGTGAACCACATAAGTGTATGTGCACACGCGTGTTTTGTGC
AGTGATTACCAACTTGCGCATGCAAGGATATCACACTCCTGTTTCTGCCTCATGTCTTT
TAAACGCCTCCACGGGACATGGGTCTAATTATGGAGAAGATCAAGCTTTGAAATGGCC
CGTTTACACATTTTGATACAACCGTAGACGGCGTCTCGTTTCAAAGACCGTGTGGTTGTC
TATCAGTATATACTCATTGTGTTTTTCAAAAAATCTCTGGGTTGTTTAGATGCCACTATA
TTTCTATTCTGATTTTATTTTATGTATACTTATTTTGTCTTATTTTCTTATACTCAGGAA
ACGTCACTTGGCTTGATATACTCGACGCTTTATCTGCAAATTCAGGTCTCAAATCTGAA
CGCGGTGGAGCCACCAAGGGATGGAGCTGGCAAAGGAACGTAATGGCCCATCAAAAAAC
ATCATGGCCAAATGTCAAAATCACTGTACTTCTCCAAACACTGTACGACAAAAACAAACAA
ACAACTCTTTGTTAGTAAAAAGAAAGGGAACCTAGTAATATGGAGACACATCGTAAAAA
AAATGTTGCACATACGCTTGGTTGTTCTTTGGAGCCATTATCCAGAACAGCAGCGACATG
GCACTAACCACTATGAATACACCAACAACAGTATAGCTAAATTGGACGCGCAGAGAGTTA
GTAGAAGAAGAAGGAAGAAAAGGGAAGCGGAGAGAAGAGATTATGACACATACAACTAC
TCATTACTCTTTGTTCTTTATTATTCTGTTGGACCTTTGTTTCTTAAAGTATAG

YCL007C, 130 aa (SEQ ID NO 24)

MELAKERNGPHQKHGQCQNHCTSPNTVRQNKTNKLLLVKKKGKLVIVRHHIVKKMLHIRL
VVLWSHYEQHGHGTNHYEYTNNSIAKLDAQRVSRRRRKREARRDYDTYKLLITLCSL
LFVGPLFLKV

YCL016C, 1430 bp, CDS: 501-1430 (SEQ ID NO 25)

ACATGACCTAATTTATAGCTTAGGGTTCTTTTTTGTCAATTCTATGCGTATGACAAAGA
GCACCACGATGGTGATCGAAATCTCTAGGAGTAGCATACCACAGCGATATTATTTAGTAG
TAGGCGGTTTATATCTTTGTCCCTTTATACTGTTGTGTTTCTTGCTTATTGCTTCAGTA
GGCAGCGTATAGTATAACCAGAAAAAAGTGAAAAATAAACTAAAAAAGCACTATGAGATG
AACGGTAAAAATCCACCAGAGATTGTCTCACTAATAATCCTGTACCATGTCCATCAACCT
ACATTCCGCACCCGAGTATGATCCATCTTATAAGCTGATCCAGTTGACACCAGAGTTACT
GGATATAATACAGGATCCGGTTCAAATCACCAGTTAAGGTTTAAGTCATTGGACAAAGA
CAAGCTCGAAGTTGTACTGTGTTGCGACGACAAGACTTGGGTGCTGCAAGCAGCGCAAAAC
ATTCAAACACAGTTCTACTAATGAGAGAATTTGTTCTGAAACAACCTATTACTTTTCGACG
AAACGCTCTTGTTTGGACTGTCCAAGCCGTACATGGACGTCGTGGGATTCCGCCAAGACTG

AATCAGAATTTGAGACCAGAGAGACACATGGCGAATTGAACTTGAATTCAGTACCAATAT
ACAACGGGAGAACTGGATTTCTCCGACAAAATCATGAAGAGGTCATCTACAAAGGTTATCG
GGACCTTGAAGAACTACTTGAAGAACTACCATGTTCTGCGCTAGAAGGTATATCAAAAT
GGCATAAGATTGGTGGATCTGTGAAAGACGGTGTGTGTGTATTCTTTTCAAGAACTTCC
TTTTCAAAGCACTGCATGTACTACTGATGAGCGCAATGGCAGAATCACTCGATCTACAGC
ATCTGAATGTTGAGGATACACATCAGCTGTGGGAAGGACATTGAGGACGAGTTCAATC
CATACACAAGAGAAATCATTGAAACAGTGTGAATAAATTTGCTGTTCAAGCAAGAGG
CTGAAAAAATACTGCGCTTGAAGTAACCGTTTATAGCTCAGTGGTACGGGATTCAAG
CGCTAAGGAAATATGTTTCTGGAATAAGCATGCCAATTGATGAGTTCCTCATCAAGTGGA
AGTCCCTTTTCCCACCTTTCTTTCCCATGTGACATTGACATTGACATGCTGCGAGGCTATC
ATTTCAAGCCTACCGATAAGACTGTCCAGTATATAGCGAAAAGCACACTACCAATGGACC
CCAAAGAACGGTTTAAAGTCTGTTTAGGCTACAGTCACAGTGGGACTTGGAGGATATCA
AGCCTCTAATTGAAGAATAAATTCAGAGGTATGAAAATAGACAGTTTCATCATGAAGT
ATGCCCGCCGTAAAAGACTGGGCAAAAAGACCGTGGTCACGAGCAGGTAG

YCL016C, 309 aa (SEQ ID NO 26)

MREFVPEQPITFDETLFLGLSKPYMDVVGFAKTESEFETRETHGELNLSVPIYNGELDF
SDKIMKRSSTKVIGTLEELLENTPCSALEGISKWHKIGGSVKDGVLCILSQDFLFKALHV
LLMSAMAESLDLQHLNVEDTHHAVGKDIIEDEFNPYTREIIETVLNKFVQEQEAENNTWR
LRIPFIAQWYGIQALRKVYSGISMPIDEFLIKWKSIFPPFFPCDIDIDMLRGYHFKPTDK
TVQYIAKSTLPMDPKERFKVLFRLQSQWLEDIKPLIEELNSRGMKIDSFIMKYARRKRL
GKKTVVTSR

YCR052W, 1952 bp, CDS: 501-1952 (SEQ ID NO 27)

GTCATCGACAGCAAATTGCTGGAAGAGTTCAAGGACAACGTGAGATACACCTTGGAAAAAT
GACCCTGAGGAAGGAGCCGATGAGGCCACTCTGCAACGCAGGAGGCAGTTGGAACAGATC
ATTACGGGAGACAACGCTGAGGAGGAGTTGGAAGGTACATCCGTGCTATGGTCAGAGAG
CAGATGCTGGGCCAGGGCTCCATGGCGGGTTCCGGGGACGAACCAGATTCCAAGAGAAGA
AAATAACGACCCAGCACAAAGGCTCTTACAGCTTGCTAAAAGAAATTGAACGCGACGCTA
CATGAACTACTTCTTCTCTTACATAGTCTTTTCCCTTATGTATCTTTTCTGTACATTAA
TAGACGTTCTTACAAGGTAAAATTTACCGCGTTTTAAATAGAATGAAAAAACGTTGT
AGAGTGAAAGAAAAGCAACAAATATACAGTTCACAAGGCAGCTTCGTATAGTAATACAGC
ACGAAAAACAGCTCATAGAAATGGTAACACAGACCAATCCGGTCCCTGTTACATATCCAA
CGGATGCTTATATCCCCACGTATCTGCCCGATGATAAGGTCTCCAATCTGGCAGATTGTA
AAAAATTGATAGAAATGGATTCCAGACTAGATTGTATCTGACAAGAAGGAGGCTGGATA
CGTCCATCAATTTACCTACAAACACCAAGACCAAGGACCATCCCCCAATAAAGAGATGC
TGAGGATTTTACGTCTACAACACTACGGAAGCAGCCCTCGCAGCGATTCTGCGACCCAG
CGGACTCAGGCAAGACTACATGGACACTGAGAATAGAAGGTAAGCTTCTGCACGAGTCCG
CAAACGGAAAGCACCCATTTAGTGAGTTTTTGGAAAGGTGTCGCGGTGACTTTAAAAGAC
TGAAACCGCTGGGCATGGGCAAGAAGAGGAAACGCGATTTCGTATTGAGCCTTCCTTTGA
ATCTGCAACAACCCGAATACAATGATCAAGATAGCACCATGGGCGATAACGACAACGGCG
AGGATGAGGACAGTGCAGAGGCAGAAATCCAGGGAGGAAATTGTAGACGCACTGGAATGGA
ACTACGATGAAAAACAACGTTGTGGAGTTTGATGGTATCGACATCAAGAGGCAAGGCAAGC
ATAATTTGCGATGCAGTATAACCATCCAGTTGAGGGGTGTCGACGGTGGAAAAGTACAGT
ACTCGCCCAACTTAGCTACCTTGATAGGTATGCAAACGGGCTCCGTTAATGACGCGGTTT
ATTCGATCTACAAGTACATTTGATCAACAATCTGTTTGTACGGAACAAACAGAGGCTC
AAGATGGTTCCAACGATGCCGAAGACAGCAGTAACGAGAATAACAATAAAAACGGTGCTG
GTGACGATGATGGCGTCGAGGGAAGTACTCCAAGGATAAGCCCGAATTGGGTGAAGTGA
AGCTAGATTCACTCTTACAAAAGGTATTGGGATACAAACGCCGCGCACCTCCCCTTGATGA
ATGTTGTGCAAAACCGTGAACAAACTGGTATCACCCCTACCGCCCATCATCCTAGATTATA
CAATTGATCTTTCAAAGATACCACCTATGGTGCTACCACCTTGGATGTAGATGTGTGCGC
ACATTTCTCCACCAGCCTCAACCCAGCCAAATTTACAAAAGAGGAAGAAACAGATGCTG
AAGACACAGCAAACTACGTGAAATCACAAGCTTGCCCTTGCAAGTTGAAGTCTAGTGCTC
AAAAATACCAGTTTTTCCACGAACTGTCTTTGCATCCAAGAGAAACGCTGACTCACTACT
TATGGTCTTCCAAGCAAAACGAGCTTGTGCTGCAGGGCGACCAATACTTCAATGAAGATG
CTGCAAGAACGAGTGACATATACAGTAACAACAATGACAGGTCACTAATGGGCAATA
TCTCACTACTGTACTCCAAGGAAGACTATAA

YCR052W, 483 aa (SEQ ID NO 28)

MVTQTNFVPVPTYPTDAYIPTYLPDDKVSNLADLKKLIEMDSRLDLYLTRRRLDTSINLPT

NTKTKDHPNKEMLRIYVYNTTESSPRSDSGTPADSGKTTWTLRIEGKLLHESANGKHPF
SEFLEGVAVDKRLKPLGMGKKRRDSSLSLPLNLQQPEYNDQDSTMGDNDNGEDEDSE
AESREEIVDALEWNYDENNVVEFDGIDIKRQKDNLRCSITIQLRGVDGGKVQYSPNLAT
LIGMQTGSVNDVYSIYKYILINNLFVTEQTEAQDGSNDAAEDSSNENNNKNGAGDDDGVE
GSTPKDKPELGEVKLDSLLQKVLDTNAAHLPLMNVVQTVNKLVSPLPPIILDYTTIDLSKD
TTYGATTLDVDVSHILHQPQPQPNLQKEEETDAEDTAKLREITKLALQLNSSAQKYQFFH
ELSLHPRETLTHYLWSSKQNELVLQGDQYFNEDAARTSDIYSNNNNDRSLMGNISLLYSQ
GRL

YCR064C, 911 bp, CDS: 501-911 (SEQ ID NO 29)

AGGTTTTAAACGCGTTATCTTTGTTCCGAAAAAACCGAAAAATATATTTTTTC
GCGTCGCGTTCTCGCGTCTGTTTTGTTTTTCGCGTTCCAATGACCAAAATGGGAAAGTG
GTCGCTCTTTGACGAAGGAGACGAAAACCTCTTCTAAAACGTTGGGAGAGAGATAATTACA
TGGCCAGAACAATACTGCAACGTGCATATAGTCGTTAGTCTGTGCTTGCACATCCACGGC
AGCCCGAGTGGACGCACTGATGGAAGGACACCTGTGTGCCCTTTTTGCGTGCTTCTTCCT
CTAACTGTGCACGAGGCACCTGCGAGATGCAAGTGCTACCGTTGTTAGTTTCGTTCTTTT
GAATGCAGCGCAGACAGCACAGTTTTTCATACCCGGTTTTGCGCCATTTGGCAATTAGCA
ATTTATCAGCATACTTTTCCTTTATCAACCAATCGTAAAGGTCTTTGGAGATGGCCTTTC
TCTTGTAGTACAGAGTATATATGTATCTAGAGCGCTGGTGGTGGAGTTGCATTATCTCCC
AGAGCTGCTCATTGGACTTTGCTGCGAGCTTAGACGACTTGTCTTTTGGGCATCTCTGA
GTTGGATTTTCAAATCTGTGAGGGTTGGCTTGATTTTTTCAAACCCGTCAGGTGCAGGCT
TGGATCTTCTGGTCTTTATGCGCGGCATGTCTGTTTTGTGAGGTGAGCTTTGCTAGTCTTG
ACGGCTGTAGAGGTGTTTACATTGATGATGAGTCCCTAAGAAAATTTTTCTTTTTTTTC
AGTATTTCACTTTCCGTTGTGAACGACAAATGTACTATGCGTTCAAGAGCCAACGCAGTA
TCATCGTCAAAGTTCCTACCACAACGCGTGTGATTGATCTTGTACTGGTTGTAAATGTGC
TAAGTCTGTGA

YCR064C, 136 aa (SEQ ID NO 30)

MYLERWWWSCIISQCSLDFAASLDDLFSWASLSWISKSVRVGLIFSNPSGAGLDLLVFM
RGMSFCEVSFASLDGCRGVYIDDESLRKFFFFFYFTFR CERQMYAFKSQRSIIIVKVPT
TTRVIDLVLVNVL

YCR073W-A, 1448 bp, CDS: 501-1448 (SEQ ID NO 31)

GTTTATGGCTGGAATGACTTGATAATCTCTTCACGAGCTTACTTGAGATGGTATGAGGAG
CCAGAACTCTCCCGCCTTCAGCCGCTTTTTGTTGCTGTGTATTAGTATATCCATCATCA
TTTTACCTACAAGGAACCTTTTATAGCCACCCTAAGTAAACAAACATTAGCTTAGC
ATCCTCAATTCTTATCGTATGTTGTTGCTGCTATTTTTATCCTATTGTTCTCGGCATCGC
TTTTTTACATAAGGTACCAAGGCAAGAGAAAAGACCCGCGAAATTTTCAATTCGAGACAT
AGGGTTAATACGAAATATGTTAAGGTCTAGTTTCCAAAAATGAAGAAAATGTGATTAGA
CATCCTGGGGAAATAGGTTTAAATAGGGCGGGCGCTACAGGGGTTTTTCTAACAAATTT
CAATGATAATAGTGGCATCATCATCGTCATATCCAGTGTAGGTATGGACTAGAACAGAAA
GCAATTTGCAGCAAGACAATATGACTACGACGGTACCCAAGATATTGCGGTTTCACGAGT
TTTCAGACGTGGCAGAGGCCGTAGCTGACCATGTAGTCCACGCGCAAGACGGTGCATTGG
CTCCAAAGAACGAGAGGAAACACTCTGTTCCCAACATCAGCATGAATGCACTGGATATGA
CGAGAGAGGCCTCTTGCAAAAGCACAGCATCTGCCGCGGAAGGGAAAAGTGGTAGCAGTG
GTAGTGGCAGTGGTAGCAGTAAGCCAAAAAGGAGAAACGGTTCAAGATTGCTCTCTCCG
GTGGGTCAATTGATCGAAGTGCTACACGAAGGTCTGCTAAAACGAGACGATGTACGGTGGG
GAGACTGGGACATTTACTTTGCAGACGAGAGACTTGTACCCTTCAGCTCGAATGAAAGCA
ATTATGGATGCGCCAAAAGGAAGATTTTGACCTGATAGACACGGCGAAGTATGGAACCTC
CGAAGGTGTACCACATTGACGAGTCATTGATTGACGACCCGCAAGAATGCGTTGATAACT
ATGAAAAGGTGCTAATCCGCGGGTTTGCCGGTAGAGATTCCGTCAAACCTCCGATGTTTCG
ACTTGTTCCTGCTTGGTTGTGCCCCGATGGTCATATCGCATCACTCTTCCCTAACTTCC
AGGACAATCTACGTGAGAACTTGCATGGTGGTGGCCGTTGGAGAACGCTCCTAGTGGGC
CCTCGAACGAAATTTGCTGACTATACCTGTAATCTGCCATTCTCACAGGGTTACTTTTCG
TTGTGCAAGGTGCAACCAAGGCGCCCATCATCAAGACCATTATGGAAGGCCTGAAAAGG
GCCTACCTAGCAGTATTGTCAACGAAGGTGCTGCTGGTGTGTATCATGGTTTGTGACG
ACGATGCTCTTACGGACGTCTCGTCACCAAAAAAAGTATAAATTCCACCAAGGTTTGT
CTATTTAA

YCR073W-A, 315 aa (SEQ ID NO 32)

MTTTPVKIFAFHEFSDVAEAVADHVHQAQDGLAPKNERKHSVPNISMNALDMTREASCK
STASAAEGKSGSSGSGSGSSKPKKEKRFKIALSGGSLIEVLHEGLLKRDDVVRWGDWDIYF
ADERLVPFSSNESNYGCAKRKILDLIDTAKYGTTPKVYHIDESLIDDPQECVDNYEVLIR
GFAGRDSVKLPMFDLFLGCAPDGHIALSPNFQDNLREKLAWVPVENAPSGPSTRISL
TIPVICHSHRVTFVVEGATKAPIIKTIMERPEKGLPSSI VNEGAAGRVSWFVDDDALTDV
LVTKKKYKFHQGLSI

YDL010W, 1196 bp, CDS: 501-1196 (SEQ ID NO 33)

TAGTAATTAGTTTCTTATGATGGATTTAATGGCGTAGTTCATCCGCGTTTAATTTAACTA
GAGGATAATCTACTTGCAGCATGAATGAAAATAGTAAGCCAGTAAGGATGCACCTGACAGA
CTCAGCTACCGATTAGTGTGTTGACTTTTCCGCAAGATCCTTTTCTCCCTCTTTGGACC
TAGTCATCCCTCCACACAAGATTGCGCTCTTAAGTAGTGGCGCAGGCTGTTTCGCTTTTAAG
CATAGTGCTTAATGTCGAAGGCTTTATAGATCCCAATACTACGCCCTTGAGAAATTGAAT
GCACTAGCAGTTAGTTAACTTTCTGGAACGCGCATGACGCGTCCCGGGCGCCTGAGGCG
GAGCGTTCGCGAAATCGGGAAAACATTATACTGGGAAAGATCACTATCTATTCTCTAAAT
GAACTTTAAAGCAAATTATCGTAAGATAGAAAAGACGAAACCTTAGCAACCTAGCGGTTT
AATATAGAAAACAAATTTTATTATGATACCTTCCAATAAGAGAAATGCTAGAAATTTAAGCA
TTACAACGCTATTATGTGTTAGTGTGTTTTCTGTAAGCGCAAAATGCGAACTTCTTGACGG
TAGAGATAAAGAGGAACTTCTAAAGCATTAGTACTAATATGGACAATATGGCTGGAG
GATCTTCCAGGGAATATGCTGCTATGCCGACTTCTACCACGAATAAGGGGAGCTCTGAAG
TAGACGAAGAAATTAATGAAATAAAACAGAAGGTGGGACTCCAACAGCCCATAGCATCGG
TTGATGATAGTTTGTGCGCCATTAAAAACGATAAAGGGTCGCGAATAACCAAAGCTTTTA
ATGTTCAAAAAGAAATCTCCCTCATACTAGACTTGTCTCCGATTATAATATTTAGTAAAA
GCACCTGTTTATATAGCAAGGGCATGAAGGAAGTCTTGAAAATGAGTATCAGTTTATCC
CAAACCTACTATATTAGAACTTGACAAACATGGACATGGGGAAGAGCTGCAAGAATATA
TCAAGTTGGTGACCGGTAGAGGAACTGTTCCAAACCTTTTGGTTAATGGAGTATCAAGAG
GAGGTAATGAAGAAATCAAGAACTGCACACTCAAGGGAAACTTTTAGAATCATTACAAG
TCTGGAGTGATGTTAAATTCTCGGTTGAGCAACGTGAAAAACCTTCCAATAATTGA

YDL010W, 231 aa (SEQ ID NO 34)

MIPSNKRNRARILSITTLTLLLVFFVAQNANFLTVEIKEETSKAFSTNMDNMAGGSSREYA
AMPTSTTNKGSSEVDEEINEIKQKVGLQPIASVDDSLSAIKNDKGSRITKAFNVQKEYS
LILDLSPIIIPSKSTCSYSKGMKELLENEYQFIPNYIIELDKHGHGEELQEYIKLVTGR
GTVPNLLVNGVSRGNEEIKLHTQKLLLESQVWSDGKFSVEQREKPSNN

YDL036C, 1889 bp, CDS: 501-1889 (SEQ ID NO 35)

TCAATCCAGCTTCTTTCAAGCAATATTGTCACAAACGATGATGAGAATAGCATTGAAG
AGGATAAGAATTTACGCTATTACAGATGCTAGTGCATCTGAAAATTATCTGGTCAAGCCCA
CAATACCAGGTACGACTCCTGATCCAATAATTGAGGCGCAGAACGATAATGATAGTAGTG
ATAGTAGCGGCATAGATTTGATAGCCTTCTTAAGAAATGGACCATTATAAAGTTTTTGTA
TCGCGATGTTTGAAAATGGAAGTAAGGAACGTAATACAAATTGACAAAGTAGCCGACATG
AATGACGCTCACTTCTTATATATGTTAGGTAGTATATGCATTATAGAATTTATTCATT
GAAGCAATGTGATTCTTCGATAAGTAAGCTTTTTTCTGTCTGGCGGCGAACCATTAGAG
AACAAAAGACCGAGTTAAGAAAAAGTTCATAAAAAAATTTTGAAAATGGATGAGTGTCTG
TATAATGGAATAGGAACTTATGCAAAGAAATAATAGGTTAAGAAATTTGTTTACAGTGC
CAGTAATAATGGCTCGACAACCTCAAAGGAATGCATTATCTGCAGGTCTTGTCTTTGTCAG
GTAATGCAACCTCAAATGAGTTTGATGAACATTTGCAAAATGAGGTTGAAAGAGAGAGGG
AAATTCAAAGAAAAAATAAAGCGAACTCAATCAAAAAATCGCCAGATTTGATTA
ATAAATCTACTTTTCAATCAGAACGATAGGCAGCAAAAAAGAGAAACATAGACAACCTAG
ATCCAGAGTATGAAATGTGATCGATGGCCCTCTAAGGAAAAATCAAGCCCTACCATTTTA
CGTACAGGACCTTTTGCAAAGAGCGTTGGAGAGATAAAAAATGGTTGATGTCTTTATAT
CTGAATTTTCGAGATCGTGAATCTGAATATTATAAAGAACAATCGAAAACGGGGACGTTT
ATATAACGATGAAACTGCGGACTTATCTACTGTAATTCGCAATGGTGACCTGATTACGC
ATCAGGTACATAGACATGAACCTCCAGTCACTTCCAGGCCTATCAAAGTTATTTTTGAAG
ATGATAACATAATGGTTATTGATAAACCAGCGGTATACCTGTTTACCCCACTGGCCGAT
ATCGGTTCAATACAATTACGAAAATGCTTCAAAAATAATCTCGGATTTGTTGTGACCCCAT
GTAATAGGTTAGATAGGCTTACAAGTGGATTAAATGTTTTTGGCAAAAACTCCGAAGGGAG
CCGATAATATCGGCGATCAACTAAAAGCTCGAGAAGTCACTAAGGAATACGTGGCCAAGG
TAGTTGGAGAATTTCCAGAAACGGAAGTAATGTTGAAAAACCTCTAAAACCTGATCGAGC
CAAGGCTTGCTCTTAATGCAGTTTGTCAAATGGACGAGAAAGGAGCCAAACATGCAAAAA

CTGTTTTTAACAGAATCAGCTACGACGGTAAACGAGTATTGTAAAGTGCAAACCGCTTA
CCGGGCGATCACATCAAATTAGAGTACATTTACAGTACTTAGGCCACCCAATTGCTAACG
ATCCTATTTATTCCAATGATGAAGTATGGGGTAACAATCTCGGAAAAGGCGGCCAGGCTG
ACTTCGATATAGTTATTACTAAGCTAGACGAAATAGGGAAAAGAAAACCTGCTAAAAGTT
GGTTCCATAGTAATGGCGGGTACGGTGAGGTATTAAGGCAAGAAAAATGTTCTATTTGTG
AATCTGATTTGTATACTGATCCTGGCCCCAATGATCTTGATCTGTGGTTACATGCCTATC
TATACGAATCAACTGAGACTGAAGAAGGAACCGAAAAGAAAAGTGGTGCTACAAAACAG
AGTATCCAGAATGGGCTCTGAGAAGATAG

YDL036C, 462 aa (SEQ ID NO 36)

MQRNNRLRNLFVPMARQLKRNALSAGLAFAGNATSNEFDEHLQNEVEREREIQKKK
IKRTQSKKSPDLINKSTFQSRITIGSKKEHRQLDPEYEIVIDGPLRKIKPYHFTYRTFK
ERWRDKKLVDVFISEFRDRESEYKRTIENGDVHINDETADLSTVIRNGDLITHQVHRHE
PPVTSRPIKVFEDDNIMVIDKPSGIPVHPTGRYRFNTITKMLQNNLGFVNPENRDLRL
TSGLMFLAKTPKGADNIGDQLKAREVTKEYVAKVVGFEFPEDEVIVEKPLKLIIEPRALNA
VCQMDEKGAKHAKTVFNRI SYDGKTSIVKCKPLTGRSHQIRVHLQYLGHPIANDPIYSND
EVWGNLGLKGGQADF DIVITKLDEIGKRKPAKSWFHSNGGYGEVLRQEKCSICESDLYTD
PGPNLDLWLHAYLYESTETEEGTEKKKWCYKTEYPEWALRR

YDL083C, 1364 bp, exon1: 501-909, intron1: 910-1341, exon2:
1342-1364 (SEQ ID NO 37)

TATTCGACTAGAAAAAATTAAATTTTCTAACTACAAAAAATTGCCTGCATATATGTAA
GGATGTAACAGGAAATGTATGGGTCACATATTAATAGCTTGTTTTACTCCATAAAAGAGT
CTGATATTTCAGAAAAAACCCATACATGTTGAAAAATAATGCATTGTGAAAAAAGTGG
TTGAAAAATGTATGCGATCTAGGAAAAACTGAATTTTCTTAGGTTGTGCGTCTCTCT
AGAAGGATGCTGTGGCCTTTGACCTGGGCGGAAATCTCTCTGTTTCCCTCTAGCTGAGG
GAAACAGAACTGGTAGCAGTTCTGTTCCGGCCAGGCCGCGTGAGCCTATACCACCGAATAT
TATCCTAGCGCAGAGAGTAACACTGGCAAAGTCAAAAGTAAATGCCATGTAAATGTATA
GGTTACGCAGTAGACTATTTAATATATACCTTTTATTATTAGCAGTGTTCGAAAAATACA
GCAAGAGAATAAGCAACAAGATGTCTGCCGTCCCAAGTGTCCAAGTATGTTAAATAATTT
AAACGATGTACGAATTTGTGAGGGATATTGAAACCATGCAGTGAGATAATTTCAATTTA
AGAACCATATCACCTGAATAAGACGGGTGGGGCAAGCACTAGATGCGAATCATAGTTTAA
GAACAACGGATCACCATTTTACACGTTAAAGACCGAGTAGAAATAACCAATAAATGTGT
GGGAAAAATTATACTTAATTTCTCTGTGGAGTAAAGTAATGAGCGTCTTTTGGCGTCTT
ATTTATTCACTTCGCTCCCTTGCATGAATTTTGAACAGAATGCTCCAAAGAGGAAGTGC
CAGGGTACCTCACTTGTCTTACCCTTTTACACAGTTCATAATATTTTGGAGGATTTGAA
TTTCTGTTTTTACTAACATGTGACACGAAATGTTTTTCATTTTTGGTTTTTATAACAGACTT
TTGGTAAGAAGAAATCAGCTACCGCTGTTGCCACGTCAAGGCCGTAAGGGTTTGATTA
AGGTCAACGGTTCTCCAATCACTTTGGTTGAACCAGAAATCCTAAGATTCAAGGTCTACG
AACCATTATTGTTGGTTGGTTTGGACAAGTTCTCCAACATCGATATCAGAGTTAGAGTCA
CTGGTGGTGGTCATGTTTCTCAAGTCTACGCCATCAGACAAGCTATTGCTAAGGGTTTAG
TCGCTTACCACCAAAAGTACGTTGACGAACAATCCAAGAACGAATTGAAGAAGGCCTTCA
CCTCTTACGACAGAACTTTGTTGATCGCTGATTCTAGAAGACCAGAACCAAGAAATTCG
GTGGTAAGGGTGCTCGTTCTAGATTCCAAAAATCTTACCGTTAA

YDL083C, 143 aa (SEQ ID NO 38)

MSAVPSVQTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIAGLVAHYHQKYVDEQSKNELKKAFTSYDRLLIAD
SRRPEPKKFGGKGARSRFQKSYR

YDL125C, 1088 bp, exon1: 501-597, intron1: 598-708, exon2:
709-1088 (SEQ ID NO 39)

TTCAAAATACGAGTAAAGGAGATCCTAGGTGTGGATTAGTAAGGGGAGTGTGGCAACTTC
CTTTTCCGGTTAATTCTCCGCGCTTTCTGTTAGACTATTTTGAAGGACCCAAATAGGAG
ACGCATGGAGGCTTCTACAAAACAGCGTGCCGTTTGTATGGCATGAGCAGGGGGCGCAAA
GGAAACACCGGTAAATCGCGCAAGACCTTGTGGCCACGTAGCCTCAAAGGTTGAATTGA
CACTTGTCTACAGAACTTGAAGAAGTACAAAAGGAGGTACATAAAACAGTAAGCTTGAGA
AGCTTTAAGATATGGTGCGAATCGTTACAGAATATTCCTTGCAGAAATAATGGCGGGTCC
GTTCTCTTCTGAAGAAGTTACCGCCCTACTGAAGCATTGCTGTACGATCGTGAATGTGA
TGTGTGTTCCGACTGGAAGCGGAGAACATTATGAAGTAAAAGGACAATCAGCACGCCTTC

CAGACTTTTAAAGAAACATTGATGGAGCCATTGATATCGGCACCGTACCTAACAACAACAA
AAATGTCGTCTCCTGCTACGCTTGATGCTGCCTGTATTTTTTGCAAGATTATTAAAAGTA
TGTCACATTACTAATAAAGAGCTTACACTCACACCAATGATGGCGATAGTCTCTATGTAG
TACATATACATAAAGCAGAATACTAACAATCGATCCGCTATGCAACAGGCGAAATTCAT
CCTTCAAATTGATTGAAACAAAGTACTCGTATGCTTTCTTGGACATCCAACCTACTGCTG
AAGTCATGCTTTAATCATTCTTAAGTACCATGGTGCGAAGTTGCATGACATCCCGGACG
AATTCCTTACCGATGCTATGCCGATTGCCAAGAGACTGGCCAAGGCAATGAAGTTGGACA
CTTATAATGTGTTGCAGAATAATGGTAAAAATTGCGCATCAAGAAGTCGACCACGTCCACT
TCCATTTGATTCCCTAAGAGAGATGAGAAAAGTGGTTTGATTGTAGGGTGGCCAGCCCAAG
AAACGGACTTCGATAAGTTGGGCAAGCTACACAAGGAATTGCTTGGCCAACTAGAAGGCT
CCGATTAG

YDL125C, 158 aa (SEQ ID NO 40)

MEPLISAPYLTITKMSAPATLDAACIFCKIKSEIPSFKLIETKYSYAFLDIQPTAEGHA
LIIPKYHGAKLHDIPDEFLLDAMPIAKRLAKAMKLDITYNVLQNNKIAHQEVDHVHFHLI
PKRDEKSGLIVGWPAQETDFDKLGLKHLKELLAKLEGSD

YDL133C-A, 578 bp, CDS: 501-578 (SEQ ID NO 41)

AAAGGTGGTTGGAGACTTGTGTGTGTAGCTTAGAATTTCTTCCACTATATGAAAGCCAAAG
ACCTCTTCTCCTCTTTTCGACACTTCGTTTATTTCCACTTTCCCTTATTTAGTATTCATCG
TTCAGAATGCTTTCTTTATTTACGACGGTTACCACACCCGTACACCTTATCTCATTTTC
ACCAGTACCTTTCTTATTAGATTTCATCTTATTTTATTTTAGGATTTTAGGTTCATTGTA
CGACGCGTGTGCGACCATGGAAAAGGTGTGCGAGCTGCGATGCTATCCATTTACCCGTCA
TCATTGCTGGCAGAAATCCCATCTTCTCTGCTGGGGTGATTATATATATGAGAGAGTTA
ACGAATGTAATATTTCTGAATGTTAAATAATTGTTATCCGTCATTATTTGTTCACTTCTC
TCTTTGAAATTTTCGCTTGTCTTTCTGTTTTCATCTTATATTTTACTTCAATCCTAAGATAG
TCATATCGACTTAATTCCAAATGAGAGCTAAGTGGAGAAAGAAGAGAACTAGAAGACTTA
AGAGAAAGAGACCGGAAGGTGAGAGCCAGATCCAAATAA

YDL133C-A, 25 aa (SEQ ID NO 42)

MRAKWRKKRTRRLKRRKVRARSK

YDL136W, 1268 bp, exon1: 501-503, intron1: 504-908, exon2:
909-1268 (SEQ ID NO 43)

CATGCGGACCTTGTGTGTTTTGTTTCTAGATTGTTTTATTTTTATGATTGTTGAAGATAT
AAACCACTGTATAGTTGTATAAGATAGGATAATGATGGTGCAGTGAATAAATAAATACTACTA
GCTCTTTAATATTGCAACGGCTTGTAACGGGCGCCATGATGACATTCAGAATTATACCAC
TACTATATGAAAAAATGAAAAGAGGCCCTGCTTTGAACCCGTACATTTTATTCTATAATA
TTGCATCTGTGGTTTGCCTGACGGCAGCGAGTCCAACACAAAGTCTGGCATATGCTACGA
ATTTTCCACCATGGATTTCAGCACCCAAACATTTGAATTTTTTTTCATGTCGATTGTGAAA
TTTTACTGAAGATGAGGGTAAATAGAGGCTGCAATCGTCATCATATGAGAAATGGATAT
ATTGAAATCTACTACATCTCTTTTTTGGGGGTTTGGTAGTACAGTGAGAACACCGATAA
AGAACCAATAGGACTAAAAATGGTATGTAGAGATGAATATACATGAAACGGACGTGATA
TAATGTGCTATGGAAGAAAAAGTCTCCTTTAATGTCTGCAGGATAAATAATCAAGTGGT
CTGAAGAAAATTTACAGCTACAGTATTACTGCAACCTTGCAGGCAAATATCAGAGAGAT
CTCACCAGCTACAACCTGGTAACAGAAATTTATAAGTTTATGGCACTTGTTAAATTTGTT
TGGGAAGTTTTCGAAATTATAATATTGGTCTTCAGAAACCTGGAACCACATGTGAACATA
TTTTTTGGATAAATGCATTGCAAGAGCGTATTAGTGATACGAGAATCTAAAAATTTGAA
ACTGGCTCATAAAAACAGGAACCTTTACTAACAGTTATGATTTTTTGTTCCTTTCTT
ATCAATAGGCCGGCGTTAAAGCTTACGAACCTAAGAACCAAATCCAAGGAACAATTAGCTT
CTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGAATTGAAGGTCCAAAAGTTGTCCAGAC
CATCTTTGCCAAAGATCAAGACCGTCAGAAAGAGTATCGCCTGTGTCTTGACCGTCATCA
ACGAACAACAAAGAGAAGCTGTTAGACAATTATACAAGGGTAAGAAGTACCAACCAAAGG
ACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAGAGCTTTGACCAAATTCGAAGCTTCCC
AAGTTACCGAAAAGCAAAGAAAGAAGCAAATCGCTTTCCCAAAAGAAAGTACGCTATCA
AGGCTTAA

YDL136W, 120 aa (SEQ ID NO 44)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGGKYQPKDLRAKKTALRRALTKFEASQVTEKQRKKQIAFPQRKYAIIKA

YDL167C, 2660 bp, CDS: 501-2660 (SEQ ID NO 45)

TGGGTGTCGTCAAACAGGATGCCGTGGAATCATACGAACCGCACATTGTGGTAGAGCTAC
AAAGCGATACGAAAGAAGATATGGTATCTAACGTATCCCGTATTGTTGCTTGGGAAAAGA
TGTGGTTAGAACAACATCCAGATGGAGTCACAAATGAATATCAAGGGCCTCGTAGCGATG
ACGAAGACGATGAAGACAGTGAGTAGGCGTTCCATAACTTTGTGTATCTACATATATACA
TATATAATTGTAAATTAGTAACAGTAGTAATAGTAGTGCCTATTATAAAGGGTTTCTTT
AAGTAATGTCATGTACTTGTTTAATGTGACTTTGGTAATATATTTTCATTCTCCGATGCC
GATGCCCAGTGGAAAAGTTTAAAGTGAAAAATTTTCAACACATACAAGTTTAATAAGTT
GGTTTTGATGCAAATAGCATTACTAAAGAAGAGCGCTAGGATAATTGTGCATTGCTATTG
TGATTTTGTATACAGAAATTATGCACTATGTGGTACTAGAGCTGCAAGTTGCGCATTGTC
CAGATACCCCCAAGGATCAATGTCGCATTGCGAATATAGCATTTCAAATTGTGAATGCTG
AAACATTAGTATGCCATTATGGGACCAATTCTTTACCGAGCATTGAAGTAAACGGGACGA
CAAAGAGTTTGGAGAGTGCAATGGTGCAATTGGACAAGGATATTCATGACGTTATTGGTA
ACGACGACTTTGTTCTTGTTCCTGTATTCAACATGGCATATCCGTGTTACCTTACCAC
GTCAAGCGAGAGATGATGGGTTTATTCTTACTTCTTATTTACAACATCCGAAAGTATTTG
ACTTATGGAAGGAATTCGATAGATGGTGTGTCAACCATCCGGAGATTTTGGGACAAAAGA
AAGCAATCTCCAACAACATTGTAATACTAAAAGTATTAGTATTAATGCAGCCAAAATA
CGAAGGATTTGGACGAAATAGTTAGAATATTGGAAGTTTCAATCCCACTGAAGAGGCAG
GCTCTGTTCCAGAGATATACTCTCTTTTAAAAAGGACAACGGATATATTAATACAATTGC
ACAAAAGTGTACTTCCCTGAAGATATGGAATCTGTCTTAACAAAACCATATGACTCAC
ACACCGATATTAGAGCGTTTTTGGCAAGAGAAATCTAAGATTTTGTACATGAACAATTTAC
CGCCCGACACAACCTCAAAGTGAGTTGGAATCATGGTTTACCCAATATGGTGTAGACCAG
TTGGGTTTTGGACTGTCAAAAACATCGTAGAAGATACGTCTAACGTTAATAATACTGGA
GTCTAAATAACAGTCCCTATGTGGAAGATCAAGATAGTATCTCAGGATTTGTTGTCTTCC
AAACACATGAAGAAGCAACTGAAGTACTAGCGTTGAATGGGAGATCAATCCTATCTAATC
TGGCAAACACTAAGCAACCAAGGGTGGTGGAAACATGTCCTTGAGCTTCAACCTTCTTCCA
CCGGAGTACTCGATAAGGCTCAAGAAATTTTATCGCCTTTCCCTCAAAGTAAAAACAAAC
CAAGACCAGGTGACTGGAATTGCCCATCTTGTGGTTTTTCAAACCTTCAAAGACGTAAGT
CATGTTTTAGATGTTCTTTTCCGGCACCATCAAATAGTCAAATACATACTGCCAAGCTCAA
ACAATAATGTTAACAGTAGTAGAAATAATTTAAACAATCGCGTGAACCTCGGGATCTTCAA
GCAATATTAGTAACACTGCAGCGAATCACCCCTATGGTGGCCCTGAGTTCAACATGATTG
CTAACAACACGCCAGCAGCTTTAACATACAATAGAGCTCATTTCCTGCAATTACGCCAT
TGTCGCGACAAAATTCATTGAACATGGCACCATCGAACAGTGGGTGCGCGATAATTATAG
CGGATCATTTCGCGGAAATAATAATATAGCCCCAAATTATCGTTATAATAATAATATTA
ACAATAACAACAATAATATTAACAATATGACCAATAATAGATATAACATTAAATAACAACA
TCAACGGTAATGGGAATGGTAATGGGAACAACAGTAATAACAATAACAATCATAATAACA
ATCATAATAACAATCATCATAATGGTAGTATCAATAGTAATAGTAATACCAATAATAATA
ATAATAATAACAATGGTAACAATAGTAATAATTGTAATTCGAATATCGGTATGGGAGGAT
GTGGCTCCAACATGCCATTTAGAGCAGGAGATTGGAAGTGTTCCACGTGCACGTATCATA
ACTTTGCTAAAAACGTAGTGTGCTTACGCTGTGGTGGTCCAAAATCAATAAGCGGCGATG
CAAGTGAACCAATCATTACATAGATTCAACATTGGACCAGCGTCGCGTACTCCCA
GTAATAACAATAATTTCTGTTAATACTAATGGTGGTAGCAATGCTGGTGCACCGATGGGA
ACGATAACAAAGGTCGTGATATTAGTTTGATGGAATTTATGTCACCACCGTTATCGATGG
CAACAAAGTCAATGAAGGAGGAGATGGGAATGGTAGCTCGTTTAAACGAGTTCAAAGTG
ACAAAGCTAACGTTAATTTTCCAATGTTGGTGATAATAGCGCTTTCGGTAATGGTTTTA
ATAGTTCAATACGTTGGTAG

YDL167C, 719 aa (SEQ ID NO 46)

MHYVLELQVAHLPTPKDQCRIANIAFQIVNAETLVCHYGTNSLPSIEVNGTTKSLESA
MVQLDKDIHDVIGNDDFVLVSLYSTWHIRVTLPRQARDDGFILTSYLQHPKVFDLWKEFD
RWCNVNHEILGQKKAISNNNCNTKSISINAANKTKDLDEIVRILEVSIPTTEAGSVPEIY
SLLKRTDILILQLHKKCTSPEDMESVLTKPYDSHTDIRAFLQEKSKILYMNLPDPTQS
ELESWFTQYGVREPVGFVTKNIVEDTSNVNNNWSLNNSPYVEDQDSISGFVVFQTHEAT
EVLALNGRSILSNLANTKQPRVVEHVLELQPSSTGVLDKAQEILSPFPQSKNKPRPGDWN
CPSCGFSNFQRTACFRCSFPAPSNSQIHTANSNNNVNSSRNNLNLRVNSGSSSNISNTA
ANHYPGAPEFNMIANNTPAALTYNRAHFPAITPLSRQNSLNMAPSNSGSPIIADHFSGN
NNIAPNYRYNNNNNNNNNNNNNNMTNNRYNINNNINGNGNGNGNNSNNNNNNNNNNHH
NGSINSNSNTNNNNNNNNNGNNSNNCNSNIGMGCGSNMPPFRAGDWKCSTCTYHNAFKNVV
CLRCGGPKSISGDASETNHYIDSSTFGPASRTPSNNNISVNTNGGSNAGRTDGNNDKGRD

ISLMFMSPPLSMATKSMKEGDNGSSSFNEFKSDKANVNFNSVGDNSAFNGNFNSSIRW

YDL184C, 578 bp, CDS: 501-578 (SEQ ID NO 47)

AACAAGAAAACCCCTCCGTTGATCTTAGATTTCTTAGAGGTTTCATGAAGTAGAAAAGCGAC
TTGAACAAAAGTCATCCTTCAAGAATCGAAATCTCAAGAGAAAAACAAAATTTAATGTAGA
TTGTCCACTATCTCATGTAAATATACATAACAGGTATTCTGAGCGTTCCGAAAATTAGAC
TGTACTTTTCTGATGCGCTCCCGTACACCTTTGACATATACAAACATCCGCACATTTTAT
AGCTTTCTTTCTAGAATTTTTTCCACGCGCTCTCGATCAATGAACTCTTAAAAGTAACTG
ACCCCTAACTTTTTTCCAGGCAAGGCTGGCCTCATTACCCTACCCGAAAAGTTTCACTTTA
CCCCATGGCAGATGGACGATATTTTAAACAAGACGAACTGACCTCGTCTTCTATAAACT
GGACTTCTAAGCAACTCTCATTATCTTATATCCGTTCCATTTTGTACTAAAAGAACCAG
ACCACATCGATTCAATCGAAATGAGAGCCAAGTGGAGAAAAGAAGAGAACTAGAAGACTTA
AGAGAAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL184C, 25 aa (SEQ ID NO 48)

MRAKWRKKRTRRLKRRKRRKVRARSK

YDL191W, 1354 bp, exon1: 501-503, intron1: 504-994, exon2:
995-1354 (SEQ ID NO 49)

TATTGACGTTTTCGCTCTCAGGTCCACCCTGTTCTCAAAAGATACTTTTAAAACCTAAAC
ACACGAAATCATATTATGATAATTCAGAATGATAGTGTGGTACTGTGTCAATTGACTGTT
CAAGACTGAAGAGGATCTTTGATTTGTTGTTACTCAACAAATAATCTTCACGAAAACCTTT
CTCAATCTGGGGACTGTATTAATCTCAGACCCATACATATCTACACCCATAACTTTTTAC
ATTTAATTTTTTATCACATAATAGGTAGCTTAAATTGTAAAGTCGAAAAAAAAAATGGCA
GCGCAGCCTCTCCGGGTGAACCCACGACAACCTTACCTGGCACTCCATGCCTAACGGGC
GGTTTTGGGCAGGATTCAGCATCAATTTTGCAAAATTCACACCTGAGTAATTCATATAT
GTAATATAATGTTAAGCATACGCTGTGCTGATTAGCACTATTATTGACCGTAGAATAGGTAC
AGTGAGACAGTATATTGAAATGGTATGTTTGAGATGAACAAAATAATAAGACTGACAA
CTGCAGAACAGAGAGGATCATAGCAACCTAGTGCAAGAAAGAGCCTCGAAGCGTTAAACT
TTTGGAACGTAATTCATCCGTTGGCTATGTCTATTCAATACAGTTAGAATACGAAAGCTG
TAATCAAGTATATCGGATTATTGCGAAGCAAAGAATCAAGGAAAAGAAAGTGAAAATAGC
ATACATCTTTTAAATTCAGAGGTTTTGCTGAATTTTAAATAGGGAAGTTTACGTTATGATTG
TTGGCCGTAGATCGCCTAGCGTTTGACCAAATTTAATTCTCCTAATTTTTTTTATTGTAAA
AAAGCCTTCCAACGAAATAAATTAGTTATTGGTTTTTTTTTCTCTGTTACGAGGGATATAT
GATGCCTGTGCTTGTAGTTTATTATAAGTGCTAATAAAATACTAACGTTAATAAAAAATT
TGGAATATTATTTTCAATTTTTTATCCTATTAATAGGCCGGTGTAAAGCTTACGAACTAAG
AACCAAATCCAAGGAACAATTGGCTTCTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGA
ATTGAAGGTCCAAAAGTTGTCCAGACCATCTTTGCCAAAGATCAAGACCGTCAGAAAGAG
TATCGCCTGTGTCTTGACCGTCATCAACGAACAACAAGAGAAGCTGTTAGACAATTATA
CAAGGGTAAGAAGTACCAACCAAGGACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAG
AGCTTTGACCAAATTCGAAGCTTCCCAAGTTACCGAAAAGCAAAGAAAGAAGCAAATCGC
TTTCCCAAAAGAAAGTACGCTATTAAGGCTTAA

YDL191W, 120 aa (SEQ ID NO 50)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTVINE
QOREAVRQLYKGKQYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

YDR103W, 3254 bp, CDS: 501-3254 (SEQ ID NO 51)

ATCAAGTTTCTTTTAAAGGATATATAACAGATTCTAAAAGTACAGAAATATTTTCGAGT
GAAGAAGAAGCGTTAAATATTGGATCTTTCCGCGAGTTCTACTCTGATACATTTTGAAGT
AGGAGAGTCATTTAGAAGGCGTATTGCTCAATAGTAGAAAGCAGGCCTGTGCACATGAAT
TAATTAATAAATATAAAGGTAGTGATTAGACGACACATGTCCATAGGTAACCTGTCTATA
TTTTGAACAATTTCCCTTCTTTTCTTTTTTTTTTTGGGTGCGCGATATGTAGCTTGT
AATTTACACATCATGTACTTTTCTGCATCAAAATATGAAAGGCGATAGTAGCTAAAGAAA
ATACCGAGAATTTCTCGAAAAGTTGACGACAAAAGAAAGGCATAAAAAAGTAATTTGAA
AATATTTTAAACTGTTTTTAACCCATCTAGCATCCGCGCTAAAAAAGGAAGATACAGGAT
ACAGCGGAAACAACCTTTTAAATGATGGAACCTCTACAGACAATATAGTTTCCCTTTTTC
ACAATTTTGGTAGCTCGACACAATATAGTGGTACCTTGTGAGAACTCCCAACCAATAA
TAGAGCTAGAGAAGCCCAGTACTCTATCCCCATTGTCAAGAGGAAAAAATGGACGGAAA
AGTTAGCCAGGTTCCAAAGAAGTAGTGCTAAAAAGAAAAGATTCTCACCTTCTCTATTT

CCTCCTCTACATTTTCGTTCTACCCCAAATCTAGGGTCACTTCTTCAAACCTCTTCTGGCA
ATGAAGACGGTAACCTAATGAATACACCTTCTACGGTTTCCACTGATTATTTGCCACAAC
ACCCTCACAGAACATCGTCTTTGCCAAGACCTAATTTCCAATCTCTTTCACGCAAGTAATA
GTAACCTATCCCGAGCAAATGAGCCCCCAAGGGCCGAAAATTTATCAGATAATATACCAC
CCAAGGTCGCTCCATTTGGCTATCCAATACAAAGAACCTCTATTAATAATCCTTTTGA
ATGCTTCTTGACGTTATGTGACGAGCCTATTTCTAACAGAAGAAAGGGAGAGAAAATTA
TAGAGCTTGACATGTGGCCACTTAAGTCACCAAGAATGTCTTATTATCTCTTTTGGCACCA
CTTCAAAGGCAGACGTTCTGTGCGCTATTTCTTTTGTACCAAATGTAAAAAAGATACTA
ACAAAGCCGTTCAATGCATTCCAGAAAATGATGAACTAAAGGATATTCTAATTTCTGATT
TTTTGATTTCATAAGATTCTGTGATTCTGAGTTATCAATCACACCTCAGTCCCGCTTTCTCTC
CTTATTACCACTCTTGCTCTCTTTTGGGTATCTTATACACCTGTGTGAAGACAAAACGA
TATATTCTCAAGCTCCAAGTCTAAACCCAAATCTCATATTGGCTGCACCCCCCAAGGAAA
GAAACCAAATTTCCACAAAAAAATCAAACCTATACATTTTACATTACCCCTGGGGCACA
GAAGAATTCGTCGAGCAAACCTCTATCTTAGCAGACACCTCTGTAGCGTTGTCAGCTA
ATGATTCTATTTCTGCTGTTTCCAATTCGGTAAGAGCAAAGGATGACGAAACCAAAACAA
CGTTGCCGCTGTTAAGGTCATATTTTATTCAAATTCCTTTGAACAATTTCCAGGAAGAAT
TGCAGGATTGGAGAATAGACGGGGACTATGGATTACTAAGGTTGGTAGACAAATTGATGA
TTTCCAAAGATGGTCAGAGATATATACAATGCTGGTGTCTTATTTGAAGACGCATTTG
TAATAGCAGAAGTGGATAACGATGTTGATGTTTGGAAATTAGACTAAAGAATTTAGAAG
TATTTACACCTATTGCCAACTTGAGAATGACTACACTCGAAGCTTCAGTACTCAAATGCA
CCTTAAATAAACAACATTGCGCCGATTTATCAGATCTTTACATTGTTTCAAGATATAAAT
CTGACGAAAGCACAACCTGTACAGAAATGGATATCAGGTATATTGAATCAGGATTTGTAT
TCAATGAGGACAATATCACTTCGACCCTGCCTATTCTTCCCATTATAAAGAACTTTTCAA
AAGATGTTGGTAATGGTAGGCACGAGACGAGTACCTTTCTAGGTTTAAATCAATCCTAACA
AAGTTGTTGAAGTTGGAATGTGACGATACTGTAATCATAAGGAGGGGATTCA
CCTTAAATTCAGGAGAATGTTCTAGGCAGAGTACTGTGACAGTATACAATCTGTTCTAA
CCACGATAAGCTCAATTCCTTCCCTTAAACGAGAAAAACCTGATAATTTGGCAATAATCT
TACAGATCGATTTTACGAAATTGAAGGAAGAAGACAGTTTAAATTGTTGTTTATAACAGTC
TAAAGCTTTAACCATTAAATTTGCGCGTTTGCAGTTTGTGTTTCTGTTGATCGAAATAATT
ATGTTCTGGACTATGGATCGGTATTACACAAGATAGATTCACTAGATTCCATCTCAAATC
TCAAATCAAAGAGTTCTCTGACACAATTTTACCTATTGTTGTTGAAATACTCTATATC
CCGAAATATTATGAACATTTGGGTATTGTTGCTGTATCAAATAGTAATATGGAAGCAA
AAAAATCCATACTATTTCAAGATTACAGATGCTTTACAAGTTTGGGAAGAAGAAGGCCCA
ATGAATTGAAGATTAAGGTGGGCTATTTGAACGTTGACTACAGTGATAAAATTGATGAAC
TAGTCGAGGCCAGCTCCTGGACTTTTGTGTTTAGAACTCTTTGCTACAGTTTCCGTCTAA
GTTTGTGATGAACATGATGACGATGACGAAGAGGATAATGATGATTGACCGGATAATGAAC
TTGATAATGATTTCAGGATCACTGTGCGATGCTGAATCTACAATACTATTATTCATTGATT
CTCCATTTGATAATGAAATGCTACCGCAAATATGGTGAATGACAGAAACCTTCTCACTG
AGGGTGAACATAGCAATATAGAAAACCTAGAAAACGTGCGCTTCTTCAGTACAGCCAGCTC
TGATTCTTAATATTAGATTTTCACTTCACTTCTGAGGAGGAAGGTACTAATGAAATGAAA
ATGAAATGATATGCCAGTATTATTACTTAGTGATATGGATAAAGGAATCGATGGCATAA
CCAGACGCAGTTCACTCTCGAGTCTTATAGAGAGCGGTAATAACAACCTGTCCCCTCCATA
TGGATTATATATAG

YDR103W, 917 aa (SEQ ID NO 52)

MMETPTDNIVSPFHNFGSSTQYSGTLSRTPNQIIIELEKPSTLSPLSRGKKWTEKLARFQR
SSAKKKRFSPPISSTFSFSPKSRVTSSNSSGNEGNLMNTPSTVSTDYLPQHPHRTSS
LPRPNSNLFHASNSNLSRANEPRAENLSDNIPKVPFGYPIQRTSIKKSFLNASCTLC
DEPISNRRKGEKIIELACGHLHQECLIIISFGTTSKADVRALFPFCTKCKKDTNKAVQCI
PENDELKDILISDFLIHKIPDSELSITPQSRFPYPSPLLPPFGLSYTPVERQTIYSQAPS
LNPNLILAAPPKERNQIPQKKSNYTFLHSPLGHRRIPSGANSILADTSVALSANDSISAV
SNSVRAKDDETKTTLPLLSYFIQILLNNFQEELQDWRIDGDYGLLRVLDKLMISKDQQR
YIQWCWFLFEDAFVIAEVDNDVDVLEIRLKNLEVFPIANLRMTTLEASVLKCTLNKQHC
ADLSDLYIVQNINSDESTTVQKWISGILNQDFVFNEDNITSTLPILPIIKNFSKDVGNR
HETSTFLGLINPNKVVEVGNVHDNDTVIIRRGFTLNSGECRSQSTVDSIQSVLTTISSIL
SLKREKPDNLAILQIDFTKLKEEDSLIVVNSLKALTIKFARLQFCFVDRNNYVLDYGS
VLHKIDSLSISNLKSKSSSTQFSPIWLKNTLYPENIHEHLGIVAVSNSNMEAKKSILFQ
DYRCFTSFGRRRPNELKIKVGYNVDYSDKIDELVEASSWTFVLETLCYSFGLSFDEHDD
DDEEDNDDSTDNELDNSSGSLSDAESTTTIHIDSPFDNENATANMVNDRNLLTEGEHSNI
ENLETVASSVQPALIPNIRFSLHSEEGTNENENENDMPVLLLSMDKIDGITRRSSFS

SLIESGNNNCPLHMDYI

YDR238C, 3422 bp, CDS: 501-3422 (SEQ ID NO 53)

CCGTGTC AAGATCTAACACGGTAGTCAGCTACTACACAAGGTCTCAGAACAGAATGAGAA
GTGGAACACTGGATAATGATTACGTGAACAGACAAAAGCTTCCTACACATATCTCTCTTC
AAGATTATCGTGATGCTAATGCTAGAAAGTAATATATCGCGTCAGGACTCTGTCTCCACAA
CGAACTCTGATGTGGTAGACCTCAGCTATTCTCTGGGGCATGGCTTGGCTGTGGCAAACC
CTGATTACAGACCCAGAATGATATCTCTCTCTGTAGTTTGTAGATGTCATATATGTACGT
TTATGGAACAGCATTTTAGAAAAGTATTACCCAGCTTATCACTTCGTTTTTTTTTTCTTT
CCGTGTACTCGCTACACGTAGAAAAGAAATCAGAAAACAACAGCTCGACAAGTGAAATTTG
ACGTTTCATTAAAGACTCAGTTAAGATTGGCTTGAGAAATAAACAAAAGTAATCACAGTTAAC
TATTGAACAAGAGTGCACCTATGACTTCACCTTTCTTCACAGCCAGCGTACACGTTGGTTT
TCGATCTCTCTCCGAGTATGGAGACTTACTCGAGTACCGATTTCAGAAAAGCTCTTGAAA
AGGGATCTGATGAACAAAAATTGACAGATGAAATCAATTTTAGTTACAAATGCTGGAAG
GAAATCCAATGCCCTGAATTGTTGATGCACATAATAAGATTTGTCATGCCCTTCTAAAAATA
AGGAATTA AAAAAGCTTTTGTACTTCTACTGGGAAATTTGTTCCCAAACCTAGCTGAAGATG
GAAAATTGAGACATGAAATGATTCTTGTCTGTAATGCCATTCAACACGATTTTGCAACATC
CTAATGAATATATTAGAGGTAACACATTAAAGGTTTTTAACGAAAATTGAGAGAGGCCGAAC
TCTTAGAACAGATGGTTCCCTCTGTCTTACCGTGTCTTGAATACCGTCATGCATATGTTT
GTAAGTATGCAATCCTAGCAGTTTCTCCATTTTCAAGGTCAGCGAACATTTACTTTCCCG
ATGCTAAAGAAATCATCAATTCGTTTCATAGTAGCTGAAACTGATCCAATATGTAAAGAA
ATGCAATTTATTGGGTTAGCTGAATTAGATCGTGAAATGCCTTACACTATTTAGAGAACA
ATATTGCTGATATAGAAAACCTAGACCCCTTTATTACAAGCTGTCTTTGTTCAATTTATCA
GACAAGATGCAAAACAGGACCCCTGCTTTGAAAGCCCAATATATCGAATTATTGATGGAAC
TGCCTTCGACCACGACTTCGGATGAAGTCATCTTCGAGACCGCATTAGCCCTAACTGTGT
TGTCTGCCAATCCAAATGTCTTGGTTCCCTGCGGTTAACAAATTGATTGACTTGGCCGTCA
AGGTTTTCTGATAATAACATTAAAGTTAATTGTTCTAGACCGTATTCAAGACATCAATGCTA
ATAACGTAGGTGCTTTTGAAGAGTTAACCCTGGATATTTGAGAGTCTTGAAATGCAGAAG
ATTTAGACGTTTCGTTCAAAGGCGCTTGATATTTCAATGGACTTGGCCACATCCAGAAATG
CTGAAGATGTTGTTTCAAGCTTTTGAAGAAAGAGCTGCAAAACAACCGTAAATAACCCAGATC
AAGACAAGGCAATGCAGTACAGACAATTGTTAATAAAAACTATTTCGTACCGTGGCTGTAA
ACTTTGTAGAAATGGCAGCAAGTGTGTTTTCGCTATTATTAGATTTTCATCGGTGATTTAA
ACTCGGTTGCCGCCAGTGGTATCATTGCCCTTTATCAAAGAAGTGATCGAAAAATACCCAC
AACTTAGAGCCAAATATCCTTGAAAACATGGTTCAAACGCTAGACAAAAGTGAGATCTGCTA
AAGCTTACCGCGGTGCATTATGGATTATGGGTGAGTATGCTGAAGGAGAAAGTGAGATAC
AACATTGTTGGAAGCACATTTCGTAACAGCGTAGGTGAAGTTCTATCCTTCAATCAGAAA
TCAAAAAAGTTAACACAAAACCAAGAACACACCGAAGAAAATGAGGTTGACGCTACCGCCA
AGCCAACCTGGTCCAGTTATTCTACCAGACGGTACGTATGCCACTGAAAGCGCTTTCGATG
TGAAGACTTCTCAAAGTCAGTTACCGATGAAGAACGTGATTCTAGACCTCCAATTCGCC
GGTTTGTTTTAAAGTGGTGATTTTCTACACAGCTGCCATTCTGGCCAACACCATCATTA AAC
TTGTTTAAAAATTCGAAAACGTTTCCAAGAACAAAACCTGTCAATGCTCTAAAGGCGG
AAGCTTTACTAATTTTAGTTAGTATTGTAAGAGTGGGTCAAAGCTCTTTGGTGAGAAAA
AAATTGATGAAGATTCTTTAGAGAGAGTTATGACATCTATTCTATTTTATTGGATGAAG
TTAATCCTGAGGAAAAGAAGGAAGATTAAACTTCTGGAGGTTGCATTCTGGACACCA
CCAAATCCTCATTCAGAGACAAATTGAAATGCAAGAAGAACAAAGCATAAGAGAGCAT
TAAAGACAGTTGCAAAAACATCGAACCAATTGATACCGCGATTCTTTTCAGGCAATTTG
CTGGTGTGGATTCTACTAATGTGCAAAAAGATAGTATTGAAGAAGATTTACAACCTGGCAA
TGAAAGGAGATGCAATCCACGCTACTAGCAGCTCTAGTATTTGAAAGCTGAAGAAGATAG
TACCTTTATGTGGCTTTTCTGATCCAGTTTACGCCGAGGCTTGTTATTACAAACAATCAAT
TTGACGTCGTATTAGATGTTCTTCTTGTAAATCAAACGAAAGAAACATTGAAAAACCTAC
ATGTGCAATTTGCAACTCTTGGTGATTTGAAGATTATTGACACACCACAGAAGACCAACG
TGATTCCTCATGGCTTCCACAAATTCAGTGTACTGTCAAAGTTTCTCTCTGCTGACACAG
GTGTCAATTTTCGGTAATATTATTATGATGGTGCCGATGGTGAAGATGCTCGTTATGTTA
TTTTAAACGACGTTTCATGTTGACATTATGGATTATATCAAACAGCCACTGCTGACGATG
AACATTTCCGTACCATGTGGAATGCATTTGAGTGGGAGAAACAAAATATCGGTCAAATCAC
AACTACCAACATTGCATGCTTATTTGAGAGAACTGGTCAAGGGAACTAATATGGGTATTC
TAACACCATCAGAGTCGTTGGGAGAAGATGATTGTAGGTTCTTAAGTTGTAATCTGTATG
CGAAGTCGTCCTTTGGTGAAGATGCCCTAGCCAACCTGTGTATCGAAAAGGATTTCCAAAA
CCAATGATGTCATAGGTTATGTTCCGTATCCGATCAAAGGGACAAGGTTTGGCTCTGTCCC
TAGGTGACAGAGTGGCATTGATTGCTAAGAAGACCAATAAACTTGCTCTCACTCATGTTT

GA

YDR238C, 973 aa (SEQ ID NO 54)

MTSLSSQPAYTLVFDPSMETYSSTDFQKALEKGSDEQKIDTMKSILVTMLEGNPMPPEL
LMHIIRFVMPSPKNEKLLLYFYWEIVPKLAEDGKLRHEMILVCNAIQHDLQHPNEYIRG
NTLRFLTTLKREAELLEQMVPSVLACLEYRHAYVRKYAILAVFSIFKVSEHLLPDAKEIIN
SFIVAETDPICKRNAFIGLAELDRENALHYLENNIADIENLDPLLQAVFVQFIRQDANRT
PALKAQYIELLMELLSTTTSDVIFETALALTVLSANPNVLVPAVNKLIDLAVKVSNNI
KLIVLDRIQDINANNVGALEELTDILRVLNAEDLDVRSKALDISMDLATSRNAEDVVQL
LKKELQTTVNNPDQDKAMQYRQLLIKTIRTAVNVFEMAASVVSLLLDFIGDLNSVAASG
IIAFIKEVIEKYPQLRANILENMVQTLDKVRSKAYRGALWIMGEYAEGESEIQHCWKHI
RNSVGEVPILQSEIKKLTONQEHTENEVDATAKPTGPVILPDGTYATESAFDVKTSQKS
VTDEERDSRPPIRRFLVSGDFYTAAILANTI IKLVLKFENVSKNKTVINALKAEALLILV
SIVRVGQSSSLVEKKIDEDSLERVMTSISILLDEVNPEEKKEEVKLLLEVAFLDTTKSSFKR
QIEIAKKNKHKRALKDSCKNIEPIDTPI SFRQFAGVDSTNVQKDSIEEDLQLAMKGDHAIH
ATSSSSISKLKKIVPLCGFSDPVYAEACITNNQFDVLDVLLVNQTKETLKNLHVQFATL
GDLKIIDTPQKTNVIPHGFKFTVTVKVSSADTGVIFGNIIYDGAHGEDARYVILNDVHV
DIMDYIKPATADDEHFRTMWNFAFEWENKISVKSQPLTHAYLRELVKGTNMGILTPSESL
GEDDCRFLSCNLYAKSSFGEALANLCIEKDSKTNVDVIGYVRIRSKGQGLALSIGDRVAL
IAKKTNKLALTHV

YDR259C, 1652 bp, CDS: 501-1652 (SEQ ID NO 55)

AAACTTTGTTCAGATTATGCTTTCTTTGTAATTTTAAACATAGTCTTGCACTTATTTTT
ACTGCATGTGGATAAAAGTTTTTCGAATCGTTTGCAGGCAAATGTAAACTATTACTTTTT
AATGATTTCTGATACTCTTTGATTCCATTCTGTCTACTTTTTTCTGCATTTGAAACGCT
AATTAAGTATTTCTTGGCCCTGCTTCTTTCTTTGATTCTTTTTTTATTCTCAAGTT
TTTAATTTCTGGAGAATCTCTTTTTTTGTTTATTTTGTAAACACAGTTAGTGGAGCCTTG
TAGTATCGAGAGTAGACTATCTTTGGAAAGCAATGCGAGTTGAGAGATTGTGGAGTGAC
TACAGAACCAATATTAAACACAATCTTTCCTCAAACCTGTAACACCGAGTTTTTTTCCCCA
CCAATCGTGAATCCGATAGCATATACTTTGTCTAGAAATTTCAATAAACAACAGAATAA
CGAAGAGTGCTAAGGGACAAATGCAAAACCTCCGTTGATTCTCGTCCCGATATGTATAATC
AGGGAAGCAGCTCAATGGCTACTTATAATGCCTCTGAGAAGAATCTAAATGAGCATCCTT
CTCCGCAAATTGCACAGCCGAGCAGCTCCCAAAAGTTACCTTATAGAATAAAATCCTACAA
CCACTAATGGGGACACCGACATATCTGTAAACAGCAATCCTATCCAGCCTCCTTTGCCAA
ACTTGATGCATCTATCTGGTCCGTCTGACTATAGATCGATGCATCAAAGTCTTATACATC
CATCTTATATCATCCCTCCGCATTCAAATGAAAGAAAACAATCAGCTTCTTACAACAGAC
CTCAAAATGCTCATGTTAGTATTCAACCTTCCGTGGTATTCCCCCTAAAAGTTATTCCA
TATCTTATGCACCTTATCAAATAAATCCCCCTTACCAAATGGACTTCGAACAGAGCA
TATCTTTGAATAAGGAGTATATTGCAGAGGAGCAACTATCAACCCTCCCATCTCGCAATA
CCAGTGTTACTACTGCACCTCCTTCTTTTCAAAACAGTGCTGATACCGCTAAAAATTCAG
CTGATAATAATGATAATAATGATAATGTAACCAAACCTGTTCTTGATAAAGACACCCAAC
TCATAAGTAGTTTCAGGCAAACTTTAAGAAATACTAGAAGAGCTGCTCAAAATAGAACCG
CTCAAAAGGCATTTAGACAAAGGAAAGAAAAATACATCAAGAATCTCGAACAAAAATCAA
AGATATTTGACGATTTACTAGCAGAAAATAATAACTTCAAATCATTAAACGATTTCATTAA
GAAATGACAACAACATTTTAAATAGCTCAGCATGAAGCTATAAGGAATGCAATTACTATGT
TAAGAAGTGAGTATGATGTCTTATGTAACGAAAAACAACATGTTGAAGAATGAGAATAGTA
TAATAAAAAATGAACACAACATGTCAAGAAATGAAATGAAACCTAAAACCTTGAGAATA
AACGCTTCCACGCTGAATATATACGAATGATCGAGGATATTGAAATACTAAAAGAAAGG
AACAGAACAACGAGATGAAATAGAGCAACTAAAAAAAAAATAAGATCCCTGGAGGAAA
TAGTAGGGAGACACTCGGATAGTGCCACGTAA

YDR259C, 383 aa (SEQ ID NO 56)

MQNPPLIRPDMYNQSSSMATYNASEKNLNEHPSQIAQPSTSQKLPYRINPTTTNGDTD
ISVNSNPIQPPLPNLMHLSGSPDYRSMHQSPIHPSYIIPPHSNERKQSASYNRPQNAHVS
IQPSVVFPPKSYSISYAPYQINPPLPNGLPNQSI SLNKEYIAEEQLSTLPSRNTSVTTAP
PSFQNSADTAKNSADNNDNNDNVTKVPDKDTQLISSGKTLRNTRRAAQNRTAQKAFRQ
RKEFYIKNLEQKSKIFDDLAEENNFKSLNDSLRNDNNILIAQHEAIRNAITMLRSEYDV
LCNENNMLKNENSI I KNEHNMSRNEENENLKENKRFHAEYIRMIEDI ENTKRKEQEQRDE
IEQLKKKIRSLEEIVGRHSDSAT

YDR294C, 2270 bp, CDS: 501-2270 (SEQ ID NO 57)

CCGACAGTACGACTTAAAAAACAACGTCAGGTGGAAAAAGCTGCCGCAATGG
TACACGGTTTAGATCAACAAGATCCAATACCCCTAATTACACATGAATGTGACGTTTCTT
AAAAGAAGTAGCCTGTATAATATAGAGAGATTTTATATACTTTCTTAATGAATTAGACTG
TTTCTACAAGTATTTGACACTGGAAAAAAGAGAAAGTACATAGAGATTGGCCAAATATT
TAAATCTACACAGTTGCCTATCGTTTATCGCCTTATTCTTCAGAAACATTTTCATCAACTA
CTCTGGTGCATTATTTTCATGTTAGTTACCATATATACCGGCCGGCCGCATCGGGGTTTTT
TGATTGAAAAAATTTGGTATATTTTCAGTACACATATAAATAAAACCCCTCAATTTGCCTCT
CCAACCGTTATAACTATTCCAGATCCTCTTTACCGAGCAAGTAGGCTAGCTTCTGTAAAG
GGATTTTTCCATCTAATACAATGAGTGGAGTATCAAATAAAACAGTATCAATTAATGGTT
GGTATGGCATGCCAATTCATTTACTAAGGGAAGAAGGCGACTTTGCCAGTTTATGATTC
TAACCATCAACGAATTAATAATAGCCATACATGGTTACCTCAGAAATACCCCATGGTACA
ACATGTTGAAGGATTATTTGTTTGTGATCTTTTGTGTACAAGCTAATAAGTAATTTTTTTT
ATCTGTTGAAAGTTTATGGGCCGGTGAGGTTAGCAGTGAGAACATACGAGCATAGTTCCA
GAAGATTGTTTTCGTTGGTTATTGGACTCACCATTTTTGAGGGGTACCGTAGAAAAGGAAG
TCACAAAGGTCAAACAATCGATCGAAGACGAATAATTAGATCGGACTCTCAGTTAATGA
ATTTCCACAGTTGCCATCCAATGGGATACCTCAGGATGATGTTATTGAAGAGCTAAATA
AATTGAACGACTTGATACCACATACCCAATGGAAGGAAGGAAAGGTCTCTGGTGCCGTTT
ACCACGGTGGTGATGATTTGATCCACTTACAACAATCGCATACGAAAAATATTGCGTTG
CCAATCAATTACATCCCGATGTCTTTCTGCGTACGTAAATGGAATCCGAAGTGGTTT
CTATGGTTTTTAAGAATGTTTAATGCCCTTCTGATACAGGTTGTGGTACCACAACCTCAG
GTGGTACAGAATCCTTGCTTTTAGCATGTCTGAGCGCTAAAATGTATGCCCTTCATCATC
GTGGAATCACCGAACCAGAAATAATTGCTCCCGTAACTGCACATGCTGGGTTTGACAAAG
CTGCTTATTACTTTGGCATGAAGCTACGCCACGTGGAGCTAGATCCAACGACATATCAAG
TGGACCTGGGAAAAGTGAATAAATTCATCAATAAGAACAATTTTACTGGTCCGTTCCG
CTCCAAACTTTTCCATGTTATTGCGGATGATATTGAAGGATTGGGTAAAATAGCACAAA
AATATAAATTTCCTTTACACGTCGACAGTTGTCTAGGTTCCCTTTATTGTTTCATTATGG
AAAAGGCTGGTTACAAAAATCTGCCATTACTTGACTTTAGAGTCCCGGGAGTCACCTCAA
TATCATGTGACACTCATAAATATGGATTTGCACCAAAGGCTCGTCAGTTATAATGTATA
GAAACAGCGACTTACGAATGCATCAGTATTACGTAAATCCTGCTTGGACTGGCGGGTTAT
ATGGCTCTCCTACATTAGCAGGGTCCAGGCCTGGTGCTATTGTCTGAGGTTGTTGGGCCA
CTATGGTCAACTGCGGTGAAAATGGGTACATTGAGTCGTGCCAAGAAATAGTCGGTGCAG
CAATGAAGTTTAAAAAATACATCCAGGAAAACATTCCAGACCTGAATATAATGGGCAACC
CTAGATATTTCAGTCATTTTCAATTTTCTTCAAAGACCTTGAACATACACGAACATCTGACA
GGTTGTCCAAGAAAGGCTGGCATTTCATGCCCCTACAAAAGCCGGTTGCACTACACATGG
CCTTCACGAGATTGAGCGCTCATGTTGTGGATGAGATCTGCGACATTTTACGTACTACCG
TGCAAGAGTTGAAGAGCGAATCAAATCTAAACCATCCCCAGACGGAACCTAGCGCTCTAT
ATGGTGTGCGCGGAGCGTTAAACTGCTGGCGTTGCAGACAAATTGATTGTGGGATTCC
TAGACGCATTATACAAGTTGGGTCCAGGAGGATACCGCCACCAAGTAG

YDR294C, 589 aa (SEQ ID NO 58)

MSGVSNKTVSINGWYGMPIHLLREEGDFAQFMILTINELKIAIHGYLRNTPWYNMLKDYL
FVIFCYKLISNFFYLLKVYGPVRLAVRTYEHSSRRLFRWLLDSPFLRGTVKEVTKVKQS
IEDELIRSDSQLMNFQPLPSNGIPQDDVIEELNKLNDLI PHTQWKEGKVS GAVYHGDDLL
IHLQTIAYEKYCVANQLHPDVFPVVRKMESEVVSMLRMFNAPSDTGCGTTTSGGTESLL
LACLSAKMYALHHRGITEPEIIAPVTAHAGFDKAAYYFGMKLRHVELDPTTYQVDLGKVK
KFINKNTILLVGSAPNFPHGIADDIEGLGKIAQKYKLPLHVDSCLGSI VSFMEKAGYKN
LPLLD FRVPVTSISCDTHKYGFAPKGSSVIMYRNSDLRMHQYYVNPWTGGLYGSPTLA
GSRPGAIVVGCWATMVNMGENGYIESCQEI VGAAMKFKKYIQENIPDLNIMGNPRYSVIS
FSSKTLNIHELSDRLSKKGWHFNALQKPVALHMAFTRL SAHVDEICDILRTTVQELKSE
SNSKPSPDGTSALYGVAGSVKTAGVADKLIVGFLDALYKLGPGEDTATK

YDR430C, 3470 bp, CDS: 501-3470 (SEQ ID NO 59)

ACGTCATTTGTTCTTGTGGAGCTGGTGGTTCTTGTGGAGCAGATTCCCTGTGGAGCAGAT
TCCTGTGGAACCTGTGGTTCTTGTGGAGCATCTGGAGCCTGTGGTGGTTCTTGGTGCTGT
TCTTCGACTGGGCATCGACAACAGATTCTGGTAGTTGCTCTACGTGAGTTTCTTGGAGCT
TCAGACATTATCCTTATGGTTTTAGCGTAATTGCTTAATTTTGATTCCCTTCAAAGTATA
TATATTTAGAAGAGAGGAAATTATTTTTCTCATGTCCTTTTTAAATCCCTTTGGGTGGCG
AAAAAAGAAATGTAAAAAATTTGCCCCTTCGTTTACAGTGATAAATATACGGAGGGGCT
CTATGATAAAGGTAGTAGTAATCATTAATTGTTGAACAAGCATTGACAGATATGATAA

CAAGCAATTGTAATCAATAAGCCACCAATTAGAAGGCTACTCAAAAGAATAAAAGTTACTA
TAAATATACTGCGGTATATATGTTGCGGTTTCAGCGATTTCGCTCCTCGTATGCCCAAG
CACAGGCCGTTAGAAAATATCCAGTTGGAGGTATATCCATGGTTATGAAGTGAGAAGAA
TTCTACCGGTTCCCGAGCTGAGACTCACTGCGGTAGATTTCGGTGCACTCCCAGACAGGAG
CCGAGCATTTGCATATTGATAGAGACGACAAGAATAATGTGTTTCAGCATTGCTTTTAAAA
CCAACCTCCAGATTCCACTGGGGTCCCTCATATTCTAGAGCATACAACGTTGTGTGGGT
CTGTTAAATATCCAGTTAGGGACCTTTTTCAAAATGCTAAATAAATCTCTAGCTAATT
TCATGAACGCTATGACAGGTCCAGATTATACATTTTTTCCCTTTTCCACTACGAACCTTC
AAGATTTTCGCTAATTTAAGAGGTGTTTATTTAGACTCCACCTTGAATCCGCTACTTAAAC
AAGAAGATTTTGATCAGGAGGGTTGGAGGTTGGAGCATAAAAACATCACAGACCCGGAGA
GTAACATTGTTTTCAAAGGTGTTGTCTATAACGAAATGAAAGGTCAAATATCAAATGCCA
ATTACTATTTCTGGAGTAAATTTCAACAGTCTATTTATCCTTCCCTGAATAACTCCGGCG
GAGATCCTATGAAAATFACAGACTTGAGATACGGCGATCTCTTGGATTTCCATCACAAAA
ATTACCATCCCTCCAATGCAAAAACCTTTCACGTACGGTAACTTGCCATTGGTGGATACGT
TAAAGCAATTAATGAGCAGTTCAGTGGTTACGGGAAGAGAGCTCGAAAGGATAAGTTGT
TAATGCCCTATTGATTTAAAAAAGACATAGATGTCAAGTTACTGGGTCAAATAGATACTA
TGCTTCCACCGGAGAAGCAGACAAAAGCCTCAATGACGTGGATTGTGGAGCGCCACAGG
ACACATATGATACCTTTTGTAAAAGTACTGGGAATTTATTAATGGATGGCCATTCTT
CTGTAATGTATCAAAAATTAATAGAATCAGGAATTGGTTTGGAGTTCTCCGTAAATTCAG
GTGTTGAACCAACTACAGCAGTAAATTTGCTAACTGTTGGTATACAGGGCGTGAGTGATA
TTGAAATATTTAAAGACACTGTAATAATATTTTCAAAACCTGTTGGAAACAGAATC
CTTTTGACCGCAAGCGTATCGATGCCAATTTGAACAATTGGAATTATCTAAGAAGGATC
AAAAGGCTGACTTTGGACTTCAATTACTCTATTCTATACTACCTGGTTGGACAAAACAAA
TCGATCCTTTTGAGAGCTTGTGTTTGAGGACGTTTTCGAAAGATTTAGAGGTGACTTAG
AAACGAAAGGTGATACTTTATTCCAAGATTTAATCCGTAAATATATCGTTTCATAAACCTT
GTTTCACGTTTTTCATTTCAGGGATCTGAAGAGTTCTCTAAATCTTTGGATGATGAAGAAC
AAACAAGACTGAGAGAAAAAATTACTGCCTTGGATGAACAAGACAAGAAAAACATCTTTA
AACGTGGTATACCTGTTACAGGAGAAACAAAATGAAAAAGAAGATTTATCCTGTTTACCTA
CCTTACAAATAAAAGACATCCCAAGAGCTGGTGATAAATATTCAATCGAACAGAAGAATA
ATACAATGTCTAGGATTACTGATACCAATGGTATCACATATGTCAGAGGTAAACGTTTAC
TAAATGACATAATACCTTTGAACTCTTCCATACTTACCTTTATTTGCTGAATCGTTAA
CTAACCTAGGGACAACAACAGAATCCTTCAGTGAATAGAAGATCAGATAAAATTACATA
CGGGTGGTATATCAACACATGTAGAGGTTACATCTGACCTAACACCACAGAGCCTCGCC
TGATTTTCGGGTTTGACGGATGGTCTTTAAATTCGAAGACCGACCACATTTTGTGATTCT
GGTCTAAGATCTTACTAGAACTGATTTCCATAAAAACAGCGATAAATTGAAAGTTCTTA
TCCGCTTATTAGCATCTTCAAACACATCTTCTGTAGCAGATGCCGGTCATGCATTTGCAA
GGGGCTATTCTGCCGCACATTATAGATCAAGTGGAGCTATAAATGAGACCCTCAATGGTA
TTGAGCAACTACAATTTATAAATAGATTGCACAGCTTGTTAGACAATGAAGAACTTTCC
AAAGAGAATTTGTGCAAGCTAACTGAATTGCAAAAGTACATTGTTGATACCAATAACA
TGAATTTTTTATCACCTCAGACTCTGATGTTTCAAGCGAAAACAGTAGAAGGCCAAATTT
CAAAATTCATGGAGAGATTACCTCATGGCAGCTGCTTGCCCAATGGACCAAAGACTTCAG
ATTATCCTCTTATTGGATCCAAATGTAAACATACTTTGATAAAATTTCTTTCCAGGTCC
ATTACACATCCCAAGCTTTATTGGGTGTGCCGTATACACATAAGGATGGCTCTGCACTTC
AAGTTATGTCAAATATGCTAACATTTCAAACATTTGCACAGAGAAGTCAGAGAAAAGGGTG
GTGCTTATGTGGTGGTGGTCTTCTATAGCGCCTTAGCGGGTATTTTCAGTTTCTATTCTT
ATAGGGATCCTCAGCCTTTGAAGAGTTTAGAAACCTTCAAGAATAGCGGGCGTTATATAC
TGAACGATGCCAAGTGGGGCGTCACAGACCTTGATGAAGCTAAATTGACAATATTTCAAC
AAGTAGACGCACCTAAAAGTCCCAAAGGAGAAGGCGTGACGTATTTTCATGAGCGGTGTTA
CAGACGATATGAAACAAGCAAGAAGGGAACAACCTTTAGACGTATCTCTCTGGACGTTT
ATAGAGTCGCCGAAAAATATCTACTAAACAAGAAGGGGTGAGTACGGTCATTGGACCTG
GAATCGAGGGGAAGACTGTTTTACCAAATTGGGAGGTGAAGGAAGTGTAG

YDR430C, 989 aa (SEQ ID NO 60)

MLRFQRFASSYAQAQAVRKYPVGGIFHGYEVRRILPVPELRLTAVDLVHSQTGAEHLHID
RDDKNNVFSIAFKTNPPDSTGVPHILEHTTLCGSVKYPVRDPFFKMLNKSANFMNMTG
PDYTFPFSTTNPQDFANLRGVYLDSTLNPLLKQEDFDQEGWRLEHKNITDPESNIVFKG
VYVNYEMKGLISNANYFWSKFQOSIYPSLNSGGDPMKITDLRYGDLDFHHKNYHPNSA
KTFYIGNLPLVDTLKQLNEQFSYQGRKRDKLLMPIDLKDDIDVKLLGQIDTMLPPEKQ
TKASMTWICGAPQDITYDTFLKVLGNLLMDGHSSVMYQKLIESGIGLEFSVNSGVEPTTA
VNLLTVGIQGVSDIEIFKDTVNNIFQNLLETEHPFDRKRIDAIIIEQLELSKKDQKADFG

QLLYSILPGWTKIDPFESLLFEDVLQRFGRDLETKGDTLFDQLIRKYIVHKPCFTFSIQ
GSEEFKSLDDEEQTRLREKITALDEQDKNIFKRGILLQEKQNEKEDLSCLPTLQIKDI
PRAGDKYSIEQKNNTMSRITDTNGITYVRGKRLNDIIPFELFPYLPLFAESLTNLGTTT
ESFSEIEDQIKLHTGGISTHVEVTSDEPNTTEPRLIFGFDGWSLNSKTDHIFEFWSKILLE
TDFHKNSDKLKVLIIRLLASSNTSSVADAGHAFARGYSAAHYRSSGAINETLNGIEQLQFI
NRLHSLLDNEETFQREVVDKLTQLKYIVDTNNMNFITSDSDVQAKTVESQISKFMERL
PHGSCLPNGPKTSDYPLIGSKCKHTLIKFFQVHYTSQALLGVYPYTHKDGSAQVMSNML
TFKHLHREVREKGGAYGGGASYSALAGIFSFSYRDPQPLKSLETFKNSGRYILNDAKWG
VTDLDLDEAKLTIFQQVDAPKSPKGEVTVYFMSGVTDMDKQARREQLLDVSLLDVHRVAEKY
LLNKEGVSTVIGPIEGKTVSPNWEVKEL

YDR438W, 1613 bp, CDS: 501-1613 (SEQ ID NO 61)

CTTTTCTCAGCACCTGTCCAGAGACATAACATCACAATCACATCGCCCCAGTAAATGCA
TACGCAAGATAAGATACAACTGGCTACGGGAACACTACGCCAACGTGATTGGCAATTGT
GCTCTAATAGTTACTCTATTATTGCTGTTAATTGACAATGTTTAGTCACGTGCAACACAA
TTCAAGTCACGTGGAAAGGCCTTCACATGGTGATCCATCTTCTACATCTTCATCGGTCCCT
GCATAAAGTCATAATATGGGGCTACTGGAATGTATGCACTTAACAGTACTATTATATGGT
GAGGCTGTAATGCTTACCGTTTTGTGGCTATTCTCGTATTCTGTAGGCCCCCCCCATACAC
ATTTTTCGGTAACTGCGGCATATAGATGAAAGTTGAAATGAATATTCAAAGAATATATA
TAATAATGCAGGAGATCAAGGAAGAATTAGATATGTATAAGAGTGATGGTAGAGGCAAAA
AATAAAAAGTAAGCAGGAGAATGAATCGTGTTGGTATAGACGTAGATCATATGATAGGGG
TCCTGCTTCTGGCCGTAGTGGTGGTGTGTTGGGTTGGCGCTTCGTGTTTGACTAATGAAT
TGCTCGAGACAAACGCGTACAATAAACCTTTCTTCTTACTTATCTAAACATATCATCGT
TTGCTCTTTATTTGACGCCAGATCTATGGAGGATAATCCAATCAAGAAGGAAGAGCTTGC
AGGAACGGACAGAACGAACATTACCTATTCACACACAAGAATCTTTTTTCAGAGTTCCTAC
CTTTACTATCTTCAACTCCTTCTACTTCTTCAAATTTGTCTTCGATAGCGGACACGAAAG
TGAAGGATACAATGAGGTTGAGTCTGCTATTTGCGTCTTGTGGTTCGTGGCAATTTGG
CGGCTAACGCTGCTTTGTGCTATACACAGTGGCTTCGTCAACAATCTTTTCATCGACAT
CCTCATTTTTTACCTTATTTCTTGCCACTAGTCTAGGAATAGAACTTTTTTCGACAAAAA
AACTGCTGGGGTTATTTGTGTCTTTGTTTGAATTATCTTAATTGTGATGCAATCCTCGA
AGCAACAGGATTCTGTGAGTGCTTCTCTCTTTTGGTAGGTAACACTTTAGCACTGCTGG
GGTCATTGGGTTACAGTGTCTATACAACCCTTTTGAATACGAAATATCATCCAAAGGTC
TCAGACTAGACATTAGATGTTTCTTGTTATGTTGGTATCTTCACGTTTCTGTTGTTT
GGCCAATTTTAATAATCCTGGATATAACACATATGGAACTTTTGAACACCAAGTAAC
TCCACATTTCTTTTCTTGTCATGTTAAATTGTATCATTATCTTTGTTAGTGACTATTTTT
GGTGTAAGCCCTCATTTTGACATCACCTTGGTGGTTACCGTTGCCTTAACCTTTACTA
TCCCGTTAGCCATGTTTCGCTGATTTTGTATGGCGAGAGGCATTTTTTACGCCTTGGTATA
TCATTGGTGTATTTTCATTTTGTTCATTCTTTCTAGTTAACCATCGGGGAGAATCTG
CTGTTGAAAAGGACTGTGCTGCGGTTGAAAAGGACCTATCTTGGATGCCTAA

YDR438W, 370 aa (SEQ ID NO 62)

MNRVGIDVDHMIQVLLAVVVVFWVGASCLTNELLETNAYNKPFFLTLYLNISSFALYLTP
DLWRIIQSRKSLQERTERTLPIHTQESFSEFLPLSSTPSTSSNLSSIADTKVKDTMRL
SLLFCVLWFVANLAANAALSYTTVASSTILSSTSSFFTLFLATSLGIETFFSTKKLLGLFV
SLFGIILIVMQSSKQDSVSASSFLVGNTLALLGSLGYSVYTTLLKYEISSKGLRLDIQM
FLGYVGIFTLLFWPILIIILDITHMETFELPSNFHISFLVMLNCIIIFVSDYFWCKALIL
TSPLVVTVALFTIPLAMFADFVWREAFFTPWYIIGVIFIFVSFFLVNHRGESAVEKDCA
AVEKGPILDA

YDR450W, 1376 bp, exon1: 501-547, intron1: 548-982, exon2:
983-1376 (SEQ ID NO 63)

CGGCCCATGAGCATAAATTGAGAACGATATTATTAATTCTAGTATATTTTAGGAACAGCA
GGCCATTATATCCAAACTTTTTTAAAATAGCATCCACATCACTTACTGGCGTACAGTTT
CGTGTCTGGCAACAAAAAGTACATTTAATTTCAATGATTAAAAAGACATTAAACATCCG
TACATTACGCACCCATGCATGCTATCTGAAAATATTCTACATGCTGCTTTTAGAAATTTG
AAGCGGCATATGGTGTTCCTTGCGGAGACGCGCGCTCAGGGGAACGCGATTCCGAAAG
ATGCCCTTCCCATGCCCATCCCAAGATCATGCCCGGAGAGCAAAATGTCGCC
CCAGCCAGGTCCGACACATCTGTCAATCGACCCTAAGTATTGTCAAAGCTAGGGTTAAT
TGAAGATAGCTCTACATGTTATTAGTAGAGTTTTTAAACGTTGAGATACTAGTGAACGTA
TACACAAGAGCGGATAAAAGATGTCTTTAGTTGTCCAAGAACAAGGTTCTCTCAACACA

TTTTACGGTATGTTTATTATTACTAGTGAGCTATGACAAAATCGGCTAAAAACTTAAAAA
TATGACAGACAAGAAAGGAAATTCATTACCTCTTTAATCGTGGCGATTATTTCGCTAACG
ACGTGATTAAATATAATAATGATGTTCCCGGGCTGGACTAAGAACGTAATAATAAGGCTG
ATGAACAAAATTTATGGTTTATGCATCAAAAAGGAACATGAATTTGGCATAAGCGCACATA
ATTACGGAACATTGCAATAGCGGTGCGAGGTAAAGTACCGGGAATGCTTTACAATGAATC
AGCTATTGGCGGATATTGACCAACCAACACTAAAATTTTATATCCTGCTCCGATTTTGT
CTTGGCCGTGAAAATCCATTATGCACATTTTACTAACGTTTATCAATAAGTTCGGTTTC
CCGTCTAAATTTTTTACGCGATTTGTTGAACACTAACGTTGACGGTAACATTAAAGATCG
TTTACGCTTTGACCACTATCAAGGGTGTGGTTCGTCGTTACTCCAACCTGGTCTGTAAGA
AGGCTGATGTTGATTACACAAGAGAGCTGGTGAATTGACCCAAGAAGAATTGGAAAGAA
TTGTTCAAATTTATGCAAAACCCAACCTACTACAAAATCCCAGCTTGGTCTTGAACCGTC
AAAATGACATCACTGATGGTAAGGACTACCACACTTTGGCTAACACGTCGAATCCAAAT
TGAGAGATGACTTGGAAAGATTAAAGAAAATCAGAGCTCATCGTGGTATCAGACACTTCT
GGGTTTTCGGTGTAGAGGTCAACACACCAAGACCACTGGTAGAAGAAGAGCTTAA

YDR450W, 146 aa (SEQ ID NO 64)

MSLVVQEQQSFQHLRLNLTNVDGNIKIVYALTIIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YDR486C, 1289 bp, CDS: 501-1289 (SEQ ID NO 65)

ACTGCATACACAATAACTGTAGATGTAGCCCCAAGGCACTACCACAGGTATTTCTGCTCAC
GACAGGTCGATGACTTGTAGGGCTCTTGACAGACTCTTCTCTACGCCAAAATCATTTTTTA
AAACCAGGGCACATCTGTCCCTTGAGAGCCGCTGATGGCGGTGTTTTCAGAGAAGAGGC
CACACTGAGGCCGGTGTGCTGATTTGTGTAAACTAAGTGGACTAAGTCCCGTCTGTTATT
GGCGAATTGGTTAACGATGACGAACAAGGAACATGATGAGATTAAATGACTGCCAAGCG
TTTGGTAAGAAACATGGCATTCCTTTGATCTCCATCGAAGAATTTGGCCCAATATTGGAAG
AAATAATCTGGTGAACATTTCTCCATTCACTTATCACAACAGACTCACACATATATAC
ATGTATATATTTGTAACCTTTGTATATATCTTTTGTTTTTTGACCTTTTTCTCTCTATG
TTTTTCAGCCATACAAAATATGGGATTTTAGCAAGAGAAAAAGTACATCTAAAAAAG
TAGTAATAGGAGGAAGCCAAGATTGGTTGAAACACAGTTATAAACTCTTCAAGGCAATTA
TGAACAGGATTTTCGGATATGGGAACAAAAGAGCCATGATCAGCTCTTACAAGAGTCGA
ATCAGTCCATGAATCAGGCCCAACAATCACTATCGAACAGAATATCCAGTTAGATACTC
AAATCGCCCAGTTAAACTTCCAGCTGCAAAATATTCAAAGAATTTGCAAAGATCAAAACA
ACAAGCAACCCTCGTTAAGAAAACAGGCTTTGAAGATTTTAAATAAACGTAAACAGTTAG
AAAATATGAAGGATTCTTTAGATTCTCAATCCTGGTCCATGACGCAAGCCCAGTTAACAA
ATGATAACTTACAGAACACAATGATCACTATAAACGCACTAAAGCAAAACAAACAATGCCA
TGAAGGCTCAATACGGCAAGATAAATATCGACAACTACAGGACATGCAGGATGAGATGC
TGGATTTAATAGAACAAGGGGATGAGCTGCAAGAAGTCTTGGCAATGAATAATAACAGTG
GCGAGCTCGACGACATTAGTGATGCAGAGCTGGATGCAGAGCTGGATGCTCTGGCACAAG
AGGATTTCACTTTGCCAACCAGCGAAAACCTATTAGGTAACGATATGCCCAGTTACTTAC
TAGGTGCGAATGCGCCACCGGCTTTTATTGATGAAGAGCCAACTTAGATACTGAAGACA
AAAATAAAGCTTTAGAAAGCGCTCAGTA

YDR486C, 262 aa (SEQ ID NO 66)

MGFLAREKVHLKKVVIGGSQDWLKHYSYKLFKAIMNRIFGYGNKKSHDQLLQESNQSMNQA
QQSLSNRISQLDTQIAQLNFQLQNIQKNLQRSNNKQPSLRKQALKILNKRKQLENMKDSL
DSQSWSMTQAQLTNDNLQNTMITINALKQTNAMKAQYVGKINIDKLQDMQDEMLDLIEQG
DELQEVLMNNNSGELDDISDAELDAELDALAQEDFTLPTSENSLGNDMPSYLLGANAPP
AFIDEENLDTEDKNKALESAQ

YDR471W, 1295 bp, exon1: 501-531, intron1: 532-915, exon2:
916-1295 (SEQ ID NO 67)

GGCAAATCAATTAAAATTCCTTTTCTCTCTACCTTTGCTAATATTA AAAAACCATAGTTGT
AAAGGGTACTTAATGCTATATTCCTGTTAAGTTTCCTATTTACCTTGTTTTTCCAATT
CTTACCAATTTGAAGACTATGTTTTTAAACACCCAATCATTTTCCACCCACACATATATT
ACCTTTTTTTTTGGGTGAAGAGAAGTATTTTTGTTTTTTCATGGGAGTGGAAGTCTTTTC
AAAATAATCCGAGCAGTAGTGCTGTCTAGGCGGAGATTATTGAAAGTCGGCATTGGCTG
CAGCTAGCGTTTTGTTTTTGGTACTACCTGTCAAACCCGGCGTCTGCCTAGATTGCGCGG
AGGGTACGTTGAAACTTTTGCCTTTCCACGTCAGTTTATAATATCAAAAGCAGCAATATA

CACATTTAATGGTTTGGCCCTTAGTGACTATTAGGGCGTTTTGGTGAAAAGAAAGAGTCGC
TCAAAGAAATCAATATAACCATGGCTAAATTTTTGAAAGCAGGTAAAGTTGGTACGTAAA
TTTAACAGAGCAAACGCTCTAATTAAGATATCGAATAAAAGGGGACTTTCAGGTGCATAA
GATGGGAAATTGTACAATCTGAGGGACAAACAATATGGAAAGCAGTACATGATTGTATTG
TCATTGTAGGAGGTACCAATTGTGCCAGTAAAAAGAGAGGGCCCGGGGAGCACCACATT
CACGACCAATCGTGTGATCTGCAAAAAGGCACATGGAAATGTAATTTATCAGTGTTC
AACACTGAGTTGAACAGATAGCTATCTAATCAATGTTAACTTTCCAGGGAACAAAAGCT
AAATCCACTTCTCTTTTATTTCAAATATCATTAGAAAATAGAAAAATTTACTAACAAATT
TTCGTATTATCGTAGCTGTCTGTTGTTCTGTTGTTACGCTGGTAAGAAGGTTGTGATCG
TTAAGCCACACGATGAGGGTTCTAAATCTCATCCATTCCGTCACGCTTTGGTTGCCGGTA
TTGAAAGGTACCCATCAAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTGCTAAGAGAA
CTAAATCAAGCCATTTCATCAAAGTCGTCAACTACAACCATTATTGCCAACCAGATACA
CCTTGGATGTTGAAGCTTTCAAGAGCGTTGTATCTACAGAGACTTTTGAACAACCATCCC
AACGTGAAGAAGCCAAGAAGGTTGTAAAGAAGGCATTTGAAGAAAGACATCAAGCTGGTA
AAAACCAATGGTTCTTCTCCAAGTTGAGATTCTAA

YDR471W, 136 aa (SEQ ID NO 68)

MAKFLKAGKVAVVVRGRYAGKKVIVKPHDEGSKSHPFGLVAGIERYPKSVTKKHGAK
KVAKRTKIKPFIKVVNYNHLLPTRYTLDEAFKSVVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YDR499W, 2744 bp, CDS: 501-2744 (SEQ ID NO 69)

TAACAATAGAAAAAATACACACACATTAGATTGGAATTAGAGCTTAAGTGGTACAACT
AGGGCTAATAAAGAGGTAACGGTCCGTTCTCTACTAAGGTTCTGATTGTGTGGCACCAGT
GTTAAGCACTTTTAAGCGGAATAACTCGAGTGGAATTTTATGTTTAGTTAGGTTTTACC
TTGAATTTTTTAAAAAAGAGTCAAGACAGGCTCGCTCTTTCTACTAAATATTAGG
AGCAAAGCAGTAAAAAGTCTCTGAATAAGGATAGTAACCTGTAGTAACCTCAAATTTAT
CTTACAAAGAGCTATTAGTATCTTGGTTCTTCTATTTTCTTCGATTATTGGTGATTTTTTC
CCGCCTCTAGCCAAATCCGAGCGTTCCATCGATTTTTTGGGGAAAACAGCACATGCAATA
AAATAAAAAGCAAACAAATACGCGATAGTGCACGAAACGTC AACACAATCATCAAACCTCT
TTTGTCATATTTCTATTATAGATGAGACGAGAAACGGTGGGTGAATTTTCTTCAGATGACG
ATGATGATATTTCTTTTGGAAATTAGGCACCAGGCCCTCCAAGGTTTACTCAAATACCGCCAT
CATCAGCAGCATTACAAACACAAATTTCCCACTACTTTGGAGGTTACAACGACCACATTA
ACAATAAACAGAGTAAAAATGATAACCAACTGGTTAACCAACTGAATAAAGCTCAAGGTG
AAGCAAGCATGCTTCGTGATAAAATAAATTTTGAACATTGAAAGGGAAAAGGAAAAGA
ATATTCAAGCCGTCAAAGTTAATGAATTGCAAGTCAAGCATCTTCAAGAGTTGGCTAAAT
TAAACAAGAAATTACAGAACTGGAAGATGAGAAGAAGTTCTTACAGATGGAAGCGAGAG
GAAAATCGAAAAGGGAAGTTATTACGAATGTAAAACCAACCGTCAACAACATTTATCAACA
ACACAACACTATAACGCCAGATTCTGTCCTCAGTTGCAATCGAAGCAAAACCTCAATCAC
CACAATCAAAAAACGTAAGATAAGTGATAATTTACTGAAAAAATATGGTTCCCTTAA
ACCCAAATAGGATTATTCCCGATGAAACGAGTTTATTTCTAGAGTCAATATTACTTCATC
AAATAATAGGCGCTGACCTGAGCACAATAGAAATATTAAATAGATTGAAGCTTGACTACA
TCACAGAGTTTAAATTTAAGAATTTCTGTCATTGCTAAAGGAGCCCCATAGGGAAGTCCA
TAGTTTCTCTACTTTTGGCATGTAAAAAGACGTTGACCCTCGACAGGTTTCATAGATACTT
TGCTAGAGGATATAGCTGTTTGTATCAAGGAAATATCAGTTTCATCCAAATGAATCGAAAT
TAGCTGTCCCATTTCTCGTTGCATTGATGTATCAGATTGTACAATTTCTGTCCTAGTGCCA
CTCATAATTTAGCACGTAAGGATTGTTTTCTTTTTTATTTGCGATTAAATAAGAATCTATC
ATCATGTATTGAAAGTACCGATACATGAATCAAATATGAATTTGCATGTAGAACCCTCAGA
TTTTCCAATATGAACTGATAGACTATTTGATAATTTCTGATTCTCTTTGATCTCTTAGAAG
GTATATTAAAGGGTACTGCAGTCGCATCCTAAGCAAACCTTATATGGAATTTTTTGTATGAAA
ATATTCTAAAATCATTTGAATTTGTCTACAACTAGCACTAACCATTTTCATACAAGCCAA
TGGTAAATGTAATATTTAGTGCAGTCGAGGTCGTTAATATTATCACTAGTATAATATTAA
ATATGGACAATTCCTCAGATCTGAAATCCTTGATAAGCGGTAGTTGGTGGAGAGATTGTA
TTACAAGATTATACGCTCTTTTGGAAAAGGAAATTAAGAGTGGCGACGTATATAATGAAA
ATGTGGATACTACAACCTTCATATGTCGAAGTACCATGACTTTTTTGGGTTAATCCGAA
ATATAGGTGATAATGAATTTGGGAGGATTGATATCAAAGCTGATTTATACCTGACCGATTGC
AAAGTGTCCCAAGGGTAATTTCTAAAGAGGATATTGGGATGGATAGCGACAAATTCCTG
CCCTATAATAGGTTACAAGATGGAATAATGGCTTTTGAAGTTAAAAGATGAAGTTTAA
ATATTTTTGAAAAATTTATTAATGATCTATGGAGACGATGCGACCATAGTAAATGGAGAAA
TGCTCATCCACTCCTCTAAATTTCTATCCAGGGAGCAAGCGTTAATGATAGAAAGGTACG

TGGGACAAGACTCCCCGAACCTTGGACCTCAGATGCCATCTTATTGAACATACTTTAACCA
TAATATATAGGCTATGGAAAGACCATTTCAAACAATTGCGTGAAGAACAAATCAAGCAGG
TAGAAAGCCAATTGATTATGTCACTATGGAGGTTTCTCGTATGCCAAACCGAAACTGTGA
CAGCAAACGAAAGAGAAATGAGAGATCATCGACACCTTGTAGATAGTTTGCATGATCTGA
CGATAAAGGATCAAGCCTCTTATTACGAAGATGCCTTTGAGGATTTACCAGAATATATCG
AAGAAGAATTGAAGATGCAATTGAATAAAAAGAACGGGGAGAATAATGCAAGTAAAGTACG
ATGAGAAATTTCAAGAAATGGCAAGAACTATTCTTGAGTCAAAATCATTTCGATCTAACCA
CACTAGAGGAGGCCGATTTCATTATATATCTCAATGGGACTGTAA

YDR499W, 747 aa (SEQ ID NO 70)

MRRETIVGEFSSDDDDILLELGTRPPRFTQIPPSAALQTQIPTTLEVTTTTLNNKQSKN
DNQLVNQLNKAQGEASMLRDKINFLNIEREKEKNIQAVKVNELQVKHLQELAKLKQELQK
LEDEKKFLQMEARGKSKREVITNVKPPSTTLSTNTNTITPDSSSVAIEAKPQSPQSKKRK
ISDNLLKKNMVPPLNPNRIIPDETSLFLESILLHQIIGADLSTIEILNRLKLDYITEFKFK
NFVIAKGAPIGKSIVSLLLRCKKTLTDRFIDTLLEDIAVLIKEISVHPNESKLAVPFLV
ALMYQIVQFRPSATHNLALKDCFLFICDLIRIYHHVLKVPPIHESNMNLHVEPQIFQYELI
DYLIIISYSFDLLEGILRVLQSHPKQTYMEFFDENILKSFEFVYKLALTISYKPMVNVIFS
AVEVNIITSIIILNMDNSSDLKSLISGSWWRDCITRLYALLEKEIKSGDVYNENVDTTTL
HMSKYHDFGLIRNIGDNELGGLISKLIYTDRLQSVPRVISKEDIGMDSDFKFTAPIIGYK
MEKWLKLLKDEVLNIFENLLMIYGGDATIVEGEMLIHSSKFLSREQALMIERYVQDSPN
LDLRCHLIEHTLTIIYRLWKDHFQRLREEQIKQVESQLIMSLWRFLVCQTETVTANEREM
RDHRHLVDSLHDLTIKDQASYEDAFEDLPEYIEEELKMQLNKRTGRIMQVKYDEKFQEM
ARTILESFSFDLTTLEEADSLYISMGL

YDR507C, 3929 bp, CDS: 501-3929 (SEQ ID NO 71)

CTCTTTAAATATTCTATGTACTTTGTGCAAAACATCATTGTCATCACATAAATGCATTCCCT
ACTATTACTAACTTGAACCTTCACTTCACTGGAAGAAGTGGGTATTCAAGGTAAAGAAAT
CATTGTGTTTTGCGCCAAGTTTCGTCTGACAAGAATTTTTTATTATTATTTCCCACTTTTC
ATCGAAGGAAACGCGTCAAATCCATTTCGTACTACGCGCAATCTGCGTTATTTCTTTTTT
CGGCATACCATCGCGAAATATCAACGGCCACACCATAGATTCCCTTTTGATGTTAAATTA
AAGCGATGAATGAAGTGCACACATTTTTTATTCTTCTTGATTTTCTTTCTATTGTTGT
TTTGCTTTCTCTTCTGTGCGACAAGTCTCAACTGTACTCACCATTAGTATTCTCGAAGGC
TTTAGCAGACTTGTGAATAATTAATTGCCCACTTTGATCAAGAAAGATATTTCGCAGCACA
ATACAATAATAACATTCAAATGGCAATCAATGGTAACAGTATTCTGCCATAAAGGATA
ATACCATCGGTCCATGGAACTAGGTGAACTCTCGGTCTAGGGAGCACTGGTAAAGTCC
AGCTTGCTCGTAATGGATCCACAGGACAAGAGGCGGCAGTTAAGGTAATATCAAAGCAG
TATTCAATACCGGTAATGTCAGCGGTACTTCGATTGTTGGCTCCACCACCCAGATGCTC
TACCATATGGTATAGAACGCGAAATAATCATTATGAAGTTGTTAAACCACCCAAATGTGT
TACGTTTATATGATGTCTGGGAAACAAATACAGATTTATACCTTGTTTGAATACGCGG
AGAAAGGTGAGTTGTTCAACTTATTGGTTGAGAGAGGTCTCTGCCAGAGCATGAAGCTA
TCAGGTTTTTTAGACAAATTATTATTGGTGTGTCGTACTGTTCATGCGTTGGGTATTGTCC
ATCGTGATCTAAAACCGGAAATCTATTATTAGATCATAAATATAACATCAAGATTGCAG
ATTTTGGTATGGCTGCTTTGGAACTGAAGGAAAGCTACTGGAGACGTCGTGCGGATCAC
CACATTATGCTGCACCAGAAATGTATCTGGTATACCGTATCAAGGTTTCGCAAGTGATG
TGTGGTTCATGCGGTGTGATCCTATTGCGCCCTTCTTACTGGTTCGGTTACCCTTTGACGAGG
AAGATGGAAATATAAGAACACTATTACTTAAAGTTCAAAAAGGTGAGTTCGAAATGCCTT
CTGATGATGAAATTTGCGGTGAAGCTCAGGATTTGATTAGAAAAATCTTAACCGTTGATC
CTGAAAGAAGAAATCAAGACCAGAGATATACTCAAACATCCGCTATTACAAAAATATCCAA
GTATAAGAGATTCTAAAAGTATTAGAGGCTTACCAAGAGAAGACACATATCTCAGCCCAT
TATCAGAAAGTAATTCTTCTATTGACGCTACGATTTTGCAAAATTTAGTAATATTATGGC
ATGGAAGAGATCCTGAAGGAATTAAGGAAAACTAAGAGAACCTGGCGCTAATGCAGAAA
AGACATTATATGCACTACTGTATAGATTTAAGTGTGACACTCAAAAAGAGCTTATTAAGC
AACAGCAAGTTAAGAAGAGGCGAGTCAATTAGTAGCGTTTTCTGTTTCCCCATCTAAAAAG
TATCGACAACCTCCACAACGCAGAGAAATAGAGAATCTTTAATTAGTGTAACATCTTCTC
GTAAAAAGCCAATATCCTTCAACAAATTCAGTCCCTCCAGTGCCTCCAGCAATCTAA
CTACACCCGGTTCTTCAAAACGCTTTTCAAAAACCTTCTTCTTCAAGAAGAAGAAATATCTA
CAATCGTTAACCAATCTTCTCCAACACCAGCATCACGTAATAAAAGAGCTTCGGTTATAA
ATGTGGAAAAGAAATCAAAAAGAGCCTCTATCTTTTCTACTACCAAGAAGAACAAAGAT
CTTCTAGATCTATCAAGAGAATGTCATTGATACCAAGCATGAAACGTGAATCGGTGACAA
CAAAATTAATGTCAACATATGCGAAATTGGCAGAGGATGACGATTGGGAATACATTGAGA

AGGAAACAAAGAGAACGAGCTCAAATTTTGCAACTTTGATAGATGAAATTTTGGAGTACG
AAAAGTACGAACAAATAAGGAAAGAGAAGGAAGAGCTAGAACGTAAAGTGAGAGAAGCAA
AAGCACGTGAAGAGCTGGAACGTAGAAGACGTAAACAAGAAGAAAAAGAACGTGCAAGAA
AATTACTAGAAAAGGAAGATCTGAAAAGAAAACAGGAGGAAGCTCAAGAAGCAAATTTGAAA
TTGATATAAGTGATCTAGAGCAAGAGCTGTCCAAACACAAAGAGGAAAAACTGGATGGTA
ATATTAGATCTATCTCTGCTCCTATGGAATGAAGAGAAAAATATCAATCATTTGGAGG
TTGATATTGACAATATTCTCCGTCGCCGCAACTTTTCTTTACAAACTAGACCTGTGTCAA

GGCTTGATCCGGGTATAATGTTCTCCAGTCCAAGTGAAGTAAGTCCAGTGGAAACAA
AGAGAACAGAAAATGAAAGACTTACAACAGAAAAGAAAATTTTAGAACTATCAGAAGAT
CAAAATTTCTGGGTTTCATCATTTAATATCGATAAAGAGTTGAAATTTGTCTAAAATGGAAT
ATCCAAGTATAATTGCACCACAAAGATTGTGAGGAGCGAGTGGTGTGAGATTCTAATG
ATGGATATGAATCTTTGATCCTCCCGAAGGATGGGAATGGCGTATCTCAATTAAGGATA
GTACCGCAACAACCTGCTCCCGTCTCTGATGGTAGGTTGAGGAAGATCTCTGAAATTAGAG
TACCACAATTTACTAGAAAATCAAGGCATTTTAGTGAGTCCAATAAAAGGCTATCTGTCC
TGTCGATGTACTCTACCAAGGAGTCGTTTACCAACTTGGTTGATATTTTGAAGAACGGTA
ACCTTGATGTCAATAACCAACAAAGCCAAAGAATTCCAACACCAAGAAGTGCGGATGATT
CAGAATTTCTTTTTGAACTGTCAACGAAGAAGCTGAATATACAGGAAATAGTTTCAAGC
ATGAGAGATTTGATCGATGTCGGTGATTCCTACTATCAAAGACAAATCCGCGTTAAAGCTGA
ACTTTGAGATCGTTTAAATGGATCGAAGCAAGCGAAACAAACTGATAACTTACATCTTC
CGATCCTTCTCCGCTTAATGGTGACAATGAATTGCGTAAACAGAATAGCCAAGAGGGTG
ACCAGGCACATCCAAAGATTAAATCGATGATACCAGAATCAGGCTCTTCTTCACATACTG
AAAAGGAAGAAGAAAATGAGGAAAAGGAAGAGAAAAAGCCAGAACAACACAAACAAGAAG
AGGATCAAGAAAAAGAGAGAAAGTAGTAGATGATATGGAGCCACCATTGAACAAATCTG
TGCAAAAAATTAGGGAAGAAAATGCTGGCTCGCAGGCAAAGGATCATTCAAAGATCACT
TAAAAGAGCATAAGCAGGATAAAAAATACAGCAATTGGAAATGGTTCTCTTTAGAAAAAT
TCTCAAAATCTTCGGACAAAACAATGGAATTGTATGCCAAGATTTCTGCAAAACAATTGT
TTAATGGTTTAGAGAAGCTGTTGCGTGTTGGACTCAGTATGGTTTAAAAAATATAAAAT
CGCACCCCAACAATCTGACCTTAACGGGTAAACTATCGAGTGATAATATATTCTCACTAC
GTTCAACACTCTTTGAGGTTAATATTTATCCGAGAGGTAAGATGAGCGTTGTGCAGTTCA
AGAAAGTTTCTGGTTCATTCAAAGCTGTCAAAAAGTTGGTCAATGAAGTTGAGAACGTCC
TGAATAAGGAAGGCGTTCTACAAAAATAG

YDR507C, 1142 aa (SEQ ID NO 72)

MAINGNSIPAIDNTIGPWKLGETLGLGSTGKVQLARNGSTGQEAHVVISKAVFNTGNV
SGTSIVGSTTPDALPYGIEREIIIMKLLNHPNVLRLYDVWETNTDLYLVLEYAEKGELFN
LLSERGPLPEHEAIRFFRQIIIGVSYCHALGIVHRDLKPENLLLDHKYNIKIADFGMAAL
ETEGKLLLESCGSPHYAAPEIVSGIPYQGFASDVWSCGVILFALLTGRLPFDEEDGNIRT
LLLKVQKGEFEMPSDDEISREAQDLIRKILTVDPERRIKTRDILKHPLLOKYPISIRDSKS
IRGLPREDTYLTPLSESNSSIDATILQNLVILWHGRDPEGIKEKLREPGANAECTLYALL
YRFKCDTQKELIKQQQVKKRQSISSVSVSPSKKVSTTPQRRRNRESLISVTSRKKPISE
NKFTASSASSNLTTPGSSKRLSKNFSKKKLSTIVNQSSPTPASRNKRASVINVEKNQK
RASIFSTTKNKRSSRSIKRMSLIPSMKRESVTTKLMSTYAKLAEDDDWEYIEKETKRTS
SNFATLIDEIFEYEKYEQIRKEKEELERKVKREAKAREELERRRRKQEEKERARKLLEKED
LKRKQEEELKKQIEIDISDLEQELSKHKEEKLDGNIRISAPMENEKNINHLEVDIDNIL
RRRNFSLQTRPVSRDLPGIMFSSPTEEVSPVEPKRTENERLTTEKKILETIRRSKFLGSS
FNIDKELKLSKMEYPSIIAPQRLSEERVVSDSNDGYESLILPKDNGVSQLKDSTATTAP
VSDGRLRKISEIRVPQFTRKSRHFSSEKRLSVLSMYSTKESFTNLVDILKNGNLVDVNNQ
QSQRIPTPRSADDSEFLFETVNEEAETGNSNDRLYDVGDSTIKDKSALKLNFADRFN
GSNEAKQTDNLHLPLPLNGDNELRKQNSQEGDQAHPKIKSMIPESGSSSHTKEEENE
EKEKKPEQHKQEEDEKREKVVDDMEPLNKSQKIREKNAGSQAKDHSKDLKHEKQD
KNTAIGNGSFFRKFSKSSDKTMELYAKISAKQLFNGLEKLLRGWTQYGLKNIKSHPNLTL
LTGKLSSDNIFSLRSTLFEVNIYPRGKMSVVQFKVSGSFKAVKKLVNEVENVLNKEGVL
QK

YDR515W, 1844 bp, CDS: 501-1844 (SEQ ID NO 73)

GAGTTGAATCTATGCGTAACCATTTTGACTACCGCTTCGTATGCTTTCTTGCACTTTGTG
GAGCTACTCATACAATAGCTTATAATCTGTGTAGTCAAATATATACTAGGCAAATTAAT
AGTAAATGCAGTATTCATATGTCTCAAACCGTTTTTTGAGTATGTTATTGATCCATCG
AATCAAAATTTTACCGCCAAGAGAAAAAGATCTTACTATTTTGTGCTTATGAAAAAA

TTAGTAAAAGTAAAGCTGGAAGCACATACAAGCGCAGCTGAATCACAAAGGAAAAATTGGC
ACATCCTTGGTTGACACTGTCTATTTATTAAAAAGGTTTAAAAAGTAGTGTTCAGCAGT
TCTATCATATTTTTTTTATTTAAAAAAAATACTGAGAGGAAGCGTATTGTTAAGACACAA
TTTAGGGTGGCGTTAAATAAACGAGAGAGCCAAAAATATAACCAAGATAAAGAAAAATCA
ATCATAAAGTGAATTCAAAAATGTCATCGCAAAACCTCAATGATAATCAAAAAATACAT
CCTCAGCAGCTGAAGATAAGAAGAAACAACTTCATCCTTAAAGTTGGCACCAATACCAA

CCACATCGCCATGGAATCATCTTCGCCAGATAGCAATACAGTAATTCCTGTAGAGGAAC
TAAGAGATATATCAAAGACTGCAAAGCCAAAGTAAAAATGGTTTCGGGGTCAATTAAATTAA
CAAGCAATACCAAATGGACTCCAATTACGCCGTCTGTTATAATCTCAGGTTCCAAGGACA
CAAATTCAAAGTCAGGAAAGAACTCTAAAAATTCTAAGACTAATAAAAAATGAAAAAGC
GTGGCAAATATAATAACGATATCAATAAAAAGGACTTTAACGGTCAAACCAACAGTACAT
CGGAAATAAGTAACGTTTCCAATCTTGAATCCAAACCTTTAGATGCTAACGCTAAAGTAA
ACATACATTCAAGCTCAGGAGCAACTGCCAATGGGAATATAAAGAGGATAACAAACAACA
CAATTCCAACCAACGGTAGACAATCAAGAAATTATCAAAACAGGAATGGCAAAACAAGAT
ACAACAACAATAGTAGACACAGTCAGGCGGCTAATAATGCCATCTCCTTCCCAATAATT
ATCAGGCTAGACCTGAATATATTCCCAATGCCAGCCACTGGTTGAACAACAATTCAAGAA
ATAGCTATAAACAACCTGTCATACTTCCGTC AACAGCAGTATTATAATAACATCAACTATC
AACAACAATTGCAACACCATATTATTACTCAATGGAACCTATTTTTAAATCTATCGAAA
GTATCAAAAACCAAATTGAATTCATTTTAGTGAAGAGAACTTGAAAACAGATGAATTTT
TAAGATCTAAATTCAAAAAAGCCAATGACGGATTATCCCCATGAGTTTGATAGGGAAAT
TTTACCGTATGGTTAATTTATCTCTTGGTGGAGACCCAAATTTAATTTTGGCATCTATGA
GAGAAGTTTTACAACATAAAGAAACAAACCATTGGAAATTGCCCTTGGAAGCATAGAAG
GTGCTCAGAAGAACATGGCAGATGATTTCAATCCATTGGAAAACCTATTTTATTAGGCGCG
AAAATTGGGCTGAATACGCTATGGAAAGTAATTTTGATGAAAATGATGACGAAACTGAAA
AATACAACATTGAGAACTATTGGGACCGAAGCATTAGACAATTATTCTTATATGGGCT
ATCCAAACTTCTTTCCAGTAATGAAAATGGGAAAAGAGTCAGAGCTATGACCAAGGTG
AAATTAGCAGGCAGTTTGAACAAAACCTTACAAATAAATGATTAA

YDR515W, 447 aa (SEQ ID NO 74)

MSSQNLDNPNKNTSSAAEDKKKQTSSLKLAPIPTTSPWKSSSPDSNTVIPVEELRDISKT
AKPSQNLNGSGSIKLTSTNTKWPITPSVIIISGSKDTNSKSGKNSKNSKTNKKMKRKYNNND
INKKDFNGQTNSTSEISNVSNLESKPLDANAKVNIHSSSGATANGNIKRITNNNNSTNGR
QSRNYQNRNGKTRYNNNSRHSQAANNAISFPNNYQARPEYIPNASHWLNNSNRNSYKQLS
YFRQQYYNNINYYQQQLQTPYYSMEPIFKSIESIKNQIEFYFSEENLKTDEFLRSKFKK
ANDGFIPMSLIGKFYRMVNLSLGGDPNLILASMREVLQHKETNHLEIALGSIEGAQKNMA
DDFNPLENYFIRRENWAEYAMESNFDENDDETEKYNIEKLLGPNLDLDNYSYMGYPNFFPS
NENGKKSQSYDQGEISRQFEQNLQIND

YDR518W, 2054 bp, CDS: 501-2054 (SEQ ID NO 75)

GCAGCAGGGGCAAGATGACAACCCCTGTTCCCTGTTCCCTGTTCCAGTAGAATCTGAGACGGC
TTTTGTGCCATCAGCATTACAGCACCACCGGTGCCAACAAAGAAGAAATCAAAAAATAA
AAAGGGTACCCAGCCATTGGCAATGGATGACTATTTTAATGAAGGCAGAGATAAGTCATC
TACCGCTGCGAAGTCAGCAGAATCTGACATCTCTCGCCCCACCACCACAAAAACAGTCATC
CTCTGATTAACCTTTCCTGGTTAGTCTTTTGGTTTTGTTTCATAGCAAAATTAATATATA
TATATAAGCTTGCTTTCCCTTCAAAACACGTAAACGATAGTTGGCAATGTACGAAAAGTA
CCGAGACTTTTTTTTCAAAGGCACGCGTGTCTTTTTTTGTTAAGACAATAGATATTTTAGC
ATTACAGAAAGTTTCAATTTCCAAGACTTGACGTTTCAATTATATGGCAATCTCCCAACAA
GCACCCGCTCATATAATACCATGCAAGTGACCACAAGATTTATATCTGCGATAGTCTCGT
TTTGCCCTGTTTGCTTCTTTACGTTGGCTGAAAACAGCGCAAGAGCTACGCCGGGATCAG
ATTTACTCGTTCTAACAGAGAAGAAATTTAAATCATTTCATCGAATCTCATCCGTTAGTCC
TCGTCGAGTTTTTTTGCTCCATGGTGTGTCATTCTCAGATCTTACGCCCTCACTTAGAAG
AGGCCGCCTCTATTTTAAAGGAGCATAACGTCCAGTTGTTCAAATTGATTGTGAGGCTA
ACAGTATGGTTTGCCTGCAACAACTATAAATACCTACCCAACCTTGAAAATCTTTAAAA
ATGGTCGTATTTTTGATGGTCAAGTCTATCGCGGTGTCAAGATCACCGATGAAATCACTC
AGTACATTACAGCTATACGAGGCTTCTGTCAATTTATTTAAATTCCGAAGATGAAATCC
AACCATACTTGAAAATGCAACTTTACCAGTAGTAATAAACAGAGGCTTGACAGGCTTGA
ATGAAACGTATCAAGAAGTCGCACTGGACCTTGCTGAGGATTACGTCTTTTTATCCCTTC
TAGATTACAGAAGATAAGTCATTATCAATCCACTTGCCAAACACTACAGAACCAATTCTGT
TTGATGGAATGTAGACTCTTTGGTCGGAAATTCGTTGCTCTAACTCAGTGGTTAAAG

TGGTAATTTTACCTTACTTTACCGACATCGAACCTGATCTCTTCCCCAAGTACATTTCTA
GCAATTTGCCGTTGGCTTACTTCTTTTATACTTCTGAGGAAGAATTGGAAGATTACACTG
ATCTTTTTCACGCAGTTAGGTAAGGAAAATCGTGGCCAAATAAATTTTCATTGCATTAACT
CTACAATGTTCCACACACCGTTAGATTCTTAAATATGAGAGAACAGTTCCCATTTATTG
CTATCCATAATATGATCAATAATCTGAAATATGGTTTACCACAACCTACCAGAAGAAGAGT
ACGCGAAATTAGAAAAACCACAACCACTAGACAGAGATATGATCGTTTCAGTTGGTAAAG
ATTACCGTGAAGGTACTGCCAAGCCAATTGTTAAGTCAGAAGAGATTCCAAAAGAACAAA
AGTCCAATGTTTATAAAATAGTTGGGAAGACACATGACGACATTGTTTCATGATGATGACA
AGGATGTCCTTGTCAAATATTACGCGACATGGTGTATTTCATAGTAAAAGGTTTGGCGCTA
TTTACGAAGAAATTGCAAATGTCTTAGCATCTGATGAATCTGTTTCGCGATAAAATCTTGA
TCGCCGAAGTAGATTCAGGGGCAAATGATATCTTAAGTTTCTCTGTGACAGGATATCCAA
CCATTGCTTTGTATCCTGCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAA
ATTTGGAAGATGTTTTCGAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGG
CAATTTATGATAAATTGCACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTAC
ATGATGAATTATAA

YDR518W, 517 aa (SEQ ID NO 76)

MQVTRFISAIVSFCLFASFTLAENSARATPGSDLLVLTEKKFKSFIESHPLVLVEFFAP
WCLHSQILRPHLEEAASILKEHNPVVQIDCEANSMVCLQQTINTYPTLKIFKNGRIFDG
QVYRGVKITDEITQYMIQLYEASVIYLNSEDEIQPYLENATLPVVINRGLTGLNETYQEV
ALDLAEDYVFLSLDSEDKSLSIHLNPTTEPILFDGNVDSL VGNSVALTQWLKVILPYF
TDIEPDLFPKYISSNLPLAYFFYTSEELEDYTDLFTQLGKENRGQINFIALNSTMFPHH
VRFLNMREQPLFAIHNMINNLKYGLPQLPEEEYAKLEKQPLDRDMIVQLVKDYREGTA
KPIVKSEEIPKEQKSNVYKIVGKTHDDIVHDDDKDVLVKYYATWCIIHSKRFAPIYEEIAN
VLASDESVRDKILIAEVDSGANDILSFPVTGYPTIALYPAGNNSKPIIFNKIRNLEDVFE
FIKESGTHHIDGQAIYDKLHQAKDSEVSTEDTVHDEL

YDR519W, 908 bp, CDS: 501-908 (SEQ ID NO 77)

GGGGCAAATGATATCTTAAGTTTTCTGTGACAGGATATCCAACCATTGCTTTGTATCCT
GCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAAATTTGGAAGATGTTTTT
GAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGGCAATTTATGATAAATTG
CACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTACATGATGAATTATAATCA
ATAAATAAGCATATATAATGCACATTTTTTAACATCTGATTACTCGCATCGTTTCTGGAA
GAAATAGCTAATATTCGTTATTTATGGCATCACGATTATTCTCACCAGTTACCCGTTTA
TGCTCTTGAAGAGATTTAGCATTACTGCCAGCGCATCTTCAAATACAGGTTTATATGAGA
CCCATTACTATAACCCTAAGAAGAGAAAAAGGAGTGCTTTTCGTTTTCAATCACATTCTAG
TTTACAGTAATTGAGTCTCGATGATGTTTAATATTTACCTTTTCGTCACTTTTTTTTCCA
CCATTCTTGCAGGTTCCCTGTGAGATTGGGAAATCGGTATTATCAAGAGAATACCGGTAG
AAGATTGCTTAATTAAGGCAATGCCAGGTGATAAAGTTAAGGTTTATTATACAGGATCTT
TATTAGAATCGGGAATGTATTTGACTCAAGTTATTCAAGAGGCTCTCCTATCGCTTTTG
AACTTGGCGTTGGCAGAGTAATTAAAGGTTGGGATCAAGGTGTTGCCGGCATGTGCGTTG
GCGAAAAAGAAAGCTGCAAATTTCAAGTTCTTTGGCCTACGGAGAAAGAGGTGTCCAG
GCGTCATTCTCCAAGTGCTGATTTGGTGTGTTGATGTGCAATTGGTAGACGTGAAATCAG
CCGCCTAG

YDR519W, 136 aa (SEQ ID NO 78)

MMFNIYLFVTFSTILAGSLSDLEIGIIKRI PVEDCLIKAMPGDKVKVHYTGSLLES GTV
FDSSYSRGSPIAFELGVGRVIKGDQGVAGMCVGEKRKLQIPSSLAYGERGVPGVIPP SA
DLVFDVELVDVKSAA

YER102W, 1103 bp, CDS: 501-1103 (SEQ ID NO 79)

CGAGCTTGCCAGCATTCCAATGCCATCGTATTGTACTCAATGGTGAAACTTACCACCAT
ATTGTTAAAAGCTATTATTTATGATTTTTACTTACCAAACATTGAAAGGAGACTGAACAC
ACCACGATAAAACGTATGTTCTGATACCCAGCAAATGAGAAAGTAGAAGGAGAAACCTAA
AAACCTGTGGCGGTCAAGACTGCTAGCAAGATGGATATTTAGATCATAAATTCTAACGCA
TGCATCCTGAGCAATGAAATCATGCAACCTAACATTTGAGGTTAATATATGAGAAATTAAC
TAGCGTTGAGGAGGTACTGCAATTTAAAGACCGAAGAATTATCGATGCAAGGAAAAATG
GGTCTAGGATGAATACGAGCAATTGAAATACATTTGGAATACCTTGTGAAAATATCACAT
ACTTTCGCCTTCTATCTCGATGCGTTATTACAAGAAAATAGTTTTACTAACAAATTAACA
AAAATTAATAAGTGTAAAAATGGGTATTTCTCGTGATTCTCGTCACAAAAGATCAGCCA

CTGGTGCTAAACGTGCTCAATTCAGAAAGAAGAGAAAGTTTGAATTAGGTGCTCAACCAG
CCAACACAAAAATTGGTGCTAAGAGAATCCACTCTGTCAGAACTAGAGGTGGTAACAAGA
AATACAGAGCTCTAAGAATTGAAACCGGTAACCTTTTCTTGGGCTTCTGAAGGTATCTCCA
AGAAGACCAGAATTGCTGGTGTTGTTTACCATCCATCCAACAATGAATTGGTTAGAACTA
ACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTGAGACAATGGTTTCG
AAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAACGTCAAGGAAGAAGAACTGTTG
CCAAGACGAAGAACGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAAT
CTTCCGTTGAATCTCAATTCAGCGCCGGTAGATTATACGCTTGATCTCTTCCAGACGAG
GTCAATCCGGTAGATGTGATGGTTACATCTTGAAGGTGAAGAATTAGCTTTCTACCTAA
GAAGATTGACTGCTAAGAAATAG

YER102W, 200 aa (SEQ ID NO 80)

MGISRDSRHKRSATGAKRAQFRKKRKFFELGRQPANTKIGAKRIHSVRTRGGNKKYRALRI
ETGNFSWASEGISKKTRIAGVVYHPSNNELVRTNTLTAAIVQIDATPFRQWFEAHYQOT
LGKKKNVKEETVAKSKNAERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCD
GYILEGEELAFYLRRLTAKK

YER153C, 1265 bp, CDS: 501-1265 (SEQ ID NO 81)

ACCCTATATGGGAGGACAACTCGCCCACTGTTTGGGTCGTGTTAGCGATAAGGTCCGAAG
TAGAAGCGGAAAGAGAAGGAGCTGAAGAGGTTAATTCATCGATGGAAGGCAACTGGGTTT
GGATTTCCGAGACATCGTTGGCATTGTTGGGCCCGTCGAATTAAATCTTTTGGCCTGAAAAG
AGATCCATGACGGATGGGGCCGGGGCAATACTATGGTTTCGAGCGGTGGCCAGTCTGGAAG
AGGCAGCAAACCTTGACGTGACGAGTCGAGAGGTGAGTTTGAACATCGTCGGGGAGGTTA
TTCTGTGGCTCCGCTTGTACGTGAACAGATACGTATAGAGGGCGAGCCACTGGTTAAATT
TTTCACTGGCTCGGATTACTTCCGTACTGCTGGCTAAAATCGAAATCTCGGCCTGCTGAGA
GTGTTTTTGAGCAATCAAGGGAACATCTGAACGTGGAAGAGCAGACGAGGCATTAGCTCTGA
ACATAAGAACGGAACACGTGATGTTGACTATCACGAAAAGACTGGTGACCACCGATGTGC
GGTCGCGAATACTGTTAAGCAGTTTAAACGGGAAAATGTCCGATGCACTGGCGCTGCTGC
GTCAGCAGCAGCAGACCAGCGTGGATGTGGAGCTGCTGCACACGATGCTAGCGCGAGCCG
CTGCGCTTGCCCATGCCGACACTATAGCATACATGTGGTATCAGCATGTGATGCCACGCC
GGTTCTCCAGTAGAGGGCCGCTGCTATGTGAAATGGCTGGCGTAGCATTGTACAGGACA
GGCTCTCTTACCCTCGCGCAGTTCCCTCCAGCACTACCAGGCGATGAATCGCGATCGTCGCA
CCAGCCCAGAAGATGAACTGATTGAGTATGAGCTTAGACGGATTAAAGTCGAAGCGTTTG
CGCGTGGCACAATGCACTCCACGGCGCTCAGGGAAGGTGGAAGGTATTCTTGACAGGAGA
TGGATACGCTACCAGGGCAGCCGCCATTAAAGGCTGCGCGACTTCCCGCAAATGACCAAGG
CTATGGGCATAGCATTGATGCAGCAAGATGAGCAAGCAGCTGCCCTGGCGTTGTTTGGAC
GACAGCCCCTAGTGATAAAGAACGAATGGTCACTACCGCTACTACTGGCTGGTGTCTTTT
GGCATGTTCCCGGCCAGCGCAGGCGCGAGCTGTGCTGGCGGAGTTCCGTCAAAGTTATC
GCGGGCTGCCGCTGCTGGATGCCGAAGTAGTGATAAAGAGAAGAGGATTGTGAATCAACA
CATAA

YER153C, 254 aa (SEQ ID NO 82)

MLTITKRLVTTDVRSRILLSSLNKMSDALALLRQQQTSVDVELLHTMLARAAALAHAD
TIAYMWYQHVMPPRLPVEGRLLCEMAGVALYQDRFLPAQFLQHYQAMNRDRRTSPEDEL
IEYELRRIKVEAFARGTMHSTALREKWKVFLQEMDTLPGQPPLRLRDFPQMTKAMGIALM
QQDEQAAALALFGRQPLVIKNEWSLPLLAGVLVHVPQAPARRVLAEFRQSYRGLPLLD
AELVIKRRGFEINT

YFL014W, 830 bp, CDS: 501-830 (SEQ ID NO 83)

GGACTAGAAGCCAAAAGCCAGAGGCGGTAAAAATAGCAAGACTAGAATATTGCTGGCATC
TGTTAAGGGGATATGTTGCAACTTGCAGGGGGCGGCACAAAATAACATAGAAACGTAGTA
AAGAGGGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAAACCCATTGACGTAGAAAT
TGAAAGAAGGAAAGGTATACGCAAGCATTAAATACAACCCACAAACACAGACCAGAAGCAC
TCTAGACGGAGAGTAAC TAGATCTACAGCCCCTGGAATTCGTTTGGTCAACTTTGAGGT
TCCGGTCGTCCTCCCTCTTGTCTGAAAGGTCTTTCTCTAAATCTATATTAAACGTATAA
ATAGGACGGTGAAATTGCGTTCTACTTCTCAATTGCGTTTGTATCTTATTTAATCTCTC
TAATATATAGAAAAAAAACCATCTGATTATTCGATAATCTCAAACAAACAACCTCAAAC
AAAAAAACTAAATACAACAATGTCTGACGCAGGTAGAAAAGGATTCCGGTGAAAAGCTT
CTGAAGCTTTGAAGCCAGACTCTCAAAGTCAATACGCTGAACAAGGTAAGGAATACATCA
CTGACAAGGCCGACAAGGTGCTGGTAAGGTTCAACCAGAAGACAAACAGGGTGTCTTCC

AAGGTGTCCACGACTCTGCCGAAAAAGGCAAGGATAACGCTGAAGGTCAAGGTGAATCTT
TGGCAGACCAAGCTAGAGATTACATGGGAGCCGCCAAGTCCAAGTTGAACGATGCCGTCG
AATATGTTTCCGGTCGTGTCCACGGTGAAGAAGACCCAACCAAGAAGTAA

YFL014W, 109 aa (SEQ ID NO 84)

MSDAGRKGFGKEKASEALKPDSQKSYAEQKEYITDKADKVAGKVQPEDNKGVFQGVHDSA
EKGKDNAEGQGESLADQARDYMGAAKSKLNDAVEYVSGRVHGEEDPTKK

YFL015C, 995 bp, CDS: 501-995 (SEQ ID NO 85)

GACCTTCAGCGTTATCCTTGCCCTTTTCGGCAGAGTCGTGGACACCTTGGAAGACACCCCT
TGTGTGCTTCTGGTTGAACCTTACCAGCGACCTTGTCCGCTTGTGTCAGTGATGTATTCCT
TACCTTGTTCAGCGTATGACTTTTGAGAGTCTGGCTTCAAAGCTTCAGAAGCTTTTTCAC
CGAATCCTTTTCTACCTGCGTCAGACATTGTTGTATTTAGTTTTTTTTGTTTGTAGTTGT
TTGTTTGTAGATTATCGAATAATCAGATGGTTTTTTTTTCTATATATTAGAGAGAGATTAA
ATAAGATCAAACGCAATTGAGGAAGTAGAACGCAATTCACCGTCTATTTATACGTTTTA
ATATAGATTTAGAGAAAAGACCTTTCAGATCAAGAGGGGGACGACCGGAACCTCAAAGTTG
ACCAAACGATTTTCCAGGGGCTGTAGATCTAGTTACTCTCCGTCTAGAGTGCTTCTGGTC
TGTGTTTGTGGGTTGTATTAATGCTTGGCTATACCTTTCCTTCTTTCAATTTCTACGTCA
ATGGGTTTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
ATGTTATTTTGTGCCGCCCCCTGCAAGTTGCAACATATCCCCTTAACAGATGCCAGCAAT
ATTCTAGTCTTGCTATTTTACCGCCTCTGGCTTTTGGCTTCTAGTCTTGTCCCAAGAG
CCAAGGGCCCGTCAACACGTCGTCAATTGCTACCGCCAGCTGGCACCCACACATCACCGAC
CCTTTTTTTCCATTTTCCGCTGGGCGGTAGTGGGATCCGCCCGCTCCCGGAGATTTTCA
CTTGGATTTGCGCGTCCCCCTTTTTTCTTCTTCTTCTGACTCCCCCTACCTTCTCCCCT
TTTCTGTGTATCAAGAGGAAAAGAAGGAGAAAAGGAGAACTCCGAAAAATACCGAACAAG
AGGGTAACAGAATGTGCATTTGGATGAGCGGGTAA

YFL015C, 164 aa (SEQ ID NO 86)

MLAYTFPSFNFYVNGFFSFLFLFLFLFPSLLRFYVILCRPLQVATYPLNRCQQYSSLAIF
TASGFWLLVLVPRAKGPSTRRHRYQLAPTHRPFFSIFGWAVSGIRPLPEIFTWICASP
FFLHSLTPPTFSHFVSFYQEEKKEKRRTPKNTEQEGNRMCIWMSG

YFR022W, 2702 bp, CDS: 501-2702 (SEQ ID NO 87)

CTGCCTTCCGTACGTCAACGCATACACAATATAGTTTATATAAACTCCTGCGTATAAT
CTATCCTTTTGCATAATATTTTCGTCAACCATATCTTGTGCGGTGTTTTTATTTAAAC
AATAGAACTCGCCTAAAGGGGAAATTTTCGATATAAAAATTCAAAAAAATGGCTTTCATG
GATCGAGTATTTGTTTGTGCAAAAAGGATCACTGGAGTGACGTTACTACGCTACGAAGCC
TCCTTCCGGCTTAGCCCTGTTGATTACGAATTTGGATCAGTTGGTATTTGATTCTCCTCGGA
AGAGTTAACTTCACGCGGGTAAATCACTTGTGATGCGGTATATTCTCTATACGGCTAATA
GATGAATCAGGGTGTTTTAAAGTGCGTATAAACCTTTTGCTATTTTCGTTTATATAATT
GGCGTTGATAAAGAGCCAATATCTATTGTTGCTACATAGAGGCAGCTCTCTTAGCAAAAT
AAAAATACAAAAGTTTCGACATGGGCTTCAGTAGCGGTAAATCAACTAAGAAAAAGCCTC
TGCTTTTTCGATATCAGACTTAAAAATGTTGACAACGATGTAATACTCCTCAAAGGTCTC
CAAACGAGGCCCCCTCGGTGCTTTTATCTGGTTGCATCGTTTTATCGATTAAACGAACCCA
TGCAGATCAAAAGCATATCATTGAGACTTTATGGGAAGATACAAATAGACGTACCATTAG
AGAGGCCCCAGGACGCTAGTTCTTCGTGCTTGTCTTCATCGCCGCCAAAGATCAGAAAGT
ACAACAAAGTTTTTATAATTACGCATGGGATAATGTTAACTCAAGGAGTATCTGAGTG
GTTTAAAGAGGGCAATCTGGCCTTGGCGGCAGTAGCTCATCAAGTAATATCTTGGGCACTC
GCCAAAGAGCTCAGTCCACAAGTTTCTTGAAGTCTTTAAAGGGGTCTCCTCACCTCTT
CATGTACTTTAGATAAGGGCAACTACGATTTTCCCTTTAGTGCTATTTTGCCTGGTTCGT
TACCAGAGAGCGTAGAATCTTTGCCAAATTGCTTCGTGACATATAGCATGGAATCCGTTA
TTGAACGCAGCAAAAATTATAGTGATTTGATCTGTAGGAAAAATATTAGAGTTCTGAGAA
CCATTTTACCCGCAGCAGTGGAGTTATCAGAAACTGTTTGTGTAGATAACTCATGGCCCCG
ACAAAGTGGATTATTCTATTTTCAGTACCCAAACAAAGCCGTAGCTATTGGTTTCAGCCACC
CTATAAATATTTCCATTGTACCTCTTTCGAAAGGTTTGAAATTGGGCTCAATCAAAGTCG
TATTATTTGAGAATTATCAATATTGTGACCCCTTCCCTCCAGTAATTTCTGAAAATAGGC
AAGTGACAGAACTAAATCTTGAAGATCCCTTGAACGAGTCATCTGGAGAATTTAATGGTA
ATGGTTGCTTTGTAAATAACCCCTTTTTTCAGCCTGATCATTTCATCCAAGACAAGTGGG

AGATTGATACCATCCTGCAAATCCCGAACAGCTTATCAAACGTGTGTGCAAGATTGTGATG
TCCGCTCTAACATTAAGGTTCCGCATAAGCTCAAATTTTTTCATCATCCTAATTAACCCAG
ATGGTCATAAATCTGAGTTAAGAGCGTCTTACCGATTCAAATTTTTTATTTACCATTG
TGGCACTTTCAATAAAACCATTGTTCATCCTCGAATTTGTATTTCGCTTTTTTAGCACCCTA
ACCAGAAAGACGAAAACATCACAAGAAGAGGAAGAGGAATATCTGTTTTCTAGATCAG
CATCAGTCACAGGGTTGGAATTATTAGCGGATATGCGTAGCGGTGGCTCTGTTCCCTACCA
TTTCAGACTTGATGACGCCCCCAAATTATGAAATGCACGTATATGATCGTCTTTATAGCG
GTTCTTTCACTCGCACGGCTGTGGAACGTCTGGAACATGTACTCCTTTGGGAAGCGAAT
GTTGCGACTGTGAGGATCAGCAACAGGATTTAGAAGATTTACGTATACGGTTGACAAAAA
TTAGAAATCAACGTGACAATCTAGGGCTACCACCGTCTGCCTCGTCTGCTGCCGCTTCCA
GATCGCTATCTCCATTACTAAACGTTCCAGCACCAGAGGATGGCACGGAGAGAATCTTAC
CTCAGAGTGCTCTTGGTCCCAATAGTGGCTCTGTGCCAGGAGTACATAGTAACGTATCAC
CTGTTTTTCACTTTCAAGATCCCCAGCCCCAAGCGTGTGAGCCCATGAAGTGTTACCAGTGC
CCTCGGGCTTAAATTATCCAGAGACTCAAAACCTGAACAAGGTTCCATCGTATGGCAAGG
CAATGAAATATGATATCATTGGTGAGGACCTTCTCCTTCCCTACCCTTGTGCGATACAAA
ATGTGCAACCAAGAAAACCCAGTAGGGTACATTCCAGGAACCTTTCGACAACATTGTTCAT
CTTCTATACCAACTAGCTTTTATTCTCTAGTTTTATGAGTAGCACTGCTTCCCTATTT
CCATAATTAAATGGCTCTAGAAGTAGTTCTAGTGGGGTATCTCTTAATACACTTAATGAGT
TAACCTTCGAAAACCTTCGAATAACCCATCCAGTAATAGTATGAAAAGGTCACCAACAAGAC
GGAGGGCTACTTCTTTAGCTGGGTTTATGGGAGGTTTTCTATCAAAGGGTAACAAACGAT
AG

YFR022W, 733 aa (SEQ ID NO 88)

MGFSSGKSTKKKPLLFDIRLKNVDNDVILLKGPPEAPSULLSGCIVLSINEPMQIKSIS
LRLYGKIQIDVPLERPQDASSSSLSPPKIRKYNKVFYNYAWDNVNLKEYLSGLRGQSG
LAGSSSSSNILGTRQRAQSTSSLKSLKSSSPSSCTLDKGNYPFSAIPLGSLPESVES
LPNCFVTYSMESVIERSKNYSDLICRKNIRVLRTISPAAVELSETVCVDNSWPKVDYSI
SVPNKAVAIGSATPINISIVPLSKGLKLSIKVLFENYQYCDPFPVI SENRQVTELNL
EDPLNESSGEFNGNGCFVNNPFFQPDHSFQDKWEIDTILQIPNSLSNCVQDCDVRNLIK
RHLKFFIILINPDGHKSELRLASLPQLFISPFVALSIKPLSSNLYSLFSTTNQKDENS
SQEEEEELFSRSASVTGLELLADMRSAGSVPTISDLMTPPNYEMHVDRLYSGSFTRTA
VETSGTCTPLGSECSTVEDQQQDLEDLRLRLTKIRNQRDNLGLPPSASSAAASRSLSPLL
NVPAPEDGTERILPQSALGPNSGSPGVHSNVSPVLLSRSPAPSVSAHEVLVPVPSGLNYP
ETQNLNKVPSYGKAMKYDIIGEDLPPSYPCAIQNVQPRKPSRVHSRNSSTTLSSSIPTSF
HSSSFMSSTASPIIINGSRSSSSGVSLNTLNELTSKTSNNPSSNSMKRSPTRRRATSLA
GFMGGFLSKGNKR

YGL011C, 1259 bp, CDS: 501-1259 (SEQ ID NO 89)

AGACAATAAAATATGGAAAATAAAACGCTTAGCACAGCAGTCAATGAAATACCTCTGATAT
ATTTTGACTCTGTGGAGCATACAGCTACCACTAAATAGGATTGTGGGGACAAATATGGAA
TGGATCAAACGTTCTTAGGATTGTGGTGGTAAACCTGTAAATCCAAGCTGAGATCTT
AAATCCAGCAAACCTTCGCCCATATTTATCTTTTATAACAGAAGAAGAGACTATATCT
CAAAACCTCGTATATTTATATACATATCCTCCAAACAACTCCCAAGTTTCACTTTCTCT
GATTTACCTTGGCATTCCTTTTCCCCATCCTCTTATAATGGTAATCGCGATCCTTAATTA
TGATATCACAATAGACGAAGGGCACACACCAATTTGCCACCGTAAGGATAGAGTAAGTTA
AATGGCTAACTCATTTATAATCTTCATGCTAAATCATATAAGGGCAGAGACGAAGCAAAGC
GAAAAAACATATTACAATCATGTGGGTGCTGCTGCTGCTGCATCTGCTGCTGGTTATGACA
GGCACATCACTATCTTTTCCCCGAGGGTCGTTTATATCAAGTAGAATATGCCTTTAAAG
CGACTAATCAAACTAACATAAACTCACTAGCGGTCAGAGGTAAAGATTGTACAGTGGTGA
TAAGTCAGAAAAAGGTCCCTGATAAACTGTTGGATCCAACCTACTGTTTCGTATATTTTTT
GTATTTCAAGAACAAATTGGTATGGTAGTGAACGGACCAATACCGGATGCAAGAAATGCGG
CCCTAAGAGCCAAGGCTGAGGCTGCAGAATTCGGTTATAAATATGGTTATGATATGCCAT
GCGATGTATTGGCTAAGAGAATGGCTAACCTTTCCCAAATCTATACTCAAAGAGCATATA
TGAGACCATTAGGTGTTATACTCACATTTGTTTCGGTAGATGAAGAATTGGGTCCCTCCA
TTTACAAAACCTGACCCGTGACGGTTATTACGTTGGCTACAAAGCTACTGCGACAGGACCAA
AACAAACAGGAGATCACAACAACTTAGAAAACCATTTCAAAAAGAGTAAATCGACCATA

TTAATGAAGAATCATGGGAGAAGGTGGTAGAATTTGCTATTACTCATATGATTGACGCAC
TGGGTACCGAATTTTCAAAGAATGACTTGGAAGTCGGTGTGCTACAAAGGACAAATTCT
TTACCTTGAGTGCTGAGAACATCGAAGAAAGGCTAGTAGCAATTGCTGAACAAGATTAA

YGL011C, 252 aa (SEQ ID NO 90)

MSGAAAASAAGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDC TVVISQKKVP
DKLLDPTTVSYIFCISRTIGMVVNGPIPDARNAALRAKAEAAEFYKYGYDMPCDVLAKR
MANLSQIYTRAYMRPLGVILTFVSVDEELGPSIYKTDPAGYVYGYKATATGPKQOEITT
NLENHFKKSKIDHINEESWEKVVEFAITHMIDALGTEFSKNDLEVGVATKDKFFTLAEN
IEERLVAIAEQD

YGL031C, 968 bp, CDS: 501-968 (SEQ ID NO 91)

CCAAGTTAAGCAAGACACCAAGACAATAACTTGAGAGGTATGTCCCTATATGATGATGAT
TCATAAATTAATGGCGACCGAGGGCAGCGTTGTGCTAGAAAAGCAATGTATTATATATGAG
AGAGCTTCAGATAGCCAATACACCGGAATTTAGACTTTGACAGGATTGTGGCTTGTTCCTCA
GTATAACTTATAATATATGTCAACCTTTGAGCAGGAAACCCAATGAAAATGC'TTCATTAC
ATATATACGATATGGAGAAGCATGAAAAATAACAGCGTGAGATGTTATCCATGTTGCAAG
AACCTAGTAAAATGAATTCTGAATTTGCAAAAAGTCCATATTTCCACGTTCTCCTCTTCC
TACAATTTTGCGAACGCCCTGAACAACCATGCGGATTACCATTTATTTATATTGACAAGATG
GCTACCTATGAAAAGCATAGACTTACTAACATTTTTTTTTTCAAATATGTTTGAAAAACG
TGGATTAATATAGTGATAAAATGAAGGTTGAAATCGATTCTTTTTTCAGGTGCCAAAATCT
ACCCAGGCAGAGGTACCTTGT'TTGTCGGTGGTGACTCCAAAATCTTCAGATTCCAAAACCT
CCAAATCTGCCTCTTTGTTCAAGCAAAGAAAGAACCCAAGAAGATCGCTTGGACTGTCT
TATTCAGAAAGCATCACAAAGAGGATACCGAAGAAGTTGCTAAGAAGAGATCTAGAA
AAACCGTTAAGGCCCAAAGACCAATTACCGGTGCTTCTTTGGACTTGATCAAGGAAAGAA
GATCTTTGAAGCCAGAAGTTAGAAAGGCTAACAGAGAAGAAAAATTGAAGGCCAACAAAG
AAAAGAAGAAGGCTGAAAAGGCTGCTAGAAAGGCTGAAAAGGCTAAGTCTGCTGGTACTC
AAAGTTCTAAGTTCTCCAAGCAACAAGCTAAGGGTGCTTTCCAAAAGGTTGCTGCTACTT
CTCGTTAA

YGL031C, 155 aa (SEQ ID NO 92)

MKVEIDSFSGAKIYPGRGTLFVRGDSKIFRFQNSKSASLFKQRKNPRRIAWTVLFRKHHK
KGITEEVAKRRSRKTVKAQRPITGASLDLIKERRSLKPEVRKANREEKLKANKEKKKAEK
AARKAEKAKSAGTQSSKFSKQQAQKGAQKVAATSR

YGL032C, 764 bp, CDS: 501-764 (SEQ ID NO 93)

CTCCCATATTTTTTTATTTCACAGGCTAGACAATGGTAATGGTGCTTTAGATGATTTTCAGT
GGATTACATTCGCACAATAGAAATAAATGACTAATTTCAAGAATTTGTTTCAACCTGCCG
GCATTACAGTTATTATAAGTTATTGTTGATGGTAAAACTTCGCCATCACCGGTTGCTGCG
TTTATTGCAAAATTAAGTAAACCATGTAATTTCCGAATACGGTAATTACACCGCAGTTTGA
AATTTGACATGCAAGTTTAACAAAAAACTTCTGTCCGCATCTAAAGCTTAATTAAGGGA
CTGTTTCATACCTTCAGATCCAATATACTGAATATCAGGCAATTGATTTCCCTTGTAAT
ATACAATATAAATAGTTGTAAGAAGAGGTGATATGTTAAGTTTCCATTTTGACGTATTCC
TCATTCTAGAATGATTGTAAGCTCTCAACAGTCACTTGTGTGCCAAAATATTATACCTAC
TTCATACATTTTCAATTAAGATGCAGTTACTTCGCTGTTTTTCAATATTTTCTGTTATTG
CTTCAGTTTTTAGCACAGGAAGTGAACAATATGCGAGCAAATCCCCCTCACCACCTTTAG
AATCGACGCCGTACTCTTTGTCAACGACTACTATTTTGGCCAACGGGAAGGCAATGCAAG
GAGTTTTTGAATATTACAAATCAGTAACGTTTGTGAGTAATTGCGGTTCTCACCCCTCAA
CAACTAGCAAAGGCAGCCCCATAAACACACAGTATGTTTTTTGA

YGL032C, 87 aa (SEQ ID NO 94)

MQLLRCSFISFVIASVLAQELTTICEQIPSTLESTPYSLSSTTTILANKAMQGVFEYYK
SVTFVSNCGSHPTTSKGSPIQYVF

YGL043W, 1430 bp, CDS: 501-1430 (SEQ ID NO 95)

TCGGGATGGTGGGTTGTTCTGTACCCCCGATTCACACCGCTCTGCCTATTCATTTTATC
GTTTTCTGCTCTTTCTTTCAATGATTGATAATTAACGTGTCTATGTGATGCTATTGGTAT
ATAGCCTTTCTTGATATCCCTCTAACAATTATTACAAGTGTTTCTGTTTAAAGCAAGTG
CTAGAAGTGACTCGGTTCTCTTAGGAAATTCTAAACGCAAGATTTCTCTTATGGTGATTG
TAACAATTATGAGATACTTCACTAGCCCACCTTAACCTTACGGACCTTCTTTTGAACGA

TGCTTCGAATGACAACGCCTTTTTGATATATAATATCCAATTTTATTATAGGGAAATTTT
CAACTCTTACCCGCCCCACTGTGCTGATATGACCAAGTGATCACTCGATGATGGGACTAC
GTATTGAAAAATATTGAATGAAAAATTACTCAAGCAGCAGAACATTACAGTGTAGTCAG
TCCGCATAAGAGCATTTCATCATGGATAGTAAGGAAGTACTGGTACATGTTAAGAATCTAG
AAAAGAACAAAAGTAATGATGCTGCAGTTCTAGAAATCTTACATGTCTTGGATAAAGAAT
TCGTCCCCACTGAAAAGTTACTGAGAGAAACAAAAGTTGGTGTGGAAGTCAACAAGTTTA
AAAAATCCACTAATGTAGAGATCAGCAAACTCGTGAAGAAAATGATTAGCTCTTGGAAAG
ACGCAATTAATAAAAAATAAGCGTTCCAGGCAAGCACAGCAGCATCATCAAGATCATGCGC
CAGGCAATGCAGAGGACAAGACAACCTGTAGGTGAGTCCGTGAATGGTGTTCACAGCCGG
CCTCTCCAGTCAGATGCCATGAAACAAGACAAGTACGTACAGCACTAAACCAAGAAATA
GTAAGAACGATGGTGTGGATACAGCTATATACCACCACAAATTACGTGATCAGGTACTAA
AAGCACTCTACGACGTTTTGGCCAAGGAAAGTGAGCATCCACCTCAATCTATTTTGCATA
CTGCAAAGGCCATAGAAAGTGAAATGAATAAAGTTAACTGTGACACCAACGAAGCCG
CTTACAAAGCCAGGTATCGTATAATTTATTCAAACGTCATATCAAAGAATAACCCAGATC
TCAAACATAAAATTGCCAACGGTGATATAACACCTGAATTCTTAGCTACATGCGATGCCA
AGGATCTGGCACCAGCGCCCTTAAAGCAAAAGATAGAAGAAATTGCCAAGCAAACTTAT
ACAACGCACAGGGTGCCACCATAGAAAGGTCAGTCACCGATAGATTTACATGTGGTAAAT
GTAAAGAGAAGAAGGTATCTTACTATCAATTGCAAACAAGATCTGCGGATGAACCATTGA
CCACTTTCTGTACATGTGAAGCATGTGGTAACAGATGGAATTCTCTTAG

YGL043W, 309 aa (SEQ ID NO 96)

MDSKEVLVHVKNLEKNKSNDAVLEILHVLDFEVPTEKLLRETKVGVEVNKFKKSTNVE
ISKLVKKMISSWKDAINKNKRSRQAQHHQDHAPGNAEDKTTVGESVNGVQQPASSQSDA
MKQDKYVSTKPRNSKNDGVDTAIYHHKLDRQVLKALYDVLAKSEHPQSILHTAKAIES
EMNKVNNCDTNEAAYKARYRIIYSNVI SKNPNDLKHKIANGDITPEFLATCDAKDLAPAP
LKQKIEEIAKQNLNAQGATIERSVTDRFTCGKCKEKKVSYYQLQTRSADEPLTTFCTCE
ACGNRWKFS

YGL102C, 929 bp, CDS: 501-929 (SEQ ID NO 97)

TGTTACGATCAACATTCTTGTCCGTAATCAGCATGGTAGTTAAACCCATTCTGTACATAT
GGTCAGATATACTTTTCGCATGGGTCAATACCATGGTCAACCCAACCAAGTTCTTCTTTGCG
TTTTCAAAGTTGTATAATATTCAAAAACGCTAACTGATAATTTGGGTGAGGTTTCGAAA
GAATTGCCAAATCTCCCTAGGTATATTCTTCTGGCTTCCAGATGTTAACTGCAGTCA
TTTTGTTTTTCTTGGTCTTTACCTCGAATAGGTTTTCTTGTGTTTTGTTATTTGTTTTCTTT
TTGGACCCTATGTTTATATATGGATTTTGAAAATCTTTTAAAAAAGCGATAAAAGCGTTG
GGATCTGCCACTGGTAACCTTCAAATAGACAAGACGAAAAAAGCGTGAATGGGTGATA
GAAATAATACAGAAGTAGATGTTGAATTAGATTAACTGAAGATATATAATTTATTGGAA
AATACATAGAGTTTTTGTGATGCGCTTAAGCGATCAATTCAACAACACCACCAGCAGCT
CTGATTTTTTTCTTTCAGCCAACCTTGGAGACGAATCTAGCTTTTGACGATAACTGGAACATTT
GGAATTCTACCCTTACCCAAGATCTTACCGTAACCGGCTGCCAAAGTGTCAATACTGGA
GCAGTTTCTTGAAGCAGATTTCAAGTATTGGTCTCTCTTGTCTTCTGGGATCAATGTC
CACAATTTGTCCAAGTTCAAGACTGGCTTCCAGAAATGAGCTTGTTGCTTGTGGAAGTAT
CTCATACCAACCTTACCGAAATAACCTGGATGGTATTTATCCATGTTAATTCTGTGGTGA
TGTTGACCACCGGCCATACCTCTACCACCGGGGTGCTTTCTGTGCTTACCGATACGACCT
TTACCGGCTGTACAAAAAATATTGTAA

YGL102C, 142 aa (SEQ ID NO 98)

MRLSDQFNNTTSSSDFFSQLGDESSFDNWNINWSTLTQDLTVTGCQSVNNWSSFLRSR
FQVLVSLVFDQCPQFVQVDWLPMSLLLVEVSHTNLTEITWMVFIHVNSVVMLTTGHT
STTGVLVSLTDTTFTGCTKKIL

YGL103W, 1461 bp, exon1: 501-549, intron1: 550-1060, exon2:
1061-1461 (SEQ ID NO 99)

AACAAGCTATAATATTGTTAAATATAGTTGATCAACAGCATTGTAATGATTACAAGAGAC
GAGGTGGAATGAACCTTATGAAATGCGTATTATATATAAACTGTAATAAGAGCTAAGTTG
AATTGAAATCTACGATACTTGATGTTGACATTATAGCACTAGTTCCCAGGAAACCTTTTC
GAAAAACACAGCAAAAAACAAGAGTACTGTAAACCAATGTAACATCTGTACACCAGGGACCC
ACACATTACCAAAATCAAAATTATTTTTCTAATGCCTGTTATTTTTCTATTTTTCTCTCT
GGCGCGTGAATAGCCCGCAGAGACGCAACAATTTTCTCGCAGTTTTTCGCTTGTGTTAA
TGCGTATTTTCCCAGATAGGTTCAAACCTTTTCATCTGTATCCCGTATATTTAAGATGGCG

TTTGCTTTCTCCGTTGATTTTTTTCCCTTCTTAGTGATTTTTTTGCATTAAATCCCAGAAC
AATCATCCAAC TAATCAAGAATGCCTTCCAGATTCAC TAAGACTAGAAAAGCACAGAGGTC
ACGTCCTCAGGTATGTAGTTCCATTTTGGAAAGAGGGAATGAAAAGAACCAAGACGGTGACTTTT
TTTTTTAGTGTTGTGCAACCAATATGTCGTGTGTATATCATGGTACAGGAGAAATGTCAAT
CAGCTAAGTGTAACAATATTTCTTTGTGTTTTGATTGCGAACTTTGTATTACCATCT
CACTGTTGAGACGGCTTATTTGAGGTAATAGCTCGAGTAAATGTACTCTTCCATCGCAA
CTGAGCAAAAAGAAAGTGTCATAGCCTTTGTCTACTTTCTCCTTTATTATACCATGATA
TTCAGAACAGTCATACTGTCTACTCATTTTACGGCTATAAAAGGTAAC TTTCATTTAGAT
TATGGAAAGCACTAATTATCGCTGTATCAAATGGTTGTAGAGAGCGCAATTATGAAAAAG
AGTTACCACGTTTCTTTTGTTCGATAAAATGTCCAGTTGAAAACCTGTTTACTAACGA
TTTAAAAATTGTATTTTCAATACAATATTTTTTTTTGTACAGCCGGTAAAGGTCGTATCGGT
AAGCACAGAAAGCACCCCGGTGGTAGAGGTATGGCCGGTGGTCAACATCACCACAGAATT
AACATGGATAAAATACCATCCAGGTTATTTCCGGTAAGGTTGGTATGAGATACTTCCACAAG
CAACAAGCTCATTTCTGGAAGCCAGTCTTGAAC TTGGACAAATTGTGGACATTGATCCCA
GAAGACAAGAGAGACCAATACTTGAAATCTGCTTCTAAGGAACTGCTCCAGTTATTTGAC
ACTTTGGCAGCCGGTTACGGTAAGATCTTGGGTAAGGGTAGAATTTCCAAATGTTCCAGTT
ATCGTCAAAGCTAGATTCGTCTCCAAGTTGGCTGAAGAAAAATCAGAGCTGCTGGTGGT
GTTGTTGAATTGATCGCTTAA

YGL103W, 149 aa (SEQ ID NO 100)

MPSRFTKTRKRGHVSAGKGRIGKHKHPGGRGMAGGQHHRINMDKYHPGYFGKVMRY
FHKQQAHFVKPVLNLDKLWTLIPEDKRDQYLKSASKEAPVIDTLAAGYGKILGKGRI PN
VPVIVKARFVSKLAEKIRAAGGVVELIA

YGL130W, 1880 bp, CDS: 501-1880 (SEQ ID NO 101)

TTTTGGTACTTGAATTTCTCGTTTCTACTAGCTGGATTGCTTGCTTTTACAATTCCTG
GGAGTTTGGCTATTGCTACCCCTGGTCTTAGCACCACCTTTTTTCCGCTATTGTATTGT
TGAAC TAATTTAGTATCTATTTCCATTTTCAATATAATTCACGTTTTTAGCAGCCTCTCTT
CTTCTAGGTAATTTGAAATCTTCTTTTAGGCATAGCGTGACCAGCTGAAAGGCAGATG
ATCTCAATATGTCCCGATAGGCCAATTTTGCCACCAGATAGTTGATGGCATTTTATTTT
TAGTCCTTTTGAAGCAATATCATAAAATATATATAGTTCTCCATGATGTTCTGGGTCAGT
CGCTCCGAAGCGTAACCTAGTATAATAAATAGTTTCAATGCAGAAAATAACGAAAGAAATG
GTGGAATACGATCTGTTATATCTAAACTAAAGCTAACTAACGGAATAAGCAATACGAAT
CGACCGCTAATTTAACAAATATGGTTTTAGCAATGGAAAGTAGAGTGGCACCGGAAATTC
CTGGGCTCATTCACCTGGGAATGTCACGCAAGACTTGAAGATGATGGTCTGTAAATTAT
TGAATTTCCCAAAACCTACGAAAACATTCCCTGGTTCCCAGCCTGTGTCTTTTCAGCATTT
CTGATGTGGAAGAGAAGCTGCTTGGCATGATTACTACGTTTGTGAGAAAACAGATGGTCT
TGCGGGTGTGATGTTTATAGTGATAAATCCTGTGACGGGTGAGCAAGGATGCTTTATGA
TTGATAGTGGGAAAATAACTATTATCTGGTTAATGGATTAGGTTTCCCAGATTACCCCAAA
AGAAGAAAGAAGAGCTGCTAGAGACTCTTCAAGATGGCACCTTATTAGATGGTGAAC TTG
TCATACAACTAACCCAATGACAAAATTACAAGAGTTGCGTTATTTAATGTTTCGATTGTC
TTGCTATCAATGGTAGATGTCTCACACAATCACCACAAGTTCTAGACTAGCCACCTTG
GAAAAGAATTTTTTAAACCATACTTCGATTTAAGAGCAGCGTACCCTAATCGTTGTACTA
CTTTTCCGTTCAAAATTTCCATGAAACATATGGATTTTCAGTTACCAATTAGTAAAAGTTG
CTAAAAGTTTAGATAAACTACCACATCTTTCTGATGGTCTGATATTTACTCTGTGAAGG
CACCTTACACTGCCGGCGGAAAAGATTCTTGTATTATAAAATGGAAGCCAGAACAAGAAA
ACACCGTGGACTTCAAATTGATTTTAGATATCCCAATGGTGGAGGATCCTTCTTTGCCTA
AAGATGATCGGAACAGGTGGTATTACAATTATGACGTTAAGCCAGTTTTCAGCTTATATG
TCTGGCAAGGCGGAGCTGATGTCAATTCACGTTTAAAAATTTTCGACCAGCCTTTTCGATA
GGAAGGAATTTGAAATATTAGAAAGAACATACAGAAAATTTGCAGAGTTGAGCGTTTTCAG
ATGAGGAATGGCAAAATTTGAAGAACCTAGAACAGCCATTAAATGGTAGAATGATAGAGT
GCGCAAAAACCAAGAGACTGGGGCGTGGGAAATGTTAAGATTTCAGGGATGATAAGTTAA
ATGGTAATCATACATCGGTGGTCCAGAAAGTTTTGGAGAGTATCAACGATTTCAGTTTCAT
TGGAGGACCTCGAGGAAATTTGTTGGTATATTAAAAGGTGCTGGGACGAGAGAAGAGCAA
ATATGGCTGGTGGTAGTGGGAGACCACTACCGTCTCAAAGTCAAATGCGACATTATCTA
CCTCTAAGCCAGTCCATTACAGCCCCCAAGTAATGATAAGGAGCCAAAATATGTAGACG
AGGATGATTGGTCGGATTAG

YGL130W, 459 aa (SEQ ID NO 102)

MVLAMESRVAPEIPGLIQPNVTQDLKMMVCKLLNSPKPTKTFPGSQPVSFQHSDVEEKL

LAHDYVVEKTDGLRVLMLFIVINPVTGEQCFMIDRENNYYLVNGFRFPRLPQKKKEELL
ETLQDGTLLDGLVVIQTNPMTKLQELRYLMFDCLAINGRCLTQSPTSSRLAHLGKEFFKP
YFDLRAAYPNRCTTFPFKISMKHMDFSYQLVKVAKSLDKLPHLSDGLIFTPVKAPYTAGG
KDSLLLKWKPEQENTVDFKLILDIPMEDPSLPKDDRNRYNYNDVKPVFSLYVWQGGAD
VNSRLKHFDQPFDRKEFEILERTYRKFAELSVSDEEWQNLKNLEQPLNGRIVECAKNQET
GAWEMLRFRDDKLNGNHTSVVQKVLESINDSVSLEDLEEIVGDIKRCWDERRANMAGGSG
RPLPSQSQNATLSTSKPVHSQPPSNDKEPKYVDEDDWS

YGL147C, 1076 bp, CDS: 501-1076 (SEQ ID NO 103)

CAATATTATAGTTACTACCTATTTGATTATTAAGATCAAAAGTAATCCTTCATCTCATAT
CAAAAAGAAAGGTTTGTAAAAGAGCATTGGGCAGAGAGTATTTGTCCTGCGTATAGAGGA
GAAAAAATTGTACTGATGCTAATTTTGGTGTCTGTTCTTTTATTTTGTAAAGACTGT
TTTCCAGAAATGTTTGGGTTTATTTTTTAATTTTTTGAACATTTTTTTCATCCTTTCTC
ATTTTGTCTATTTTCTGTGTGAAAATTTCACTGACGCGAAGAAGCGATGAAATTTTC
CAACATCCTCCCATCATCCCAATATTGGCATAACACACATGCAGCACAGCGGAATGCG
GAGGTCAGAGGCAATGTGGCAGAGACGCTGGCGCGCCTGTATTGTATAATAGTATATTTT
ACACTCAATTCAATTTTTTGTATTTAAATTAGTGTGTAAAAGCTTCTGAAATCAAGAAG
CCCGTACCAGAAGTTCAATCATGAAATACATCCAACTGAACAACAAATCGAAGTCCAG
AAGGTGTCTGTCTGAGCATCAAGTCCAGAATCGTCAAGGTTGTTGGTCCAAGAGGTACTT
TGACCAAGAAGTTGAAGCACATTGATGTTACCTTCAACAAGGTCAACAACCAATTGATCA
AGGTTGCTGTTTCAACAACGGTGGCAGAAAGCAGCTTGCTGCTTTGAGAACCGTCAAGTCTT
TGGTTGACAACATGATCACTGGTGTACCAAGGGTTACAAGTACAAGATGAGATACGTCT
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCCAAATTCATTGAAG
TCAGAAACTTTTTGGGTGACAAGAAGATCAGAAACGTTCCAGTTAGAGATGGTGTACTA
TCGAATTTTCCACCAACGTTAAGGACGAAATTGTCTTGTCTAGGTAACCTGTGCAAGACG
TTTCCCAAAACGCTGCTGACTTGCAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTA
AATTTTTGGACGGTATCTACGTTTCTACAAGGGTTTTATTACTGAAGATTTATAA

YGL147C, 191 aa (SEQ ID NO 104)

MKYIQTEQQIEVPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTFKVNQLIKVAVHNG
GRKHVAALRTVKSVDNMITGVTKGYKYMRYVYAHFPINVNIVEKDGAKFIEVRNFLGD
KIRINVPVRDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQICVRNKKDIRKFLDGIY
VSHKGFITEDL

YGL213C, 1694 bp, CDS: 501-1694 (SEQ ID NO 105)

AATCAAAACGATCGTTATACAATTCATTGAGGAACCTCTCTAGTCCGATCCGTCCTTCAT
CGATCATTTCCGGATCATCATATCTTCTTTGCCACCTCCTGTCCAATACACCGGGCTTTT
CAGGGAAGTCATATGGGATGGTGTCTTCTACATCTCTCTCCAATCGTGTCTTCAGTTTCC
AAAACCTCGGATACCTTTTGTAAAGGCGCTTGTGTTGGTGTACTAACACCGTATAAAACAT
ACTTGGGGTTGATTTTAACATCGTCCACCTTGATTCTTAACTTTTCACTCATTTTCCCTA
CAGAATTAGCTGCCATCAATATCAATTATCAACCTTATATGACTTTTATTGTTTTTGT
TTGTTGGCTAATTAATTGATACAAATCTTTAGGCGAAAAATAAAAAAATAAAGTAAA
GAAGGAAAAATTAGGCGATATTAAAACAAATCTAAAATAAAGACAAGAAACGAAAAAGAG
GTTAATCAAGTATTGGAAAAATGTCCAAAGTGTATTATGCCACAGCAAATGCAGGTAAAG
CTCATGACGCTGATATTTTCTCGGTTTCTGCTTGCAATTCATTTACGGTAAGTTGTTTCAG
GTGACGGTTACTTAAAGGTGTGGGATAATAAGCTGTTAGATAATGAAAAATCCAAAAGATA
AGTCATATTCTCACTTTGTCCATAAGTCCGGATTGCACCATGTCGATGTCTTGCAAGCTA
TTGAGAGAGATGCATTTGAATTATGCCCTTGTGCTACCACTTCATTTTCTGGCGATTTAC
TCTTCTATCGTATCACTAGAGAAGATGAGACTAAAAAAGTTATATTTCGAGAAATTGGATC
TTCTAGACTCAGACATGAAAAAGCATTCTTTTGGGCATTAAAAATGGGGTGCCTCAAATG
ACAGACTACTTTCCCATAGGCTGGTTGCTACAGACGTCAAAGGGACCACTTACATTGGA
AGTTTCAACCGTTTGCAGATGAGTCAAATTCCTTTAACTAAATTTGGAGCCCAACGTTAG
AATTACAAGGCACTGTGCAATCGCTATGACTCCAAGTCAATTTGCCACTTCTGTGGATA
TCTCTGAACGAGGACTAATTGCCACAGGTTTAATAATGGAACAGTACAAATTTCAGAAC
TATCTACATTACGCCCGTTGTACAATTTGAATCTCAGCATTCTATGATTAATAATTCGA
ATTCCATCAGATCGGTGAAATTTTCTCTCAAGGATCCTTATTAGCCATTGCTCAGGATT
CAAATTCATTTGGTTGCATCACTCTATATGAAACTGAATTTGGTGAAAGAATAGGCTCCT
TATCCGTACCAACCCATAGCTCGCAGGCAAGTCTGGGTGAATTTGCACATTCTAGCTGGG
TCATGAGTCTATCGTTAATGATTCTGGTGAAACATTATGCAGTGCCGGATGGGATGGTA
AATTGAGATTTTGGGATGTAAAACAAAGGAAAGAATCACTACATTGAATATGCATTGTG

ATGATATTGAAATTGAAGAGGATATCTTAGCTGTTGATGAACATGGAGATTCTTTAGCTG
AACCTGGTGTCTTTGACGTGAAGTTTTTGAAAAAGGTTGGAGATCTGGTATGGGAGCTG
ATTTAAATGAAAGTTTATGCTGTGTTTGTAGATAGAAGCATCAGGTGGTTTAGAGAAG
CTGGCGGTAAATAA

YGL213C, 397 aa (SEQ ID NO 106)

MSKVFIATANAGKAHDADIFSVSACNSFTVSCSGDGYLKVWDNKLDDNENPKDKSYSHFV
HKSGLHHVDVLQAIERDAFELCLVATTSFSGDLLFYRITREDETKKVI FEKLDLLDSDMK
KHSFWALKWGA S NDRLLSHRLVATDVKGTTYIWKFPFADESNSLTLNWSPTLELQGTVE
SPMTPSQFATSVDISERGLIATGFNNGTVQISELSTLRPLYNFESQHSMMNNNSIRS VK
FSPQGSLLAIAHDSNSFGCITLYETEFGERIGLSVPTHSSQASLGEFAHSSWMSLSFN
DSGETLCSAGWDGKLRFDVKERITTLNMHCDDIEIEEDILAVDEHGDSLAEFGVFDV
KFLKKGWRSGMGADL NESLCCVCLDRSIRWRFREAGGK

YGL235W, 1037 bp, CDS: 501-1037 (SEQ ID NO 107)

CTGGTTCCAACCATATCTTATGGGAAGATCTATCAGGAAACCTTAGAATCTTAGCTTCGA
TGGAGGGACAATAGCGGGGGCCTTTGATGGTCTGTCTGAATATGAATGGATTGATGCA
AGTTATTGCGCAAAAAGTCGTGCATTTGAGGTGTGGTATGTGTGCCAAAGCAATCCAGTT
GCTTCGTGGGTTGCACTGACACGGTTTCATTTCAGAAAACCTCATAGGGACAGGCAACGCAT
CTCCCTTCTGGACCTCCAGAGCGCTGAAATCAATGGATTCTTTGGCCAGCCTAGCCGGAG
TGCCTGTTTTTCAAACGCCCTAACTGAAAGCCACCTCATTTTGTAGAGTATTGCTGATCC
CATATGTTGGCTGCTCGCCAATTCTTCTGCTGCAATACGCTTGTGCGCCGATGTGAATTT
CTGCACTGAGAAACGTACCTGTAGTGATTATGACCTGATCTGCCCCAACCTGGGTACCGT
CATCCAGAACCACACCTTTGATGACCTTGTGGCCACATCCGGGGTCATACAAGATCAAGT
CAGCAACTTTGTTCTGCAGCAGAGACAAGTTGGGGTGTGCTTTCTTGTGCGAAAGTTCCC
TTTGCATGTATTTCTTATATAACTCTCTGTCTATCTGGGCTCTGGGCCCCCACACAGCAG
GACCCCTTGCTTCTGTTTCAGCATTTTGAATTGCACTCCAGCGAGATCAGTTACTTTGCCCA
TCAGCCCATCGAGAGCGTCGATTTCTTTACAAGGATGCCCTTACCCACTCCACCAATAG
AGGGGTTGCACGAACACTTACCAATATCTGTTAACGATGGTGTAAATGAGAGTAGTATGCG
CACCAGTCCTAGATGACGCAGCTGCAGCTTCGCAGCCTGCATGTCCAGCACCGATGACCA
CGACCTGTGTCTTGGTTGTGGGTGGAAGCTTGTCAAAGAAGATATGGTCAACCGCCTCC
TGAGGACCTGTAAGGGAAATGAAGTACACGAAGACGCCAAGGTTGTTACACGCAGCATCG
TTCTTTGGGGCGTTTAG

YGL235W, 178 aa (SEQ ID NO 108)

MTLWPHPGSYKIKSATLFC SRDKLGCAFLSESSL CMYFLYNSLSIWALGPHTAGPLLLFS
ILNCTPARSVTLPI SPSRASISFTRMPLPTPIEGLHEHLPISVNDGVMRVV CAPVLDDA
AASQPACPAPMTTTCVLVVGWKL VKEDMVNRLRLRCKGNEVHEDAKVVTRSIVLWGV

YGL260W, 731 bp, CDS: 501-731 (SEQ ID NO 109)

TACCATGGAACACCGGTGATCATTCTGGTCACTTGGTCTGGGGCAATACCAGTCAACATG
GTGGTGAAGTCACCGTAGTTGAAAACGGCTTCAGCAACTTCAACTGGGTAGGTTTCCGTT
GGGTGGGCGGCTTGGAACATGTAGTATTGAGCCAAGTGAGCTCTGATATCAGAGACGTAG
ACACCTAATTCAACCAAATTGACTCTTTCGTGAGCTGAGCTAGAGTGGTGGTTGCGGAA
GCAGTAGCAGCGATGGCAGCGACACCAGCGCGATTGAAGTTAATTTGACCATTGTATTT
GTTTTGTTTTTTAGTGCTGGTATAAGCTTAACAGGAAAGAAAGAAATAAAGATATATTCT
CAAAAGCATACAGTTGAAGCAGCTCTATTTATACCCGTTCTCTATCAGTCATCACTACT
TAAACGATTTCGTTAACAGATGCTCATTTAGCACCTCACATATCCTCCATATCTCATCTTT
CACACAATCTCATTATCACTATGGAGATGCTCTTGTTCGTAACGAATCATACATCTTTT
ATAGACTTCGTATGTGGAGTATTGTATTATGGCACTCATGTGTATTTCGTATGCGCAGAAT
GTGGGAATGCCAATTATAGGGTGCCGAGGTGCCTTATAAAACCCTTTTCTGTGCTGTGA
CATTTCTTTTTTCGGTCAAAAAGAATATCCGAATTTTAGATTGACCCTCGTACAGAAG
CTTATTGTTAA

YGL260W, 76 aa (SEQ ID NO 110)

MEMLLFLNESYIFHRLRMWSIVLWHS CVFVCAECGNANYRVPRCLIKPFSVPVTFPFSVK
KNIRILDLP RTEAYC

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 111)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTT

TTTTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCCCT
GTGTAGCCTAATGTTTAATGCCTAATTTTTTCTAAAATGCAGCAACATACATATGTTGA
GTCGTATAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTTCAGGACA
TTTTAAACATCCGTACAACGAGAACCCATACATTACTTTTTTTAATATTCTTTTTGTTTT
CACCGCCTTCTTTTTATTTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAA
GCTAGGATACCAAATTGAACTTGGACATAACTCATCTAAAGAAGTATACTGTTAAGA
GAGGCATTCAATTCGTGTATTATAACGTTTAGCATCAGTTACCCCTGAAAGCCCAACATA
TACAAAAATACGCGTCCAAGATGTCTACTAAAGCCCAAAACCCATGCGTGATTTGAAGA
TCGAGAAATTGGTCTTGAACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCT
CCAAGGTTTTTAGAACAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTCCGTATCAGAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAAACTTCTCTGCTACCGGTAACCTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTCTATGTCGTATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACTGTTGGTAACTCCACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGACGCTGATGTGCTCGATA
AATAA

YGR085C, 174 aa (SEQ ID NO 112)

MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTEFGIR
RNEKIAVHVTVRGPKAEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKRCCKGTGVGNSHKTTKEDTVSWFKQKYDADVLDK

YGR118W, 1258 bp, exon1: 501-565, intron1: 566-885, exon2:
886-1258 (SEQ ID NO 113)

AGCCATGTCGGTCGCACTAGACTTTTCTTCTCACTGTCACTTACCTGTTTGAAATCATGT
CCTTTTTTTTTTTTGCCATTCTTATACATTTTCTTTCTTCTGAAATTAACGTGTACACCCA
TACCCTATATACACCCATACCCCTATTTTTAAATATAAAAAGTAACTTCATTTTGAAAGA
CCACTCTGCATCAGCACGCGGGCTCTGGAAGGAAGAAATGACGTTTCGGCGGAATACCCCT
TTCAGAAGGTCTGCTCTTGTGGCTGGTTTCATGGGAGACACCCAGCGGAGCTCCTCCCGAG
AAAGGCCCTTCATCTCTGCCGATTGCTGACGGAAGCAGTAGCGGAGGTTTGAGTTCTC
TACGCCGAGAGTACACTGCGGTAATATCACAAATGTTTCGACTAACGGTTACAGTACGTTA
AATTAGATACTGCCTATGAATTGACATATTAGATAATGTCAAATTTTACAAAAACCTAAG
ACAACAGGAAATAAACAAGATGGGTAAAGGTAAAGCCAAGAGGTTTGAACCTCTGCTAGAA
AGCTACGTGTCCACAGAAGAAACAAGTATGTTGACTATTTCAAAATTAAAAAAACTATC
AACCCCTATTGTGATATCGTTTTAGGTGAAGGAAATGTTGTGAGCTCTGGAGTGATAAA
TTTATCAAGTAACATATCTTGGCGCAAATCAGTTTGGAGAGGCTTAAATGACACGTACAC
AGTGATAAAAAAGTAATGAATAGTGAACGGTCAGCTTCGGCCATTCTTCCCAATCTATAGT
GTGGAAAATAAACCTTTTCTTCCCAAATAAATCAGAAAGTCACAGGAGGCCGTTTTTTA
CAACGGAATCATTTTTTTTACTAACAGTTTTTTTTTATTATTATAGCCGTTGGGCCGAAAA
CAACTACAAGAAGAGATTGTTGGGTACTGCCTTCAAGTCTTCTCCATTCCGTTGGTTCTTC
TCATGCCAAGGGTATCGTCTTGGAAAAATTGGGTATCGAATCCAAGCAACCTAACTCTGC
TATCAGAAAGTGTGTTAGAGTTCAATTAATCAAGAACGGTAAGAAGGTCAGTGTCTTCGT
TCCAAACGATGGTTGTTTGAACCTTTGTGCGACGAAAATGATGAAGTCTTGCTAGCAGGTTT
CGGTAGAAAGGGTAAAGCTAAGGGTGATATTCAGGTGTTAGATTCAAGGTCGTTAAGGT
CTCTGGTGTCTCTTGTGGCTTTGTGGAAAGAAAAGAAGGAAAAGCCAAGATCATAA

YGR118W, 145 aa (SEQ ID NO 114)

MGKGKPRGLNSARKLRVHRRNNRWAENNYKKRLLGTAFAKSSPFGGSSHAKGIVLEKLGIE
SKQPNSAIRKCVRVQLIKNGKVTAFVPNDGCLNFVDENDEVLLAGFGRKGAKGDI PGV
RFKVVKVSGLLALWKEKKEKPRS

YGR142W, 1733 bp, CDS: 501-1733 (SEQ ID NO 115)

GGACTACTTTACAGGGTAATGAATATTTGGGCGTTTTTCGCTATTTTAGCATGCTGTAGT
GTATGTACTGTGCATCGTCATGTAGCACTATTTACGCCGTATTTTCTTTTTTCTTTTCG
CACCGTCTGTGGTTGTAAAGTTACTGACACTTTTTTTTTCTAGAAAGTTCCGGAAAATTGC
GACACTCGGTGGAGCTCGAGAGTTGTATCCAGTTTTCTTGTTCGGCGATATTCCGAACCA
GGTCGGGTTGGGCTAACAGCCGCCAGGATGGAAGAATTAAGAATTTCATAGAAGCCTTC
AGTTCCTGGCGAAGTAAAGTGGCAAAACAAATGGAAGATCTATTGCATTACATATATAAA
AGCATTAGAACAATCTTTTCTCATTGACAGGTATTCTCATTGCTCTATATATATTTTCTT

CTTCTTGAAAGAAATATCAGTATTACAATCATAACAACAACCAAGAAATAACTAATA
GACCCCATTACAATATAGAAATGTTTTCCATATTCAATTCACCATGTGTTTTTGAACAGC
TGCCATCTTTTAGTCAGCCCTACATTCGCGTTATTTTGATTGCAGTTCTCCAGTGAGCT
ATTATCCAGAATGTAAGGAGGAAAGCAATAAAGCTAACCTAAGAGCTCCAAAAA
GCGATGCAAATTGTTTCAAGACCTTTGAGGTATGCACTTGCTGAAACACCAAATGGTTATA
CATTAAAGCTTGTCTAAGCGGATTCCATATGAACTTTTTCAAAGTACGTTAATGAGAAAT
TAGGTGAGCTAAAGGAGAACCATTACAGACCAACTTACCATGTTGTCCAAGATTTTTTGTG
GAAACCAGTATTATGTTGAAGATGAAGCGGATGAAGATGCTCTATTGAGATCTGCATTGA
AAGATCTGGATTTTAGAGCCATAGGAAAGAAAATTGCTAAGGATCTTTTCCAAGACTACG
AAATAGAATTGAATCATAGAGGTGATGAATTGAGCATATTGAGTAAGAAGGATAAAATCT
TTAAGGAATTCTCTCTAGACCAAGTGTGTTGAAGATGTTTTGTTATTGGCTGTGGAGTTG
AAAACATAGATGATGGCTCGAGAGAAAAATATGCACTTTTAAAGATTGGTTTAGTTAAGC
ATGAGGAAGAAATTTCCGAAGGTGGCATCAACGAACCAAAGATGCCAATAATTGAATCCA
AAATAGACGAGTCTCAGCATGATGTTAATCTGCTGAATCTTTGAAGGAGGAAGAAGCGG
AGAAAGCGAAAGAACCCTAACCAAGAAAGACCAAATAAAAAAATGGATAGAGGAAGAAA
GATTGATGCAGGAGGAAAGCAGAAAATCAGAACAGGAAAAAGCTGCCAAGGAAGATGAAG
AAAGGCAAAAGAAAGAGAAGGAAGCCAGATTGAAGGCAAGGAAAGAATCTTTGATAAATA
AGCAAAAAACCAAGAGGTCCAGCAAAAAAATTGCAAAATTCCAAATCATTGCCTATCT
CTGAGATTGAGGCCAGCAATAAAAAATAATAAGCAATTCTGGTTCAGCAGAAAGTGATA
ATGAAAGTATAAACAGTGATTCTGATACGACTTTGGATTTCTCTGTGTCTGGTAATACAC
TAAAAAAACACGCTTACCCCTATTAGAAGACGTTGAGGATGAGGAAGTTGACAGATACA
ACGAGTCCCTAAGCAGATCTCCCAAGGGAACTCTATTATTGAGGAGATATAA

YGR142W, 410 aa (SEQ ID NO 116)

MFSIFNSPCVFELPSFSQPLHSRYFDCSSPVSYYPECKRRKAIKANLRAPKSDANCSE
PLRYALAEPTNGYTLSLSKRIPYELFSKYVNEKLGELENHYRPTYHVVDFFGNQYVE
DEADEDALLRSALKDLDFAIGKKIAKDLFDQYEIELNHRGDELSILSKDKIFKEFSLD
QVFEDVVFVIGCGVENIDDGSRKYALLKIGLVKHEEEISEGGINEPKMPIIESKIDESH
DVMNSESLEKEEAKEKEPLTKEDQIKWIEERLMQESRKSEKEKAKEDEERQKKEK
EARLKARKESLINKQKTKRSQKKLQNSKSLPISEIEASNKNNSNSGSAESDNESINSD
SDTTLDFSVSGNTLKKHASPLLEDVEDEEVDRYNESLSRSPKGNIIIEI

YGR236C, 890 bp, CDS: 501-890 (SEQ ID NO 117)

CAAAAAGTTTTTCGGATGAACCGGATTAATACAAGTAAATCAGCAAAGATATAGAAGAC
AAAATAAGCGTGAAAACAATCATAAACCCTCACAACGGGGTTTTTCAGCTGTTACTCCT
CCATACATACATTTTGATAAAGATATAATGTTATATTTCTTTTCGTAATTTTGTCTTACT
TCGGTTTGCTCTATAGATTTTATCAGCCGCACCGAAAAGGGAGATCAATAAGGTACCCTT
TAAAAGGGATAAGAAGCCTACATCACCCCAATAAATGGAGTAATGGCCAGCATGGATGA
AGAGAAGAATTACGGGATACTGGGATAACACTGTTAAAAAATGCTTCGCGACGTGAGGGT
CTTCTTCATATAAATTGAACTGCCAAATCTCTTTCACATTATCCAGGATAGTTTGGAAATG
TGTGTTACTGAAGGATCAGAATCAATAAATACAATCAATACAAATATTTAGCGCATAAAA
TTCAAACAAAGTTTACTGAAATGAAGTTAGATTAGGAATATACTCAGAGGCACAAAGAG
TTGTGAGAACTCCAAAGTTTAGATATATTATGTTAGGGCTGGTGGGCGCTGCTGTGGTAC
CGACCGCATACATGAGGAGAGGCTATACGGTTCCTGCACATAGCTTAGACAACATCAACG
GCGTAGACACAACCTAAGGCGTCTGTTATGGGTACAGAACAGAGAGCAGCTATGACGAAGG
GTAAGAGTTTACAAGAGATGATGGATGATGATGAAGTAACGTATTTGATGTTCTCTTCA
ATCATGTAAGGGAATTTGTACTTGGTTCCTGCATTTATGTTCTTTGCATTTTGTCTTCG
CATTTAATCATAGTACGACAAACGGGGAAGGGGATTGTGATTTTACATAA

YGR236C, 129 aa (SEQ ID NO 118)

MKLDSGIYSEAQRVVRTPKFRYIMLGLVGAADVPTAYMRRGYTPAHSLDNINGVDTTKA
SVMGTEQRAAMTKGKSLQEMDDDEVTYLMFLFNHVREFVLGSLHLCSLHFVFAFNHSTT
NGEGDCDFT

YGR277C, 1418 bp, CDS: 501-1418 (SEQ ID NO 119)

AATCTTTGCGATTGAATTGCTGCACGAACATTAACATTAGTTCTTTTGCTAAAGTTTCTC
CAATATCTGGAATATCAGAATTTAGCAAGGCAATCAAAGCGGATAAAGCAGGGATTAGCC
TGCCATTCTGTTTGTTCAGAGTAAAATCCACAACATTTTACAAATTATGTTGCGGCCAA
TAAGTATATTGACTTGAAATAAGTCTCTGTGCGATTCTGTAAAGTTGTCCATTGTTAAAT
TGGATATTATGGGTGAAACGTGTGACCTTATCATTTCCAGTTTTCTCTCTGAAATTTAA

TGCTCTTCATCCTGTATGGTAGCGGTAGACATGCTGGTTTGTAGCCTTTTTATTCCTTTTT
AGGTTTTCTTACTCACAATGCCAAAATAAATATCAGTGTAAATAAATTTTTCAAGAGTACG
TAATGGAAAAAGATAAAAAAAGGACCGTCATAAAAAAGAGACGTGATTAAACCTAAAAAT
CTAAAGTAAAGAAGTGTAAAGATGGTTGAGGAAAAATCCAGAGTTTTGATTGTTCTTCCTT
ATACACCGCCTAGTGC'TAC'TTTGCAGAGGATTATAGGGCAAAC'TATTCGGTTCTTAAGAG
AATGTCAAAGTCAACTAGACATCGTGATTGTACCTGAATTCAAAACCTCATTCCAGTTGG
ATTCTGCGCTAGGGAAGATGTACAGTATTACCAGGGATGTCTTTTTGGGCTATGGAATGA
TCAACAGCGGAATCAACATCATATTCAACAATATTCATTTTCGTGAGAGTAATTTGCAAT
GGAAAGTGGTTTTATTTGCCACAGGAATCCACTTTTGAAACTTGGAAGCTAGAGTTGGGAC
AAGGACAATACCATAGTATAGAACATTATGCATTACACGATAATATAATGGAAGAGATAG
AAGGTCCCAAAGATGCTAACAAATTTTCATGTCACCGCATTTGGGCGGAACGTTTCGACCACA
TTCACGATGGACATAAAATATTGTTGAGCGTCTCTACATTTCATCACGTCACAAAGGTTAA
TTTGTGGAATTACGTGCGATGAGCTCTTGCAAAACAAGAAATACAAAGAGTTGATTGAAC
CTTATGATACAGATGCAGGCACGTACATCAATTCATCAAGTTGTTAAAACCGGATCTCT
CCGTAGAACTAGTTCCCTTAAGGGACGTGTGCGGCCCCACAGGGAAAGTACCCGAGATAG
AATGTTTTAGTTGTGAGTAGAGAAACCGTCAGTGGGGCAGAGACTGTGAATAAGACTAGGA
TTGAAAAAGGCATGAGCCCATTTGGCAGTACATGTGGTTAATGTACTTTGGAGGAAGGGAGG
AAGACGGCTGGAGCGAGAAGTTAAGCAGCACGGAAATCAGACGCCCTACTTAAGTCTCTG
CTTCGCCAACGTGCACTCCACAAAACCCTTGCGGTATAA

YGR277C, 305 aa (SEQ ID NO 120)

MVEENSRVLIVLPYTPPSATLQRIIGQTIPLRECQSQLDIVIVPEFKTSFQLDLSALGKM
YSITRDVLLGYGMINSGINIIIFNNIHVESNLQWKVLLPQESTFETWKLELGQGYHSI
EHYALHDNIMEEIEGPKDANKFHV'TALGGTFDHIHDGHKILLSVSTFITSQRLICGITCD
ELLQNKKYKELIEPYDTRCRHVHQFIKLLKPDLSVELVPLRDVCGPTGKVP EIECLVSR
ETVSGAETVNKTRIEKGMSPLAVHVNVNLGGREEDGWSEKLSSTEIRRLKSSASPTCTP
QNPCV

YGR284C, 1433 bp, CDS: 501-1433 (SEQ ID NO 121)

AGAGAGCCATCCGTAACCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGGCCA
CCACGATTGACGAACAAGTTGGTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAGTGT
CCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTTGAAGGAATCTG
CAAAGACTATTGTCGATTCTGGCAAACCTACCATCCAGCTTGTGTGTCCTACTTCGTGTGAA
TACCGTAAGAAATGGAATAGAAATATATACGAATGTATACGAATATTATAGAGAACGTTCT
CTTTTATTTCTATAATGAATAGGTTCCGGTAACGGTTCCCTTTTTTAGGTATTTCTAGAAG
ATGAGAGAAGAGGGAATAATGAGAAAGGCGAAAAATAAAGGACACCTTTAACGAAAGATC
AAAGGTGTCCTTATTTACTTACAATAGCTGCAATTAGTACGACTCAAAAAAGTGAAAAC
AAAACCTGAAAGGATAGATCAATGTCTTACAGAGGACCTATTGGAAATTTTGGCGGTATGC
CAATGTCAATCATCGCAAGGACCATACTCTGGCGGTGCACAATTCAGATCAAACCAGAACC
AATCCACTTCTGGCATCTTAAAGCAATGGAAGCATTCCTTTGAAAAGTTTGCCTCCAGAA
TTGAGGGGCTCACTGACAATGCAGTTGTTTATAAATGGAAGCCTTACATTCCAAGTTTGT
CAAGATTTTTCAATTGTGGCCACCTTTTATGAAGATTCTGTTAGGATCTTATCACAATGGT
CAGATCAAATTTTTATCTGAATAAGTGGAAGCATTACCCATACTTCTTTGTCTGTTGTGT
TTCTAGTGGTTGTTACCGTTTCCATGTTGATTGGCGCCAGTTTGTTAGTTTTTAAGAAAGC
AAACCAATTATGCCACCGGTGTGTTATGTGCTTGGCTTATTTCTCAAGCATTAGTTTATG
GGTTGTTTACGGTTTCATCATTTGTCTTAAGAACTTTAGTGTATTGTTGGTGGGTTGTTAA
TTGCATTTCAGCGATTCAATTGTTCAAAAACAAGACAACATTCGGTATGCTTTCCTGAATTAA
ACAGCAAAAACGACAAAGCGAAGGGTTACCTGTTGTTTGTCTGGTAGAATTTTAATTGTTT
TAATGTTTATCGCTTTTCACTTTTCACTAAATCATGGTTTACTGTTGTTTGGACATTATCG
GCACAATATGTTTCGCCATTGGTTACAAGACAAAATTCGCATCCATTATGTTGGGTTTGA
TACTAACTTTTTACAATATCACGCTAAACAACCTACTGGTTTTATAACAATACTAAGAGAG
ATTTCTTGAAGTATGAGTTTTTACCAGAACTTAAGCATCATTTGGTGGGCTTCTATTAGTTA
CTAATACTGGCGCTGGTGAATTATCCGTTGATGAAAAGAAGAAGATTTACTAG

YGR284C, 310 aa (SEQ ID NO 122)

MSYRGPIGNFGMPMSSSQGPYSGGAQFRSNQNSTSGILKQWKHSFEKFA SRIEGLTDN
AVVYKLPYIPSLSRFFIVATFYEDSFRILSQWSDQIFYLNKWKHPYFFVVVFLVVTV
SMLIGASLLVLRQTNYATGVLCAVISQALVYGLFTGSSFVLRNFSVIGLLLI AFSDSI
VQNKTTFGMLPELNSKNDKAKGYLLFAGRILIVLMFIAFTFSKSWFTVVLTIIGTICFAI
GYKTKFASIMLGLILTFYNTLNNYWFYNNTRKDFLKYEFYQNL SIIGLLLLVTNTGAGE

LSVDEKKKIY

YGR285C, 1802 bp, CDS: 501-1802 (SEQ ID NO 123)

CATTTAGTTCTGATTACAGCAGAAATCGTAGCGGATGAGACATTTTCATCAAATGGCCTT
TTTTTTTTTGGGCAATTTTTTTTATATCTTGAAATGATAGTTGCCTTGTACTTTCAACCGTT
CATTTTCATTAAGAAGCTTGACTAAATATGAACATTTCTTAAAAAAGGTTGACATATAAA
AATAATCGAATATAAACGATGGAATTTTTATAAAATTAACACATATATATATATATATT
AACTATAAATATGTCAAAGAAACCATACAATCATAGATTTATAACTATCTTTTGGATGAC
ATTAATGAACATAACGCTCCTAATACAAATGTCCAAAAAATATTACCCGCAAATACGAAT
CTTTTTTTTTTCTCGATGAAATTTTGCAAAGAGTTCGAAATTTTTATTTCAGAGCTGGT
AGAGAAAATTTTATAAGGTTTTCTACCGATGCTTTTATAAAATCTTCGTTTTGTCTCAC
ATATACCAACAAGAGTAACGATGTTTTCTTTACCTACCTAACCTCAGACATCACTGTTG
AAGTCAACAGTTCGGCTACCAAACCCCATTCGTCGGTCGTCGGTCCGAACCGGTTGGTA
AGTTCTTTTTGCAACATGCTCAAAGAACTTTGAGAAACACACCTGGTCTGAATTTGAAA
GAATTTGAAGCTGAAAAGAAGCTCAAACCGTTGATGAATCCAATGTCGACCCAGATGAGT
TGTTATTTCGACACTGAATTGGCCGATGAAGATTTACTGACTCATGATGCTAGAGACTGGA
AACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAGTTGCGTTTCAGAGCTACTGAAA
GTCAAATCATCAAGGCTCACAGAAAACAAGTTGTCAAGTACCATCCAGACAAGCAATCTG
CTGCTGGTGGTAGTTTGGACCAAGATGGCTTTTTCAAGATTATTCAAAGGCCTTTGAAA
CTTTGACTGATTTCAAACAAGAGAGCTCAGTACGACTCATGTGATTTTGTGGCCGATGTTT
CTCCTCCAAAGAAGGTTACCGATTATGACTTTTATGAAGCTTTGGGGCCCGTTTTCGAAG
CTGAAGCTCGTTTTTCTAAGAAGACTCCTATTCTTCTCTAGGTAACAAAGATTCTTCCA
AGAAGGAAGTTGAACAATTCTATGCTTTCTGGCACAGATTTGACTCCTGGAGAACCTTTG
AGTTCTTTGGACGAAGATGTCCAGATGACTCTTCTAACAGAGACCACAAGCGTTACATTG
AAAGAAAGAACAAGGCCGCAAGAGACAAGAAGAAGACTGCTGATAACGCTAGATTGGTCA
AACTTGTGTTGAAAGAGCTGTCAAGTGAAGATCCCGTATCAAATGTTCAAAGAAGAAGAGA
AGAAGGAAAAGGAAAGAAGAAATGGGAAAGAGAAGCCGGTGCCAGAGCTGAAGCTGAAG
CTAAGGCCAAGGCCGAAGCTGAAGCGAAGGCTAAAGCTGAATCTGAAGCCAAGGCTAACG
CCTCCGCAAAAGCTGACAAAAGAAGGCTAAGGAAGCTGCTAAGGCCGCCAAGAAAAAGA
ACAAGAGAGCCATCCGTAACCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGG
CCACCACGATTGACGAACAAGTTGGTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAG
TGTCCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTGAAGGAAT
CTGCAAAGACTATTGTGCGATTCTGGCAAACACCATCCAGCTTGTGTCTTACTTCGTGT
GA

YHR285C, 433 aa (SEQ ID NO 124)

MFSLPTLTSDITVEVNSSATKTPFVRRPVEPVGKFFLQHAQRTLNRNHTWSEFERIEAEKN
VKTVDENVDDELFDTELADEDLTHDARDWKTADLYAAMGLSKLRFATESQIIKAH
RKQVVKYHVPDKQSAAGGSLDQDGFKKIIQKAFETLTDNKRQYDSCDFVADVPKKGT
DYDFYEAWGPVFEAEARFSKKTPIPSLGNKDDSSKEVEQFYAFWHRFDSWRTFEFLDEDV
PDDSSNRDHKRYIERKNKAARDKKKTADNARLVKLVERAVSEDPRIKMFKEEEKKEKERR
KWEREAGARAEAEAKAKAEAEAKAKAESEAKANASAKADKKKAKEAKAAKKKKNKRAIRN
SAKEADYFGDADKATTIDEQVGLIVDSLNDDELVSTADKIKANAAGAKEVLKESAKTIVD
SGKLPSSLLSYFV

YHR010W, 1472 bp, exon1: 501-531, intron1: 532-1092, exon2: 1093-1472 (SEQ ID NO 125)

GACTCGGACGGAACCGTCTCATATTATACGTTTCAGTGAATATTTTTTCACGGAAGAATGGA
AAGGGCCTCGAAAGACGTTAATGCATCCGTACACCTACATCTTTACATTTTTTGTGTG
CACCTACACTGTTTTTTTTTTTTTTTCCACTTATGAGTCTGTATTTCTTGAAGAGCCGAT
AACAATATTCCAGGTGGAGTCCCGAGGCAGAAATCAAGCTGCGGAGAGAAGTTCTCTCA
AACTAATGGGAGTGATCCGCTCAGTTCTCCCATCACGACAGAACTGTCTGAGACAAAGTC
TTTCCAGCAGAGTCCGCCCTACGCTCTTGCTGCAGAGATTGCCCCGAAGGCAGGTTTCTG
AAATCTTTTCACTAGTAAAGTGTTCGTTTCATGTAAACATACTGCCGTAGTTTGTAGCT
AAAATTAAGATATATTAGATTTTTAGAAATTTCTTAGATAGTCTCAACGTGTTAAACAA
AAGCATACCAAAGAAAAAATGGCTAAGTTCTTGAAGCTGGTAAAGTTGGTACGTATC
ATTTTCAGTTTTTTGGACATCAACAAAAACCGTCAACTGTGGTATTAGAAATCCAAGTT
ATTAGCAGTTGATGTTGTATAATTTGAGTTTGAATTCGAGTATTGTATCTTCATATGGGA
GTAGGAGGAAAAAGCGTGGAGATGTTAGATCTGGGAAAAAACCTTTAAATTTGAATGAT
AGCTTATTATAAGAAATATTGGACAAAAAGATGAATGATTTAGGAGCGAAACCTAACGATT

ATTCATATTTCATTGAGCTATACGAGGCAGTGGGAAGGGTTATCAAAAAGTTGTAATTTAAA
AGAAAAAGCATCAATAGCCACCAAATAAGATGGTGAAAGTTCCGCGATATATTGCTAA
GACCATAGGCACATGTACGCAGGCGACCAGGGCCTTTTATTTACTGTAGTTCTTTCCATG
CCCTATTAAAAAATTCGTGGGCCCTATGATAATTTTCTCTCCCTAGTATTGAAGAACAAAA
TTGAGAATTCGCCAACTTTAAGAAGGGTTCACATTTACTAACTATTTCTTTCTCTCT
TTTTTTTACACAGCTGTCGTTGTCCGTGGTTCGTACGCCGGTAAGAAGGTTGTTATCGTTA
AACCACATGATGAAGGTTCCAAGTCTCACCATTGGTTCACGCTTTGGTTGCCGGTATTG
AAAGATACCCATTGAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTTGCTAAGAGAACCA
AGATCAAGCCTTTTCATCAAGGTCGTCAACTACCAACCATTTATTGCCAACCAAGATACACTT
TAGATGTTGAAGCTTTCAAATCCGTTGTTTCTACTGAAACTTTTGAACAACCTTCCCAAC
GTGAAGAAGCTAAGAAAGTCGTCAAGAAGGCTTTTGAAGAAAGACACCAAGCTGGTAAGA
ACCAATGGTTCTTCTCTAAGTTGAGATTTTAA

YHR010W, 136 aa (SEQ ID NO 126)

MAKFLKAGKVAVVVVRGRYAGKKVVIKPHDEGSKSHPFHALVAGIERYPVKVTKKHGAK
KVAKRTKIKPFIKV/VNYNHLPLTRYTLDEAFKSVVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YHR021C, 1299 bp, exon1: 501-503, intron1: 504-1053, exon2:
1054-1299 (SEQ ID NO 127)

TTACTTACGTCCTATTATAACCTTCCGCGTAAAAAAGAAATATTGACATCCTTTCTTGTAT
TTAGCCCATACATTTTCACCCATGCACCATTTGGATTATAAAGAAAAAAATTTAATAAAAA
TCTGCCGGGGAATTTTCAGAAGAAAAAGGAAGGTGTGTTCCGATTTAACACGGGCCACC
ATAAACTTTTGTTTGCCACCCATCTAGACGGGATCCGCCCCGCCCAAGGCTCTCTTCCTC
TAGCTAGGCAATGTGGCTCTCGGAAAGGAACTCCCAACAGGACGTGGTGGGAAATGCAG
CAATTCCTCTGCTTCCCGCTGACCTTTCTTGGGCCAGTTTAGTAAGTATGCTCTCAT
CTTTCATGTGTGCTGTAACCTTGCAAGTCATTAACACTATCTATAATTGATATTAGACGTT
AAAAGTTCTATATAGCATTTGCTTTTATTTAGAGAATACGAAAACACACCAGATAATTAG
TGCATATATATTAGATCAATATGGTATGTGAAAGAGATATTAACATAAGATGTGAAGGA
AACAGAAGAGAAACAATATTTGAGGAATGAATTCGGATGAAATTCTAGTAGAAGAAAAAAG
CCTAAAAATAAAAAAGAAAGAAAGGAAAAATAAAGCAGTAATCAACCTCTGACATTTGATAGG
AGTATGCGTTTCCGCAAAATCAACAAATCATGCATTAACTGGTAACGGAGACTTTAAAG
ACGTGCAAAAGAAAGCAATTAATTTTGTAGATAGGGAATTTGAAAGGCTCTGTATAGCAGAAA
ATTTGAGATCTACTGTGGAGATAAGCATATGGTGTGAGTTATGGGTAATCTAACAATAA
TAGAACTTATAGCAGTTGAAGATGGCGGATCATGATGCCGATACTGCTGGGTAATGAT
TTATCCTTCTTTTGGAGCACAAATGCTCACTTTTCTCTGCTCTCTAATTTTCTG
ATGTATCCTACCCAACCTTACAGTTTTCAAATTACTAACATCAATTTTTTGTGAAACGA
CTTTCGTTTTCTGTTCTATTTATTTTCAATTACAGGTTTTAGTTCAAGATTTGTTGCACCCA
ACTGCTGCTTCTGAAGCCAGAAAGCACAGTTAAAGACTTTGGTTCAAGGCCCAAGATCC
TACTTCTTGGATGTCAAATGCCAGGTTGTTTGAACATCACCAGTGTTTTTTCTCATGCT
CAAAGTGTGCTCACTTGTGAATCATGCTCTACTGTCTTATGTACTCCAACCGGTGGTAAG
GCCAAATTATCTGAAGGTACTTCTTTCAGAAGAAAGTAA

YHR021C, 82 aa (SEQ ID NO 128)

MVLVQDLLHPTAAASEARKHKLKTLVQGPRSYFLDVKCPGCLNITTVFSHAQTAVTCESCS
TVLCTPTGGKAKLSEGTSFRRK

YHR141C, 1262 bp, exon1: 501-504, intron1: 505-945, exon2:
946-1262 (SEQ ID NO 129)

TAAACATGGCATTTTAAATAGTACTGCCAAAATTTAATGCAATGGCAATTAGTTGGCTA
TGTGTGTACATATTATTTTCCATAGCATTCTCTGTACAAACTTCAAAATAAAAGACAGT
GACATCCGAACATCCGATACACCCATACATCATGAAAAATAAATCCTGACATTGGAAGAAG
TCTTGATACAAAAAAGATCGCTGTCAAAAATGCGGCCAGACTGCCGCTGCATCGTACCA
ACAGTGCCTATGTTTACAGACGGAGAGACGACCTCTAGAGAGACGTCCGTCGGTGCGGCAAC
GCTGACGGTTTAGTTGTTTGCACGGGATGATGGGTTCCGCCAGGGGGAGGGAAGGCTTTCC
ACCAAGAGAGGTAATAATTATTCGTGCAAAATGAACTCAGAGATACATCCATATTGTTGACA
ATGTATATCTTAATTGATGTGGTATTTTCACTGTTTAAACGTAAATTGAAGGAGATTAAAG
CAAAAAACAATCAGTAATAATGGGTATGTGGACGATTAGGAATAGACAAACCATGTTAT
TTATCTCCATTAGGGCGTGAGAGTGTAATTAGTACACAGGTAATACTAGTAATGCTAAAGA
ACTTTTTTAAATATCCTGAATCGTAGGGCAAATCCATGTCAAGCAAGAACTAATAGTTA

TTAAACTTCATTTACTTTTGTAGCTAGTTAAATATTTTCATCATTTTCCTAAAGTACTGAAC
ACCTGAATGATACTTTATTGGCCCTTTTAATAAGAACTCTGGTTAGAAAATATATTGAG
GATATCATTTAGTAATACTCATTAGATATTTGTGAATTTAGCCGTTTCCCCATTACAGAAA
AAAGATACAACATAATTACATGTGCAGTCAAATTACTTTTTTTTAAAGATCAATTACTAAC
AATCAACTATCATGCTAAATTTGCTGTGATATCATTTTGAACCAGTTAACGTCCCAAAGA
CCAGAAAGACCTACTGTAAGGGTAAGACCTGTCGTAAGCACACTCAACACAAGGTTACTC
AATACAAAGCTGGTAAGGCTTCCTTGTTTCGCTCAAGGTAAGAGACGTTATGACCGTAAAC
AATCTGGTTTTCGGTGGTCAAACCAAGCCTGTTTTCCACAAGAAAGCTAAGACTACCAAGA
AGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACTAGAGCCCAATTAACCTTGAAGA
GATGTAAGCACTTCGAATTGGGTGGTGAAAAGAAGCAAAGGGTCAAGCTTTGCAATTCT
GA

YHR141C, 106 aa (SEQ ID NO 130)

MVNVPKTRKTYCKGKTCRKHTQHKVTOYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHK
KAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YHR217C, 962 bp, CDS: 501-962 (SEQ ID NO 131)

CATCGCTTGATTTCCGGCCTGCAAAAATAAAGTAGTCGGTACGTACTTTCGTTTTCAATT
TCCATGGTGCACAGTATCTTAACATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTTCGT
TGCTCAGCCGCTTCGTGGATATCTCTTGGATACTTTAAACATGGACCTACGTTCCGCTC
TCGAAAAGACCAATATAATAAAAAGTTATAAATTACATTTTCTTATTAGGTATACGACCT
CGCGCTTCGAAGTAGAGGAGCCCTTTTTGGCGGTACCTACATATGGCGCGTCAGACAGACA
AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATTACCCACGAC
GTATCAAGTTACTTCTTGGTGCAATGTCCCACTATAAAAAAATTCCTTGACGCTAGATC
GTTGGACTAAAATCTGCGTCACAATCGCCTAAACAGGAAATATTGCCTATTTTCGTACAA
GGTTACTTCCCTAGATGCTATATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAAT
ACAGTGACATATATATACACACACCCACACCCACACCCACACCCACACCCACACACACCC
CACACACACACCCACACACCCACACCCACACCCACACCCACACCCACACACACCCACACC
CACACACACACCCACACCCACACCCACACCCACACCCACACCCACACACCCACCCATCTA
ACCTGTCTCTTAACCTACCCCTCACATTACCCTACCTCCCCACTCGTTACCCTGCCCCACT
CAACCATACCCTCCCAACCACCATCCATCTCTCTACTTACTACTACCATCCACCGCCCA
TCATAACCGTTACCCTCCAATTACCCATATCCAACCTCCACTACCATTACCCTGCTATTAC
CCTACCATCCACCATGTCTACTCACTGTACTGTTGTTCTACCCTCCATATTGAAACGTT
AA

YHR217C, 153 aa (SEQ ID NO 132)

MSLRPCLTPSSMQYSDIYIHTPHPHPHPHPTPTHHPHTPTPTPHPHPHPTPHPHPTPTPT
TPHHTHTPHHTLSNLNLSLNLPSHYPTSPVLTLPHSTIPLPTTIHLSTYYHHPPPIITVTLQ
LPISNSTTITLLLPHYHPPCPTHCTVVLPSILKR

YIL112W, 3752 bp, CDS: 501-3752 (SEQ ID NO 133)

TTCCATAGGGCTTATTTTCCAGTTGATGGAATGGGAGGTTGCTCTTAACGCGAAGACTAA
CGTGCAAGCCAACAGTTATAGAAAAGTACCGTGAGAGAGAAAAAAGATATAGCA
TTCAATGAGGCTTTATTGAGGGGCACGATGCTCTTTTTTTCTTCTGTACTTTATAAATAA
TTCCGTATTTCTTCGCTTTGTTTTCATGCTCTGTTCTGAGCTTTTAGTTTCTCTTATTGAG
AGCCTTTTCCAAATCAAGGCTCAGGAAGTGACTCGTCCTTAGAAGAACAAGGTTTGGATT
TGGTAGGGTTCTTGTACGAAGTTCTCAATATAATTTGCGCATTTACTGTACGGTTCATAC
TAGTTTATTCCGGGTAACAAGTTTCTTGTGATGCTAAATCAATGTGTATATTGAGAAAA
CTATGTAGTAAGTTACACAAAGCAACAAAGGATATTATTATATGTGACAGAGAAGAATTG
CTGTAGAGATTTCATGACAATATGAATGAGACTACTACAAAACAGCCGCTAAAGAAAAGGT
CCCTGAGCAGCTATCTTTCAAACGTGAGCACGAGACGGGAGGAGCTGGAAAAGATTCTA
AACAAGAAACATCCGAAGAGGAAGATACTGCCGGAAGCATGAACAAAGGGAAACACTGT
CGGAAGAAGTAAGTGATAAGTTTCCAGAAAATGTTGCATCGTTTCGCTCACAGACTACAA
GCGTTTCATCAAGCCACCCAAAATAACCTGAATGCAAAGGAATCCGAAGACCTGGCCCAT
AGAATGATGCGAGTTCACACGAAGGAGAGGTTAATGGGGACAGCCGTCGGGACGATGTTT
CTGAAACGAATGAAAAAATAAGCCAAGCAATACGAGCGAAAATTCGTCATCATCATCAT
CACCCAATGACGTAATGTTGATATCCAAAACCATCAACCTTTTCGAGAGACCAACTTC
GAGCGATGTTGAAAGAACCAAAAAGGAAAACCTGTTGATGATTTCATAGAAGAAGAGGGTT
TGGGAGCTGTTGAAAGAAGAGGATTTAAGTGATGAGGTACTTGAAAAAATACAACAGAAC
CAGAAAATGTGGAAGAAGATATAGAGTATAGCGACTCAGATAAGGACACAGACGATGTGG

GAAGCGATGATCCACGGCACCCAACCTACCAATAAACTTGGTCGTCGCAAACTGGTTA
GAGGTGACCAACTTGATGCAACAACAAGTTCCATGTTTAATAACGAATCAGATTCTGAAT
TATCAGATATCGATGATAGCAAGAATATTGCTTTATCCAGTAGCCTATTAGAGGCGGTT
CTTACCTGTGAAAGAGACAAACAACACCTTTCAAATATGAATTCTTCACCAGCACAAA
ATCCAAAAAGGGGTTCTGTCTCCAGGAGTAATGATAGTAACAAGAGTTCTCATATAGCTG
TTTCCAAGCGCCCCAAACAGAAGAAGGGCATATATAGGGATTCTGGTGGTAGAACAAGAC
TACAGATTGCCTGTGACAAGGGCAAATATGATGTAGTCAAAAAGATGATTGAAGAAGGAG
GTTACGATATTAATGACCAAGACAATGCTGGTAATACAGCATTGCATGAAGCGGCGTTGC
AAGGTCATATTGAGATTGTGGAAGCTGTTGATAGAAAATGGTGCAGATGTAATATCAAGT
CTATTGAAATGTTTCGGCGATACTCCCTTGATCGATGCTTCCGCCAATGGACACTTGGATG
TTGTCAAGTATCTTCTTAAAAACGGTGGGACCCAACTATACGTAACGCTAAAGGGTTAA
CTGCGTTTGAATCTGTGATGATGAATCTGAATTTGATGATGAAGAAGACCAAAAGATTT
TGCGTGAAATAAAAAAAGGTTGAGTATAGCCGCTAAAAAATGGACTAACAGAGCAGGAA
TTCATAATGACAAATCTAAAAATGGCAATAATGCTCACACAATAGATCAGCCACCTTTTG
ATAATACCAAAAAGCCAAAAACGAAAAGGCGCTGACTCACCTTCAATGGCTTCCAATA
TTGATGAGAAAAGCTCCGGAAGAGGAATTCTATTGGACAGATGTTACTTCTAGAGCGGAA
AAGAAAACTGTTTAAAGCTTCGAAGGAGGGACATTTACCATACGTTGGTACGTATGTAG
AAAATGGTGGTAAGATAGACTTAAGGTCATTTTTCGAAAGCGTTAAGTGTGGCCATGAAG
ATATTACAAGTATCTTTTTGGCATTTCGGATTTCCCGTAAATCAAACCTTCAAGGGATAATA
AAACATCCGCTTTAATGGTAGCTGTAGGTCGTGGCCATCTTGGAACTGTTAAACTGCTAT
TAGAGGCAGGTGCAGATCCAACCAAAAGAGATAAAAAGGGTCGTACCGCTTTGTACTATG
CCAAAAACAGCATAATGGGAATAACAAACAGTGAAGAAATTCAATTGATTGAAAATGCTA
TAAATAACTATTTGAAGAAGCACTCTGAAGATAATAATGATGATGATGATGATGATA
ATAATAATGAAACATATAAACATGAAAAAAGAGAGAGAAAACGCAATCACCCATATTAG
CAAGCCGAAGAAGTGCCACTCCTAGAATTGAAGACGAAGAGGACGATACGAGGATGCTCA
ATCTGGCAGACGATGACTTTAATAACGATCGTGATGTCAAGGAATCTACAACCTTCGGATT
CGCGCAAGAGATTGGATGACAATGAAAATGTTGGTACTCAATACTCATTGGACTGGAAAA
AACGTAAAAACAAATGCCTTGCAAGATGAAGAAAAATTAAAAAGTATCTCACCCTCTCTA
TGGAACCTCATTCTCAAAGAAGGCAAAATCTGTAGAGATAAGTAAAATACATGAAGAAA
CGGCTGCTGAAAGAGAAGCAAGACTCAAGGAAGAGGAAGAATACAGAAAGAAAAGATTAG
AAAAGAAAAGAAAAAAGAACAGGAAGTACTACAAAAGCTGGCCGAAGATGAGAAAAAAA
GGATCGAAGAACAGGAGAAGCAGAAAGTCTTAGAAATGGAAGATTGGAAGAAAGTACTT
TAGAGAAAGCAAGAAAAATGGAAGGGAAAAAGAAATGGAAGAAATCTCTTAGAAGGG
CAGTAAGGGACTTATATCCGTTAGGACTGAAGATTATTAACCTCAACGATAAAGTTGATT
ACAAAAGATTTTGGCCGCTATATTATTTGTAGACGAAAAAACGATAAATTTGTGCTCG
ACTTGCAAGTAATGATATTGTTGAAGGATATCGACTTGCTCTCAAAGGACAACCAACCA
CTTCTGAGAAGATTCCCGTCGATCCCTCGCACCTGACTCCATTGTGGAATATGTTGAAAT
TCATTTTCTGTATGGAGGTAGTTATGATGATAAAAAGAACACATGGAAAAATAAAGAT
ATGTTTAAACTTTGATGGGGTTGATTGAGACACAAAGATTGGGTATGAGCTTTTGGAGT
ACAAAAAATTTGTTAGTTTGGCCATGGCGTGGATTAAATGGGATAACGTTGTTATTGAAA
ACCACGCAAAAAGAAAAGAAATTGAAGGAAATATGATTCAAATATCAATAAACGAATTTG
CACGATGGAGAAACGATAAGCTGAACAAAGCGCAGCAGCCGACGCGCAAACAGCGTTCTC
TAAAAATACCTCGAGAGTTACCGGTTAAATTTCAACACCGTATGAGCATATCTCCGTC
TCCAGCAGACATCCAAAGAACCATTTTGGTAA

YIL112W, 1083 aa (SEQ ID NO 134)

MNETTTKQPLKKRSLSSYLSNVSTRREELEKISKQETSEEEDTAGKHEQRETLSEEVS
DKFPENVASFRSQTTSVHQATQNNLNKASEDLAHKNDASSHEGEVNGDSRPDDVPETNEKI
SQAIRAKISSSSSPNVRNVDIQNHQPF SRDQLRAMLKPKRKTVDDFIEEEGLGAVEEE
DLSDFNLEKNTTEPENVEKDIEYSDSKDITDDVGSDDPTAPNSPIKLGRRKLVRGDQLDA
TTSSMFNNESSDSELSIDDSKNIALSSSLFRGGSSPVKETNNLNNMNSSPAQNPKRGSV
SRSDNSNKS SHIAVSKRPKQKKGIYRDSGGRTRLQIACDKGKYDVVKMIEEGGYDINDQ
DNAGNTALHEAALQGHIEIVELLIENGADVNIKSIEMFGDTPLIDASANGHLDVVKYLLK
NGADPTIRNAKGLTAFESVDDSEFDDDEEDQKILREIKKRLSIAAKKWTNRAGIHNDSK
NGNNAHTIDQPPFDNTTKAKNEKAADSPSMASNIDEKAPEEEFYWTDVTSRAGKEKLFKA
SKEGHLPYVGYTVENGKIDLRSSFESVKCGHEDITSIFLAFGFPVNQTSRDNKTSALMV
AVGRHLGTVKLLLEAGADPTKRDKGRTALYYAKNSIMGITNSEEIQLIENAINNYLKK
HSEDNDDDDDDNNNETYKHEKKREKTQSPILASRRSATPRIEDEEDDTRMLNLADDDF
NNDRDVKESTTSDSRKRLDDNENVGTQYSLDWKKRKTNALQDEEKLKSI SPLSMEPHSPK
KAKSVEISKIHEETAEREARLKEEEYRKKRLEKKRKKEQELLQKLAEDEKKRIEEQEK

QKVLEMERLEKATLEKARKMEREKEMEEISYRRAVRDLYPLGLKIINFNDKLDYKRFPLPL
YFVDEKNDKFVLDLQVMILLKDIDLLSKDNQPTSEKIPVDFSHLTPLWNMLKFIFLYGG
SYDDKKNMNMENKRYVNVNFDGVDLDTKIGYELLEYKFFVSLPMAWIKWDNVVIEHAKRKE
IEGNMIQISINEFARWRNDKLNKAQQPTRKQPSLKIIPREL PVKFQHRMSISSVLQQTSKE
PFW

YIL115C, 4883 bp, CDS: 501-4883 (SEQ ID NO 135)

TTTCAATGCGCTACAACCTGACTGAACCAGTCCACAAATTTGGCTGGTCTCTATCGTTCTC
GCCCTGAGAGATTTTATTTTCTTATAAAATTTTACTAAATAAGGATTTGTACTTTTGATAG
AGTTTATTTTCTGACGTTTGTAGTTAATATTATATAATAGTATTTAGGAACTA
GGTGGGAGGGGACATCGCAACTTTTATCGTGACCTACGACCAGTGTCTTTTCAATTGTTT
GATCAAAAGAGAAAAAAGACAAAGGACCGAAGGATAGTTGCACGCATAAACTGGAGAAA
AAATTTGTGTTTGACATCGGCGTTTAGGCTTGTGTTCTGTCTACACATACGCTGCTTCAC
ACCAATTTCATATTTCTCAGGTTAATTTGTCTCTCTCCAACCTTCAATAACGATTTTGGCT
GAAGTTTAAATTTCAATTATGCAATTTTACGAGAGAAACGCACATAAATATATATATATT
GATTACAGAACCATTATAACATGTCTTCTTTGAAGGATGAAGTACCCACTGAGACTTCCG
AAGACTTCGTTTAAAGTTTGTAGGTCAAAAACAAATTTCTACCTTCTTCAATGAAAAAC
TGCCATTTGCATCTCTACAAAATCTCGATATTTCAAACAGTAAGTCTTTATTCGTTGCTG
CCTCTGGTAGTAAGGCGGTGGTTCGGCGAATTAACAATTACTGAGAGATCATATCACCTCCG
ACTCTACTCCGTTAACGTTCAAGTGGGAGAAAGAAATCCCAGATGTAATATTTGTGTGCT
TTTATGGTGATCAGGTTTGTGTTTCAACCAGAAATGCATTATATTCGTTAGACTTGGAGG
AATTGAGTGAAATTCGAACGGTCACTTCTTTTGAAGAAGCCAGTTTCCAATTGAAGAAGC
TTAATAACACTTTAGTAATTTTAAATTCAGTCAATGATTTATCAGCACTGGATTTAAGAA
CAAAATCGACTAAGCAACTGGCACAAAACGTTACCTCTTTTGATGTACAAAATTCGCAGT
TAGCAGTTCTACTAAAAGATAGAAGTTTTCAAAGTTTTCATGGCGAAATGGCGAAATGG
AAAAACAATTTGAGTTCTCTTACCGTCAGAATTAGAAGAGCTTCCAGTAGAAGAATATT
CCCCTTGAGTGTTACCATTTCTCTCTCCACAGGATTTTGGCGGTTTTCGGTAAATGTTA
TATCAGAGACCGATGACGAAGTTTCTACAGATCAAAAAATGTACATTATAAAGCACATAG
ACGGCAGCGCTCATTTCAAGAACTTTTGATATTACACCTCCATTCGGGCAATAGTAA
GGTTCCCATATATGTACAAAGTTACCTTGTCTGGTTAATTGAACCTGATGCAAAACGTAA
ATGTGCTAGCATCATCATGTTCAAGTGAAGTAAGTATATGGGACTCGAAAACAGTTATG
AACCTTCCAGGATTTCTGAACGAGCAGTATTGCCCATCAGTGAGGAAACAGATAAGGACA
CAAATCCAATAGGTGTGGCAGTTGACGTCTGTTACTTTCAGGCACTATTCTAGAACCTTGT
CCGGTGTGATACGATAGAGCGATTGCCGCTCGTTTACATATTGAATAACGAAGGTAGCT
TACAGATAGTCGGGTTGTTTCTGTGGCAGCAATCAAAAGCGCCATTATAGCATAAATC
TGGAATCTTTAGAACATGAGAAATCTCTCTCTCTACATCAGAAAAAATTCCTATTTGCTG
GACAGGAGCAGGAAGAAAAAAGAAAAATAATGAATCAAGTAAGGCTTTATCAGAGAATC
CTTTCACATCAGCAAATACATCAGGCTTCACTTTCTTAAACACAACCAGCCGCTGCCA
ATAGCCTGCAGTCTCAAAAGTTCTTCAACCTTTGGTGCTCCCTCATTTGGATCATCCGCAT
TTAAATTTGACTTGCCATCAGTCTCATCTACCAGTACTGGTGTAGCGTCCAGTGAACAAG
ACGCAACAGATCCTGCTTCTGCTAAGCCAGTATTTCGGCAAACCCGCTTCGGAGCTATTG
CCAAAGAACCCTCAACATCAGAATATGCCCTTTGGCAAGCCATCTTTTGGTGCTCCCTCCT
TTGGCTCTGGAAGTCACTGTGTAATCGCCTGCCTCCGATCTGCCTTTGGTAAGCCCT
CTTTTGGTACTCCTTCTTTGGCTCTGGAATTCATCTGTTGAGCCGCTGCCTCCGGAT
CTGCATTTGGTAAGCCCTCTTTTGGTACTCCTTCTTTGGCTCTGGAATTCATCTGCTG
AGCCGCTGCTTCCGGATCTGCCTTTGGTAAGCCCTCTTTTGGTACATCTGCATTCGGAA
CTGCATCAAGTAACGAACTAACTCTGGATCCATATTGGAAAGGCTGCATTTGGTTTCAT
CATCTTTTGCACCCGCCAACAATGAACCTTTTCGGATCAAACTTTACTATTTCAAAACCTA
CAGTTGACAGCCCAAAGGAGGTAGATTCAACGTCACCTTTCCCATCTTCTGGCGATCAAA
GTGAAGATGAGTCTAAGAGTGTAGTACTCTTCTCGACACCTTTTGGTACGAAACCTA
ACACCTCTACGAAACCAAGACCAATGCTTTGATTTTGGGAGTTCTTCTTTTGGATCTG
GATTTTCAAAGGCTCTGGAATCTGTTGGTTCCGATACAACCTTTTAAATTCGGTACTCAGG
CTTACCTTTCTCTTACAGTTAGGAAACAAATCACCATTAGTTTCTTCAAAAAGATG
ATACTGAAAAATGGATCTTTAAGTAAGGCTCTACCAGTGAAATCAATGACGATAATGAAG
AACACGAAAGCAATGGTCCCAACGTAAGCGGTAATGATTTGACAGATTTTACGGTTGAGC
AAACATCTTCTACTAGATTACCGGAACTCCCTCGGATGAAGATGGTGAAGTTGTCGAGG
AGGAAGCGCAAAAAATCCCCATAGGCAAGCTAACTGAAACTATAAAAAAAGATGCCAATA
TTGACATGGCTGGTTTAAAAAATCCTGTATTTGGAAATCATGTCAAAGCAAAATCCGAAT
CGCCGTTTTCAGCATTTGCAACAAATATTACCAAACCAAGCTCTACAACACCTGCTTTTT
CGTTTGGTAACCTCCACAATGAATAAAAGTAATACATCTACGGTTTACCAATGGAAGAAG

CTGATACTAAAGAACTAGTGAAAAGGGCCCCATAACCTTGAAGAGTGTGGAGAATCCGT
TTCTACCAGCGAAAGAAGAAAGAACTGGAGAAAGTTCTAAAAAGGATCATAACGATGACC
CAAAAGATGGTTATGTATCAGGAAGTGAAATATCTGTAAGGACTTCTGAAAGTGCTTTTG
ATACCACAGCAAAACGAAGAAATTCCAAAGTCACAGGACGTGAACAATCATGAAAAAAGCG
AAACAGACCCAAAATATAGTCAACATGCTGTGGTTGATCAGGATAACAAGTCTAAAGAAA
TGAATGAAACTTCGAAGAATAATGAAAGGAGCGGTCAACCAATCATGGTGTCCAAGGAG
ATGGAATAGCATTGAAAAAAGACAATGAAAAAGAGAATTTTGATTCAAATATGGCAATAA
AGCAATTTCGAAGACCACCAATCTTCAGAAGAGGACGCGAGCGAAAAAGACAGTAGACAAA
GCAGTGAAGTTAAAGAATCAGATGATAACATGTCACTCAACAGTGACCGGGATGAAAGTA
TATCTGAGTCTTACGATAAACTGGAAGATATTAATACTGATGAGCTACCTCATGGTGGAG
AAGCTTTTTAAAGCACGTGAAGTGAGCGCTTCCGCTGATTTTGATGTACAAACTTCATTAG
AAGACAATTATGCTGAATCTGGCATAACAGACAGACCTTTCAGAAAGTTCCAAGGAAAATG
AAGTTCAAACGGATGCCATACCCGTGAAACACAACAGTACACAAACTGTTAAGAAGGAAG
CAGTCGACAATGGTCTGCAAACTGAGCCTGTTGAAACATGTAATTTTTCTGTTCAAACAT
TTGAAGGTGACGAAAATTATTTAGCAGAGCAATGCAAAACCAAGCAATTGAAAGAATATT
ACACAAGTGCAAAAGTATCAAATATTCCTTTCGTTTCACAAAATTCTACGTTAAGGTTGA
TTGAGAGTACATTTTCAGACGGTCGAAGCTGAGTTTACTGTTCTGATGGAAAACATCCGGA
ATATGGATACTTTTTTTACTGATCAATCGAGCATCCCTTTGGTGAAGCGTACAGTGCGGT
CTATCAATAATCTGTATACTTGGAGAATACCAGAGGCTGAAATTCTATTAAATATTTCAGA
ATAATATCAAGTGTGAACAAATGCAATAACAAATGCTAACATTCAAGACCTGAAGGAAA
AAGTTACAGATTATGTGAGAAAGATATTGCACAAATAACTGAAGATGTAGCCAATGCAA
AAGAGGAGTATCTGTTTTTAATGCATTTTGATGATGCTTCGAGTGGATACGTTAAAGATC
TCAGCACGCATCAATTTAGAATGCAAAAGACATTACGTCAAAAGCTATTTCGATGTGTCCG
CCAAAATTAATCATACTGAAGAGTTGCTGAACATTTTAAATTTGTTCACTGTAAAGAATA
AGAGATTGGACGATAATCCATTAGTGGCAAACTAGCTAAAGAATCTCTTGCACGTGACG
GTTTACTAAAAGAAATCAAATTATTGCGTGAGCAAGTGAGTAGGTTACAATTGGAGGAGA
AAGGTAAAAGGCTTCGTCGTTCCGATGCATCCTCTTCAATAACAAAGGACATGAAAGGAT
TTAAAGTAGTAGAAGTTGGGTTGCCATGAATACGAAAAAGCAAATTGGTGATTCTTCA
AAAATTTGAACATGGCAAAATAG

YIL115C, 1460 aa (SEQ ID NO 136)

MSSLKDEVPTSETSEDFGFKFLGQKQILPSFNEKLPFASLQNLDISNSKSLFVAASGSKAV
VGELQLLRDHITS DSTPLTFKWEKEIPDIVFCFHGDQVLVSTRNALYSLDLEELSEFRT
VTSFEKPVQLKNVNNLTVILNSVNDLSALDLRTKSTKQLAQNVT SFDVNSQLAVLLKD
RSFQFAWRNGEMEKQFEFSLPSELEELPVEEYSPLSVTILSPQDFLAVFGNVISETDDE
VSYDQKMYIIKHIDGSASFQETFDITPPFGQIVRFPYMYKVTL SGLIEPDANVNVLASSC
SSEVSIWDSKQVIEPSQDSERAVLPISEETDKDTPNPIGVAVDVVTSGTILEPCSGVDITIE
RLPLVYIILNNEGSLQIVGLFHVAAIKSGHYSINLESLEHEKSLSPSEKIPIAQEQEKEK
KKNNESSKALSENPF TSANTSGFTFLKTQPAANSLQSSSSTFGAPSFSGSAFKIDLPS
VSSSTSGVASSEQDATDPASAKPVFGKPAFGAIAKEPSTSEYAFGKPSFGPSFGSGKS
VESPASGSFAGKPSFGTPSFGSGNSSVEPPASGSFAGKPSFGTPSFGSGNSSAEPPASGS
AFGKPSFGTSFAGTASSNETNSGSIFGKAAGFSSSFAPANNELFGSNFTISKPTVDSPE
VDSTSPFPSSSGDQSEDESKSDVDSSSTPFCTKPNTSTKPKTNADFSGSSSFGSGFSKALE
SVGSDTTFKFGTQASPFSSQLGNKSPFSSFTKDDTENGSLSKGSTSEINDDNEEHESNGP
NVSGNDLTDSTVEQTSSTRLPETPSDEDGEVVEEAQKSPIGKLTETIKKSANIDMAGLK
NPVFGNHVKAKSESPPSAFATNITKPSSTTPAFSFGNSTMNKSNTSTVSPMEEDTKETS
EKGPITLKSVENPFLPAKEERTGESSKKDHNDPKDGYVSGSEISVRTSESADFDTTANEE
IPKSQDVNNHEKSETDPKYSQHAVVDHDKSKEMNETSKNNERSGQPNHGVQGDGIALKK
DNEKENFDSNMAIKQFEDHQSSSEEDASEKDSRQSSEVKESDDNMSLNSDRDESI SESYDK
LEDINTDELPHGGEAFKAREVSASADFVQTSLEDNYAESGIQTDLSESSKENEVQTD AI
PVKHNSQTQVKKEAVDNLQTEPVETCNFSVQTFEGDENYLAEQCKPKQLKEYYTSKVS
NIPFVSNSTRLRIESTFQTVAEFTVLNENIRNMDTFFTDQSSIPLVKRTVRSINNLYT
WRIPEAEILLNIQNNIKCEQMQITNANIQDLKEKVTDYVRKDIAQITEDVANAKEEYLF
MHFDDASSGYVKDLSTHQFRMQKTLRQKLFVSAKINHTEELLNLIKLFVKNKRLDDNP
LVAKLAKESLARDGLLKEIKLLREQVSRLQLEEKGKASSFDASSSITKDMKGFKVVEVG
LAMNTKKQIGDFFKNLNMAK

YIL148W, 1321 bp, exon1: 501-508, intron1: 509-942, exon2:
943-1321 (SEQ ID NO 137)

TCGATCAACTCTATCCAACAATTCATATAATATCCACTGTTCAATTAACGAATATTGGTCTT

TTTCCCTTATGGTGAAGTAAATTTTCATGCAATATCCGGGTAAGCTATCGACAAGTTTA
TTGACTGCAATTTGAGTTTATTACATCCGTACATTACTAAGATGTATGGTTTTTCTATTT
TTGTGCTCCGTGTCGATATTTCTGAGGAGCAAAACAGAAAGATGCGGAACCTCTTAGCAC
TCCGCCCTGGACATAGGCGGAGCATATTTCTCTCTATGGGATGGGTTTTGTTGTACTCTTTT
CTCTCTAGACAGGACCTCCGATTGCCTCCCTGAGGGTGAGATGGTTTTCCGGCCTCAGGAC
GGCCTTCTCCAGTTTCTAGCGAGGCATACATTCCAACCAAGGTGTATCAAGAATATCTG
AAATTAAGGTAGTTGAATCTCTATTTGTTGTTGTTATTACCGCTTATTATCCCATAGTT
GAGACGACCAAGATTCAAACATGCAAAATGTATGCACCATATCCATTCTAAACATAGTTTT
TCGAACGTTTCAAGCTTAAAGGGACAATTATTTAGAACTGAATTTTTACCCAGTGGAA
TAACATCGTATCTGTAAAGTCTACAAAATTTTTATCCATCAAAAATTAACAAAGAAA
ACTGCCAAAAGTGAATATGAGGAACCTTCTCTCTAGGAATGACTTAGTGAATGTACAGTG
ACTTGTGGAAAATATGATTAGATTTTGTAGCGGGTGATGCGACTTAACAGTCTCATTGCCT
AAGAAATATCCAAATTTGTGGTTTCATGCTCTCCCCAAGATATGACGATGAGAGCTCGTT
TAAATTTTGTCTTCTTCCGAACAGTTATGAAAAACTATTACGTGTTTTTATGATATCC
TTACTAACTTGTCTATTTTTTATAAAATATTTTTTTAACAGTTTTGTCAAGACTTTGAC
TGGTAAGACCATCACTTTGGAAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCAAA
GATTCAGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCA
ATTGGAAGACGGTAGAACCTTGTCTGACTACAACATTCAAAAAGAATCCACTTTGCACCT
AGTCTTGAGATTGAGAGGTGGTATCATTGAACCATCTTTGAAAGCTTTGGCTTCCAAGTA
CAACTGTGACAAATCTGTTTGCCGTAAGTGTTATGCTAGATTGCCACCAAGAGCTACCAA
CTGTAGAAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTAAATG
A

YIL148W, 128 aa (SEQ ID NO 138)

MQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQQLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLGGIIIEPSLKALASKYNCDKSVCRKCYARLP PRATNCRKRKCGHTNQ
LRPKKKLK

YIL150C, 2216 bp, CDS: 501-2216 (SEQ ID NO 139)

AATATTCAACCTGAAGTTGCAGTCAAAGCGGCGATTAACTTTTCCAACGTAACCGATCTA
ACTAACAATAGCACCGATGGAGCAAAAATAACAGAAATTGGAAGTACATCTAAACGGCCA
ATTGAGAGCGGTACATCTTCTGATCCAGACACCAAAAAGGTTAAAGAGAGTCCAGCAAT
GATCAAGCTTCCAACGAGTGATGTAATATTAACAATGTAATTATATAAATATGAAACAT
CTACATATTTTAAATGTCATAATGTATTACAGAGGACATAAAGTGATTTATGACACAT
CCGTACTAGTAGTTAAGTATGAACAAATTTTGGGTTTTATTGTCATTTTTTTTACGCGG
GTTTCTTGGATGCGCAAACCCACCTTTTCTAACACCACTAAGAAATATCAACTTTATAGG
CCATCGAAGATAAAGGAACGTAAGTTTGTCAATTCAACCTCACATTTTCAACGCACATTA
AGCACTTGGTTTCGTGGAGAAATGAATGATCCTCGTGAAATTTTAGCGGTTGATCCGTACA
ATAATATTACTTCTGATGAAGAGGATGAGCAAGCCATCGCGAGAGAAGTTGAATTTATGG
AACGAAAGAGGAGGCTTAGTGGAACGATTAAAAAGAAAGCAAGAATTTAAGAAACCCC
AGGATCCCTAATTTTGAAGCCATCGAGGTACCTCAATCTCCTACCAAAAACCGTGTGAAG
TGGGGTCTCATAATGCTACACAACAAGGCACAAAATTCGAAGGTTTCAATATTAATGAAG
TAAGGTTATCTCAATTACAGCAGCAACCAAAACCAGCTAGTACAACCACATACTTTA
TGGAGAAATTTCAAACGCAAGAAGAAGCAAGATAAACAATTTGCCAAGTTTGAAGCA
TGATGAATGCAAGAGTACATACGTTTCAAGTACCGATGAGAAGAAATATGTGCCGATAATCA
CAAACGAATTAGAAAGCTTTTCAAATCTTTGGGTTAAAAAGAGGTACATACCTGAAGATG
ACTTAAACGGGCTTTGTCATGAGATCAAAATCCTTCGGTTGGGCAAACTTTTTGTAAAA
TTCCGCCACCTAAATTTCAAGAGCCTGAATACGCCAACTGGGCCACCGTAGGCCTCATT
GCCACAAATCGGACATCAAATTTACATCATCTGAAAAGCCAGTCAAATTTTCATGTTCA
CCATAACGGACTTTTCAAGCATACACTAGATGTTTATATCTTCGGGAAAAAGGGTGTAGAAA
GATATTATAATCTTCGCCTGGGTGATGTGATAGCAATATTAACCCAGAAGTACTACCAT
GGAGACCTCAGGGCGAGGAAATTTTATCAAATCCTTCAACCTTCAAGTTAGTCACTGACT
TCAAATGATCCTGGAGATAGGTTCAAGTAGAGATTTAGGTTGGTGTCCCATAGTGAATA
AAAAGACTCACAAAAATGTGGCTCTCCCATTAACATATCTCTTCAATAGTGTGCGATT
ACCATAGAGAAGTGCAATTTCTGTGGAACAAGTGCTAAAAGAATTGAATTAATGGTGGGT
ACGCCTTGGGCGCGCCTACGAAAGTGGACTCTCAACCAAGCCTATATAAGGCCAAAGGGG
AAAACGGGTTTAATATAATCAAAGGTACTCGTAAGCGCCTGTCAGAAGAGGAGGAAAGAC
TTAAAGAGAGCTCTCACAATTTTACGAATAGTAATTTCTGCCAAAGCATTTTTTCGACGAGA
AATTTTCAAGATCCAGATATGCTGGCAAACTTAGACAATAAAGAAGGAAAAATAAGAAA
CTAAGAAATCGACAGCACTGAGCCGCGAAGTGGCAAAATTTATGAGAAGGAGGGAATCCA

CGCGATTAGAAGATAAGAGCGTCGGAGAGCGACAGAAAATGAAACGAACCACAGAAAGTG
CCCTCCAGACAGGGCTTATCCAACGCCTAGGATTTCGATCCCACCTCATGGAAAAATTTCCC
AAGTACTCAAGTCTTCTGTATCAGGGAGCGAACCTAAGAACAACCTTACTCGGTAACAAAA
AAACTGTTATAACGATCTCTTGCATTACAAGAAGGAAAAAGTCATTCTCGCACCTTCAA
AGAACGAATGGTTCAAGAAAAGAAGCCATCGCGAAGAAGTTTGGCAAAAACATTTCCGGAT
CCAAGGAACTAAAGAACTTCTGACGGTAGTGCCAGCGATCTTGAGATAATATAA

YIL150C, 571 aa (SEQ ID NO 140)

MNDPREILAVDPYNNITSDEEDEQAIARELEFMERKRQALVERLKRKQEFKKPQDPNFEA
IEVPQSPTKNRVKVGSHNATQOGTKFECSNINEVRLSQLQQPKPPASTTTYFMEKFQNA
KKNEDKQIAKFESMMNARVHTFSTDEKKYVPIITNELESFNLWVKRYIPEDDLKRALH
EIKILRLGKLFKIRPPKFQEPYANWATVGLISHKSDIKFTSSEKPVKFFMFTITDFQH
TLDVYIFGKKGVERYNLRLGDIVAILNPEVLPWRPSGRGNFIKSFNLRISHDFKCILEI
GSSRDLGWCPIVNKKTHKKCGSPINISLHKCCDYHREVQFRGTSKRIELNGGYALGAPT
KVDSQPSLYKAKGENGFNIIKGRKRLSEEEERLKKSSHNFTNSNSAKAFFDEKFNPD
LANLDNKRRIIETKKSTALSRELKIMRRRESSGLEDKSVGERQKMKRTTESALQTGLI
QRLGFDPTHGKISQVLKSSVSGSEPKNNLLGKKTVINDLLHYKKEKVLAPSKNEWFKK
RSHREEVWQKHFGSKETKETSDGSASDLEII

YIL167W, 1133 bp, CDS: 501-1133 (SEQ ID NO 141)

GACATTTTGAACAAATTACATTTATAGAAGTTTATTATAACGTAACAGTTAACAACAAAG
GCTCATAGTCCGAGATCAATATAATAAATTATTCAAGGTTTAAGGAAGAAGTTACCATGG
AAATGACTTACTATGAAAAGACACCTTTGATTTCGTCAATTTTTGAACAATGGTAAGACAA
ATTCTGTGGTTTTACGTTAAGCATGAGATGTTACAACCAGGTGGAAGTTTCAAATCGAGAG
GAATCGGGCATTGTAAGGAAGAGTAATGAAGAAGCGCTAAGCGAGGGTTCTGGGAAGC
TTGCTGTATTTCTAGCTCTGGGGGAAATGCTGGTTTAGCAGCAGCAACTGCCTGCAGAT
CGATGGCACTTAATTGCAGTGTAGTGGTTCTCTAAACTACAAAACCTAGAATGGTAAAGA
AAATTCAAAGTGCAGGAGCCAAAGTCATTATCCATGGTGATCATTGGGGGGAAGCAGATG
AATACTTGAGGCACGAATGAATGGCGCAAGAAAGCCAACATGGTTTCAAGACACTATATG
TGCACCCGTTTGATAACGAGACAATTTGGGAAGGTCATTCTACGATTGTGGATGAAATCA
TAGAACAATTGAAGGAAAATGATATATCCTTACCTAGGGTGAAAGCTTTGGTTTGTAGTG
TTGGTGGTGGTGGGCTATTTAGTGGCATAATTAAAGGCCCTAGATAGGAATCAGCTTGCTG
AAAAAATCCGGTCGTTGCTGTAGAACTGCCGGTTGTGACGTATTGAATAAGTCTCTCA
AAAAGGTAGTCCAGTTACTCTTGAAAATTGACAAGTGTGTGCAACTTCTTTGGCCCTCCC
CATAACATGATCATTTCGCGTTTGAGAGTTTTTAACAAGTATGGATGTAAGTCTGTAGTTT
TATCAGATCAAGACGTTCTGGCAACATGCTTGAGATATGCCGATGACTACAATTTTATAG
TGGAACCAGCCTGTGGAGCATCCTTACATTTATGTTATCATCCAGAGATTCTTGAAGACA
TTCTGGAACAAAAATATATGAGGATGATATCGTTATTATAATCGCATGCGGTGGATCAT
GTATGACGTATGAAGACTTGGTGAAAGCGTCGAGCACATTAAACGTATCATAA

YIL167W, 210 aa (SEQ ID NO 142)

MAQESQHGSKTLYVHPFDNETIWEHSTIVDEIIIEQLKENDISLPRVKALVCSVGGGGLF
SGIIKGLDRNQLAEKIPVVAVETAGCDVLNKSLLKGGSPVTLEKLTSVATSLASPYIASFA
FESFNKYGCKSVVLSQDVLATCLRYADDYNFIVEPACGASLHLCYHPEILEDILEQKIY
EDDIVIIACGGSCMTYEDLVKASSTLNVS

YJL034W, 2549 bp, CDS: 501-2549 (SEQ ID NO 143)

CCATGAACCTCAGCATGTGCTACTCCAGTTAATGACTTGTTCGTATCGTTCATGCCATAAG
CCATCACCTGGCCAGTTGGCGTATGTACAAAGATGCAAGCTACCGGTGTCTCATCGTGGT
CAAGAGCGTATCTAGCCAAACGGACAGCTGTCTCATATGTTTAATATGCTGCATAGTGT
GAGTCTCTAGTTTTTACCGCAGCCACCAGCCGCTTCTCGAGCAAAGTGTAGATCCCATT
AGGACTCATCTTCAATTTTGTCTATGTTAGCTGCAACTTTCTATTTTAATGAACC
TTCTGGAATTTTACCCGGCGCGGCAACCGAGGAAGTGGACAGCGTGTGCAAAAAGTTGC
TTTTTTATATAAAGGACACGAAAAGGGTTCTCTGGAAGATATAAATATGGCTATGTAATT
CTAAAGATTAAAGTGTACTGTTTTACTTTTTTAAAGTCCCCAAGAGTAGTCTCAAGGGA
AAAAGCGTATCAACATACCATGTTTTTCAACAGACTAAGCGCTGGCAAGCTGCTGGTAC
CACTCTCCGTGGTCTGTACGCCCTTTTCTGGTGAATATTACCTTTACAGAATTCTTTCC
ACTCTCTCAATGTTTTAGTTAGAGGTGCCGATGATGTAGAAAACCTACGGAAGCTTATCG
GTATTGACTTAGGTACTACTTATCTCTGTGTTGCTGTGATGAAAAATGGTAAGACTGAAA
TTCTTGCTAATGAGCAAGGTAACAGAATCACCCCATCTTACGTGGCATTACCCGATGATG

AAAGATTGATTGGTGATGCTGCAAAGAACCAAGTTGCTGCCAATCCTCAAAACACCATCT
TCGACATTAAGAGATTGATCGGTTTGAAATATAACGACAGATCTGTTTCAGAAGGATATCA
AGCACTTGCCATTTAATGTGGTTAATAAAGATGGGAAGCCCGCTGTAGAAGTAAGTGTC
AAGGAGAAAAGAAGGTTTTACTCCAGAAGAAATTTCTGGTATGATCTTGGGTAAGATGA
AACAAATTGCCGAAGATTATTTAGGCACTAAGGTTACCCATGCTGTCGTTACTGTTCTCTG
CTTATTTCAATGACGCGCAAAGACAAGCCACCAAGGATGCTGGTACCATCGCTGGTTTGA
ACGTTTTGAGAATTGTTAATGAACCAACCGCAGCCGCCATTGCCTACGGTTTGGATAAAT
CTGATAAGGAACATCAAATTATTGTTTATGATTTGGGTGGTGGTACTTTTCGATGTCTCTC
TATTGTCTATTGAAAACGGTGTTCGAAGTCCAAGCCACTTCTGGTGATACTCATTTAG
GTGGTGAAGATTTTGACTATAAGATCGTTCGTCAATTGATAAAAGCTTCAAGAAGAAGC
ATGGTATTGATGTGTCTGACAACAACAGGCCCTAGCTAAATTGAAGAGAGAAGCTGAAA
AGGCTAAACGTGCCTTGTCCAGCCAAATGTCCACCCGTATTGAAATTGACTCCTTCGTTG
ATGGTATCGACTTAAGTGAAACCTTGACCAGAGCTAAGTTTGAGGAATTAACCTTAGATC
TATTCAAGAAGACCTTGAAGCCTGTGCGAGAAGGTTTTGCAAGATTCTGGTTTGGAAAAGA
AGGATGTTGATGATATCGTTTTGGTTGGTGGTCTACTAGAATTCCAAAGGTCCAACAAT
TGTTAGAATCATACTTTGATGGTAAGAAGCCCTCCAAGGGTATTAACCCAGATGAAGCTG
TTGCATACGGTGCAGCCGTCAAGCTGGTGTCTTATCCGGTGAAGAAGGTGTCGAAGATA
TTGTTTTATTGGATGTCAACGCTTTGACTCTTGGTATTGAAACCACTGGTGGTGTCTATGA
CTCCATTAATTAAGAGAAATACTGCTATTCTTACAAAGAAATCCCAAATTTCTCTACTG
CCGTTGACAACCAACCAACCGTTATGATCAAGGTATACGAGGGTGAAAGAGCCATGTCTA
AGGACAACAATCTATTAGGTAAGTTGAATTAACCGGCATTCCACCAGCACCAAGAGGTG
TACCTCAAATTGAAGTCACATTTGCACTTGACGCTAATGGTATTCTGAAGGTGTCTGCCA
CAGATAAGGGAACGGTAAATCCGAATCTATCACCATCACTAACGATAAAGGTAGATTAA
CCCAAGAAGAGATTGATAGAATGGTTGAAGAGGCTGAAAAATTCGCTTCTGAAGACGCTT
CTATCAAGGCCAAGGTTGAATCTAGAAACAAATTAGAAAACCTACGCTCACTCTTTGAAA
ACCAAGTTAATGGTGACCTAGGTGAAAAATTTGGAAGAAGAAGACAAGGAAACCTTATTAG
ATGCTGCTAACGATGTTTTAGAATGGTTAGATGATAACTTTGAAACCGCCATTGCTGAAG
ACTTTGATGAAAAGTTTGAATCTTTGTCCAAGGTGCGCTTATCCAATTACTTCTAAGTTGT
ACGGAGGTGCTGATGGTTCTGGTGCCGCTGATTATGACGACGAAGATGAAGATGACGATG
GTGATTATTTTGAACACGACGAATTGTAG

YJL034W, 682 aa (SEQ ID NO 144)

MFFNRLSAGKLLVPLSVVLYALFVVILPLQNSFHSSNVLVRGADDVENVYGTIVIGIDLGTT
YSCVAVMKNGKTEILANEQGNRITPSYVAFDDERLIGDAKNQVAANPQNTIFDIKRLI
GLKYNDRSVQDKIKHLPFNVVNKDGKPAVEVSVKGEKKVFTPEEISGMILGKMKQIAEDY
LGTKVTHAVVTPPAYFNDAQRQATKDAGTIAGLNLVRIVNEPTAAAIAYGLDKSDKEHQI
IVYDLGGGTFDVSLLSIENGVEVQATSGDTHLGGEDFDYKIVRQLIKAFKKKHGIDVSD
NNKALAKLKREAEKAKRALSSQMSTRIEIDSFVDGIDLSETLTRAKFEELNLDLFKKTLLK
PVEKVLQSGLEKKDVEDDIVLVGGSTRIKPVQQLLESYFDGKKASKGINPDEAVYGA
QAGVLSDGEEGVEDIVLLDVNALTGLIETGGVMTPLIKRNTAIPTKKSQIFSTAVDNQPT
VMIKVYEGERAMSKDNNLLGKFELTGIPAPRGVPIEVTTFALDANGILKVSATDKGTGK
SESITITNDKGRLTQEEIDRMVEEAKEKFASEDASIKAKVESRNKLENYAHSKLNQVNGDL
GEKLEEDKETLLDAANDVLEWLDNDFETAIAEDFDEKFESLSKVAYPITSKLYGGADGS
GAADYDDEDEDDDDGYFEHDEL

YJL035C, 1253 bp, CDS: 501-1253 (SEQ ID NO 145)

TACCTAAGTCAATACCGATAACAGTTCCGTAGTTTTCTACATCATCGGCACCTCTAACTA
AAACATTGGAGGAGTGGAAGAATTCTGTAAAGGTAATATTACCACGAAAAGGGCGTACA
GGACCACGGAGAGTGGTACCAGCAGCTTGCCAGCGCTTAGTCTGTTGAAAAACATGGTAT
GTTTGATACGCTTTTTCCCTTGAGACTACTCTTGGGGACTTTAAAAAAGTAAAAACAGTAA
CAGTTAATCTTTAGAAATTACATAGCCATATTATATCTTCCAGAGAACCCTTTTCGTGT
CCTTTATATAAAAAAGCAACTTTTTTCGACACGCTGTCCAGTTCCTCGGGTGCCGCGCGG
GTGAAATTTCCAGAAGGTTCTATTAAAATAGAAAGTTGCAGCTAACATAGCAAAATTAGA
TGAATGATGAGTCCTAATGGGATCTACACTTTGCTCGAGAAGCGGCTGGTGGCTGCGGTA
AAAACCTAGAGGACTCACACTATGCAGCATATTAAACATATGAGGACAGCTGTCCGTTTGG
CTAGATACGCTCTTGACCACGATGAGACACCGGTAGCTTGCATCTTTGTACATACGCCAA
CTGGCCAGGTGATGGCTTATGGCATGAACGATACGAACAAGTCATTAACTGGAGTAGCAC
ATGCTGAGTTTCAATGGGGATCGATCAGATCAAGGCGATGTTGGGCTCCCGAGGAGTTGTTG
ACGTGTTCAAAGACATTACTCTATATGTTACTGTAGAACCGGTATATAATGTGTGCATCTG
CTCTCAAGCAATTAGACATTGGAAGGTGGTGTTCGGTTGTGGCAACGAGAGATTGGAG

GCAACGGTACTGTCTTGTCTAGTAAATCATGATACGTGTACATTAGTGCCCAAGAACAATA
GTGCGGCAGGGTACGAGAGTATACCGGGGATCTTGAGGAAAGAAGCAATAATGCTGCTGA
GATAC'TTTTATGTAAGACAAAATGAAAGGGCGCCAAAGCCACGGTCCAAGAGTGACAGAG
TGTTGGATAAAAACACGTTTCCGCCATGGAATGGTCAAAGTATCTTAATGAAGAAGCAT
TCATTGAGACTTTTGGTGATGATTACAGGACTTGT'TTTGCGAATAAAGTTGACTTGTCCA
GTAATAGCGTCGATTGGGATTTGATTGACTCCCAAGATAAATAATCCAAAGACTGG
AAGAACAATGCAAAATGTTTAAGTTAATGTACATAAGAAATCTAAGGTTTGA

YJL035C, 250 aa (SEQ ID NO 146)

MQHIKHMRTAVRLARYALDHDETPVACIFVHTPTGQVMAYGMNDTNKSLTGVAHAEFMGI
DQIKAMLSRGVVDVFKDITLYVTVEPCIMCASALKQLDIGKVVFVCGNERFGNGTIVLS
VNHDTCITLVPKNNSAAGYESIPGILRKEAIMLLRYFYVRQNERAPKPRSKSDRVLDKNTF
PPMEWSKYLNEEAFIETFGDDYRTCFANKVDLSSNSVDWDLIDSHQDNI IQELEEQCKMF
KFNVHKKSKV

YJL070C, 3167 bp, CDS: 501-3167 (SEQ ID NO 147)

TCCCCTGATGGTCAAATACTGTGCATGGCATCCCGTGCAGTCAAGGATGCTTTGAGACTA
GTTTCATCTGCC'TTCTTTGTAGCGTGTTCAGCAACTGGCCTACCAGCGGGACGCC'TTTGGGT
AAAGTTACCAGTGTTCGCATTTTCCGCATCTGGTGGGCTACTGGCCGTGGGTAACGAACAA
GGTAAAGTGAGGCTCTGGAAATTAACCACACTACTAAATTTCCATTTATAGACAAACTTAG
ATATTAAGCAATGTACAAATACATACACAAATATCACTGTAAAAAATTTGCGAAGAA
ACTTGAATTTGAATATGATTCTGCCACTTTT'TTCTTGTCTGTCATTTATAGTCAGAAATG
AAAAATGTCCGAGAAATTAATATAATATATGGAAGGACATTGAGTTTAAAG
AATTTGATTAATAATGTCTCTCAATATCCTCTGTAAAGAGTTATCTAAATCTCACTTTACT
TATTCATCTCGCTGGGAATTATGCAGGCGGTAGAGAGAAGGCCCTCGTTACTCTTTGACG
AATATCAAAATTTCTGTACTAAGCCTAATGAGACGAAGAATAAAGAAGCCAGGGTCTTTGT
CAGAGAAATGACGGTGTGTCTCCCATCTGT'TTTGAAACAGAAGGAAATATCAGTCGATG
ATATGGATATGATTTCTTTGCCACCGGAATTTGACAGGCAAATGGT'TTTAGGTTTCCCTA
TGTTTTCGATCTTGAAGACGAAGAAACAAATTTGATCCACTTCTTTCAGTTTCCCATC
ATTATGGAAATGGAGAAAGTGACAGCTTTGTCTCATCGTACACGCCCTCAAATCTGAAAA
CGGGTGAAGAACTAAAGATCTTTTCAATTAATCCGTTTGAATTTGGTTTCTCAAATGAGAA
AAAGATACATTGCTGCTTCCAAACAAGATGGCATTTCAAACATAAAAAATGACACTGAAA
AGTGGT'TTTTATACCCAAAACCACTGCCAAAGTTTGGAGATT'TGAAGACGATAAACGAT
TCCAAGATCCCTCTGACTCTGACTTAAATGACGATGGAGACAGTACTGGGACCGGAGCCG
CTACACCGCACCGCCATGGCTACTATTACCCAAGTTACTTTACCGATCACTACTACTACT
ACACAAATCTGGTTTGAAGGAAAAGGAAATATAAAGTACCATACACCGGTGAATAT
TCGATTTAGAGGATTACAAAAACAATACATTTACCATTTAAGTAATCAGGAAATACGC
AAAACCCACTTTTACCTTATTCTAGTAAGGAGGAGTCACTAGAGGAAGAA'TTTTAAACAG
ATGTGCCCTACGTTTCAAGAATTTAGGGATGATTTTGCATACATAATAGAGTTAATCCAAT
CTCATAAATTCACGAGGTTTTCACGAAAGCGATTATCTTATTTATTAGATAAATTTGAAT
TGTTTCGATACCTAAACTCTAAGAAAGAAATTTTAGCTAATAAAAAATGTTCCCTACAGAG
ATTTTATAATTTCTCGTAAGGTAGATCGAGACTTGTCTTTAAGTGGTTGTATTTCTCAAC
GTCAATTGAGTGAATATATATGGGAGAAAATAAATTTAGAACC'TGAAAGGATAGTTTATC
AAGACCCGAAACGTCAGGAAACTCAGTTTGAGAGACATTTTTCAGTTTGGTTGTCTT
CTAATGACCAACCCATTTGCGATTGGGTTGAAATGATTGATGATGAATTTCTGGATTGGT
ATAGAAATATTTACCTAATAGATTACCATCTAATCTCTAACAAAGTAGCAAAGTTGGTCCG
GCAAAGAAATGAGGTTTACCTATTAGCCAAAGTGT'TTCTGGAGTTTGATAATTTCAATTG
AAGGTGAGTACCTAGCAGAAATTTTCAATAAATACGTTATTCATATCTTCGAAAAATCAA
AGTACCAATTTGGCCCAAGTATCAGTTAATTTTCAATTTCTATTCCAGTGGTGAAGACTGGT
ACAAGAAATTTTCTCAATGGTTGCTACGATGGAAGCTAGTATCGTATAATATCCGCTGGA
ATATACAAATTTGCCAGGATTTTCCCAAAC'TATTCAAGGAAATGTCTGTCAAATTTCC
AGGAGTTT'TGGATCTTATCTTCAATCTTTATTCACTCTGGAAAAGGAGCAGTTACCAA
TAGATTCACTGTAAATACTGATATCATTTGGTCTGCAGTTT'TTTTATCAAATGTGTGTT
CTATGGATCTGGTCATTAAAGAGTCGGATGAATATTACTGGAAAGAAATTTACTGATATGA
ATTGTAAGCCAAAATTTTGGACAGCACAGGGTGACAATCCAAC'TGTTGCGCATTACATGT
ATTATATTTATAAAAGTTTAGCGAAAGTTAATTTTCTGCGGTACAAAAATCTTCAAATA
CAATCACCC'TAAGAAATTTATGTTCTCCACTATCCAGCAGAACTTCCCAATTTGGAGTGG
ATTTATATTTTACAGATCAAGTTGAATCGTTAGTGTGCAACTTACTGCTTTGTAATGGTG
GTCGTGATACAGGTAGAACCCTTTGGGATAC'TGCAACAATGATTCAATATTTTATC
TCTTTCAAATACCCATTTTAGCTGCGCCATTATCATCTGT'TTCACTTGAATTCGCAAA

AATCGACCTTTTTGAAGAATAAAAAACGTGCTTCTAGAACATGATTATTTGAAAGACCAGG
AAACAGCCAAAATCAATCCTTCTAGAGATATCACTGTGGGCGAACAAAGATCATATGAGA
CAAATCCTTTCATGAAAATGTTTAAAGATGGGACTAAAAATTTCTTTATCATCAAAATCGA
TTCTTTACAATAGTTCATACACGCTAGAACCTCTCATTGAAGAATACAGTGTAGCAGCAA
GTATTTACTTGTGAACCCAACAGATTTGTGCGAGTTGTGCGAGAACAAGTGTGCTATCTA
GTGGCTATGAAGGTTGGTACAAGGCTCATTGGATTGGCGTTGGAGTTAAAAAGGCGCCTT
ACTTTGAGGAGAACGTGGGTGGGATAGATAATTGGTACGATACAGCGAAAGATACCTCGA
TAAAGCACAACGTTCCGATGATTAGAAGAAGATATAGAAAGGAGACATTGGATCAAGAGT
GGAACCTCGTTCGGGATCACTTTGGAGTAATTAACCTCATTGGTAG

YJL070C, 888 aa (SEQ ID NO 148)

MQAVERRRPSLLFDEYQNSVTKPNETKNKEARVLSNDGDVSPSVLKQKEISVDDMDMISL
PTEFDRQMVLGSPMFFDLEDEENKIDPLPSVSHHYGNESDSFVSSYTPSNLKTGEETKD
LFINPFELVSQMRKRYIAASKQDGISNIKNDEKWFLYPKPLPKFWRFEDDKRFQDPDS
DLNDDGDSTGTGAATPHRHGYYPYFTDHYYYTKSGLKGKGNIKVPYTGFEYFDLEDYK
KQYIYHLSNQENTQNPLSPYSSKEESLEEEFLTDVPTFQEFRDDFAYIIELIQSHKFNEV
SRKRLSYLLDKFELFQYLNKKEILANKNVPIYRDFYNSRKVDRDLSLSGCISQRLSEYI
WEKINLEPERIVYQDPETSRKLSLRDIFQFGCSNDQPIAIGLKLIDDEFDLDWYRNIIYLI
DYHLTPNKVAKLVGKEMRFYLLAKVLEFDNFIEGEYLAEIFIKYVIHILEKSKYQLAQV
SVNFQFYSSGEDWYKKFSQWLLRWKLVSYNIRWNIQIARIFPKLFKENVVSNFQEFDLI
FNPLFTLEKEQLPIDSSVNTDIIGLQFFLSNVCSMDLVIKESDEYYWKEFTDMNCKPKFW
TAQGDNPVTAHYMYIYKSLAKVNFRLRSQNLQNTITLRNYCPLSSRTSQFGVDLYFTDQ
VESLVNLLLCNGLLQVEPLWDTATMIQYLFYLFQIPILAAPLSSVSLNSQKSTFLKN
KNVLLHNDYLDQETAKINPSRDITVGEQRSYETNPFMFMKGLKISLSSKSILYNSSY
TLEPLIEEYSVAASIYLLNPTDLCELSRTSVLSSGYEGWYKAHWIGVGKAPYFEENVG
GIDNWDYDTAKDTSIKHNVPMIRRRYRKETLDQEWNVFVRDHFVINSIW

YJL078C, 3146 bp, CDS: 501-3146 (SEQ ID NO 149)

TTTTTCTTCGCACATGGCTGGTTCTGCTGGAGCGGCTGGGTGTTTATAGTTACCGCAAT
GCAGGTCGCTTCGTTTACTTTTCTCTGCGTGCTCGAGAACTGATAAATACTGGTTTAGGA
AAACCGTCCACTTATGGATTAAACAAGGAGGTGAAAGGTAGGTACCATGGCAATATAGCT
AGCAACGCTACGCACTAGCTGTGTGTGCTTGCTCTCTTGTGTTCTGTTTTCGTATATTGC
GGGTTCCCGCGGTTAATTCAACAACAAATATGGTATCTAGGCAGGGACCCAGCAACGGAA
GGATGTAATTGCTATATAGGGCCGATGAAACAGTTCTCATGTTTCAACTCGGTGCAAGAA
TTCTCTAAAACATATTCTATACTTCAAAGTTTTAGCTTCTTGTCTTTTCGGTAGTTGCCA
AACCAATATCGGCATAAAATTATAATTGCTGCACCCCTGCAACTCCAAACAACCTAAAC
AACTTAAACGAAAACGCTTATGCTGGAGTTTCCAATATCAGTTCTGCTAGGATGCCTAG
TAGCCGTCAAGGCACAAACCAGTTTCCAAACTTCGAGAGCGATGTGCTGAACGAGCATA
ACAAGTTCAGAGCGCTACATGTTGACACAGCGCCGCTCACCTGGTCCGACACTCTGGCCA
CCTATCGCGAGAATAACGCGACCAATATGATTGTTCCGGTGTCTTAACGCATTCCGATG
CCCCATCGGTGAGAACCTTGCCCTGGTTACACAGACACGGGAGCGGTGGACGCTGGT
ACGGGGAGATAAGCAAGTATAATTATTCAAATCCCGGATTTTCTGAATCCACGGGTCACT
TCACACAGGTGGTTTGGAAAGTCAACCGCCGAGATTGGATGTGGTTATAAATATTGTGGTA
CGACATGGAACAATTATATTGTGTGCTCCTACAACCTCCTGGAAACTACCTGGGTGAGT
TTGCAGAGGAAGTGAACCACTTATAAGCACTGTTTCTCCTCGTCTCATCTCGTCTCTT
CTACCTCAACTACATCAGACACAGTCTCCACCATCTCATCCAGTATTATGCCCGCTGTAG
CGAAGGTATACAACAACGGTATCGTCTGCGGCTAGCAGCAGTTCTTTAAAATCGACGA
CCATAAACCTGCCAAGACCGCTACCTCACTGCGTCTCTTCTACCGTAATTACTAGTA
GCACAGAATCAGTTGGATCCTCCACTGTCTCATCAGCCTCAAGCTCTTCTGTCACTACTT
CCTATGCTACCTCCTCGAGTACCGTCTCTAGTGATGCTACTTCATCCACTACCACCA
CCTCATCGGTTGCTACATCGTCCAGTACCACTTCTTCCGACCCTACCTCGAGCACTGCTG
CTGCTTCTTCTTCTGATCCTGCCTCAAGTTCCGCTGCCGCTCCTCCAGCGCGAGTACCG
AGAACGCCGCTTCTTCTAGCAGCGCCATCTCGAGCTCTTCATCAATGGTTTCTGCTCCTT
TGAGTAGTACTCTTACTACTTCCACCGCAAGCTCCAGAAGTGTAACCTCCAATTCAAGTA
ATTCTGTTAAGTTTGCAAACACAACGTGTTTCTGCTCAAACAACCTCTTCTGTAAGCG
CCTCATTATCATCATCTGTAGCTGCTGACGATATTCAAGGTAGCACTTCCAAGGAGGCCA
CAAGCTCAGTTTCCGAACATACTAGTATAGTAACTAGTGCAACTAATGCTGCCCAATATG
CAACGAGACTTGGGTCACTTCCAGAAGTCTTCCGGGGCCGCTCTTCTCCTCAGCTGTGT
CGCAATCTGTTCTGAATTCGTTATAGCCGTCAACACCGACGTATCTGTAACTCAGTTA
GTAGCACAGCCCATACCACAAAGGACACCGCCACCACTTCAGTAACCGCCTCAGAAAGTA

TCACTTCGGAACTGCTCAGGCTTCAAGTTCAACAGAGAAGAATATTAGTAACAGTGCCG
CCACATCGAGTAGCATTTACTCCAACAGTGCTTCTGTGTGTCAGGACACGGTGTAACATACG
CTGCCGAATACGCCATTACATCCGAGCAATCCTCTGCGCTTGCCACATCTGTGCCTGCTA
CAAATTGCTCTAGTATCGTGAAGACCACAACCTTTAGAAAATTCGAGTACCACAACCATCA
CAGCCATTACTAAGAGTACTACAACCTTGGCCACTACTGCTAACAACCTCCACAAGGGCAG
CTACCGCAGTAACCATAGATCCACATTGGACCCTACCGACAACCTCAGCTAGTCCAACCG
ACAATGCTAAACACACCTCTACATATGGATCTTCTTCCACAGGCGCATCTTTAGATAGCT
TACGCACAACCACCAGTATTAGTGTCTCAAGCAACACCACACAGTTAGTCTCTACCTGCA
CTTCCGAGAGCGATTATTCCGATAGTCTAGCTTCGCCATCTCCACTGCCACCACCCTG
AAAGCAATCTGATCACAACACCATTACAGCTTCTTGTAGTACGGATAGTAATTTCCCTA
CCTCCGCTGCTTCTTCTACAGATGAGACGGCCTTCACTAGAACAATCTCGACATCTTGTA
GCACTTTGAACGGCGCCTCAACCCAAACAGTGAGCTAACCACATCGCCTATGAAAACCA
ACACGGTGGTTCCAGCTTCTTCTTTCCCTTCAACTACAACCACTTGTCTAGAAAATGATG
ACACTGCCTTTTCTAGTATCTACACTGAAGTCAACGCCGCAACTATCATTAAACCCCGGAG
AAACATCTTCTCTCGCTAGCGATTTGCCACATCTGAAAAGCCAAACGAGCCCACTTCTG
TCAAATCCACCTCAAACGAAGGCACCTCTTCCACAACAACCACTACCAACAGACTGTTG
CTACACTGTATGCCAAGCCCTCCAGCACAAGCCTAGGTGCAAGAACAACACTACTGGTAGCA
ACGGTCGTTCAACTACCAGCCAACAAGACGGGTCTGCCATGCATCAGCCAACCTTCTCGA
TCTACACTCAACTAAAAGAAGGCACATCAACCACCGCAAACTTTCTGCATACGAAGGTG
CTGCAACACCTCTTTCCATTTTCCAGTGCAATAGTCTAGCTGGAACGATTGCCGCTTTTG
TCGTAGCTGTTCTGTTTCGCTTCTAG

YJL078C, 881 aa (SEQ ID NO 150)

MLEFPISVLLGCLVAVKAQTTFPNFESDVLNEHNKFRALHVDAPLTWSDTLATYAQNYA
DQYDCSGVLTHSDGPYGENLALGYTDTGAVDAWYGEISKYNYSNPGFSESTGHFTQVWWK
STAEIGCGYKCGTTWNNYIVCSYNPPGNYLGEFAEEVEPLISTVSSSSSSSSSTSTSD
TVSTISSSIMPAVAQGYTTTVSSAASSSSSLKSTTINPAKTATLTASSSTVITSSSTESVGS
STVSSASSSSSVTTSYATSSSTVSSDATSSSTTTSSVATSSSTSSDPTSSTAASSSDP
ASSSAAASSSASTENAASSSSAISSSSSMVSAPLSSTLTSTASSRSVTSNSVNSVKFAN
TTVFSAQTTSSVSASLSSSVAADDIQGSTSKEATSSVSEHTSIVTSATNAAQYATRLGSS
SRSSSGAVSSSAVSQSVLNSVIAVNTDVSVTSVSSSTAHTTKDTATTSVTASESITSETAQ
ASSSTEKNISNSAATSSSIYSNSASVSGHGVTYAAEYAITSEQSSALATSVPATNCSSIV
KTTTLENSSTTTITAITKSTTTLATTANNSTRAATAVTIDPTLDPTDNSASPTDNAKHTS
TYGSSSTGASLDSLRTTTSISVSSNNTQLVSTCTSESDYSDSPSFAISTATTESNLITN
TITAGCSTDSNFPSTAASSTDETAFTRTISTSCSTLNGASTQTSLETTSPMKTNTVVPAS
SFPSTTTTCLENDDTAFSSITYEVNAATIINPGETSSLASDFATSEKPNEPTSVKSTNE
GTSSTTTTYQQT VATLYAKPSSSTSLGARTTTGSNGRSTTSQQDGSAMHQPTSSIIYTQLKE
GTSTTAKLSAYEGAATPLSIFQCNSLAGTIAAFVAVLFAF

YJL179W, 830 bp, CDS: 501-830 (SEQ ID NO 151)

TTGCATTATCAACTATAATTCCATTTCCCTAGAGGAGTTTTTATAGTCCTGCCATCTAATT
GTAGAGCAATCTTTCTTTCTCAACATCCCTATTTAGTGACACCTTTTCCCAAACTTCT
GTGAAGTTTTGCTCAATCTATTTGTTTCCGTAGGAGTGTTATTCTCAATCGTGTGTCTG
TCCCCAGTGGCTGGGCATTTAATGAGTAGAATCGGGGCAGTTTCAATCTTATGGAATTCA
CAATGAAGCATCCCTTCTTAATGATGGCAGCATTCGGTATTCTCTTTTGTAGGGTTTCG
TTTGCCTTCAAGTGTTTTGTTCTTATTTAGCCTTTTCTTTACCTTAATTTTTTCTTTT
CTCTGAAGAAAATGAATGAGTTTAAAGATATAGCAATTAAAAAGTAACAGTGAAGAAATT
TCTCAGATGAGCAGATGGGAATTAAAGAACTATCTACAGAGCTCTTTACTAAATTGAATC
AATAATACATACTTACAAACATGTCACAGATAGCACAGAAGAAATGACAGTGAGCTTAAGAA
ACGCCAGGACACAATTGGATATGGTCAATCAGCAGCTAGCATATTTGGACAGACAAGAAA
AGCTTGCTGAATTGACAAAGAAAGAACTAGAGTCTTATCCAACGGACAAAGTATGGAGAT
CTTGCGGTAAATCGTTTATCTTACAGGATAAATCCAAATACGTTAATGATTTATCAGATG
CCGAACTGTTCTTCTGGATCAAAGAAAAACATTAAAGATAAAGAAGAACTATTGAGAAA
CTACTGTTGAAAAACAATAGACAATCTAAAGGCATTGATGAAGAATTAA

YJL179W, 109 aa (SEQ ID NO 152)

MSQIAQEMTVSLRNARTQLDMVNQQLAYLDRQEKLAELTKKELESYPTDKVWRSCGKSFI
LQDKSKYVNDLSHAETVLLDQRKTLKIKKNYLETTEKTIDNLKALMKN

YJL180C, 1478 bp, CDS: 501-1478 (SEQ ID NO 153)

AATAGTTCTTCTTTATCTTTAATGTTTTCTTTGATCCAGAAGAACAGTTTCGGCATGTG
ATAAATCATTAACGTATTTGGATTATCTGTAAAGATAAACGATTTACCGCAAGATCTCC
ATACTTTGTCCGTTGGATAAGACTCTAGTTCTTTCTTTGTCAATTCAGCAAGCTTTTCTT
GTCTGTCCAAATATGCTAGCTGCTGATTGACCATATCCAATTGTGTCTGGCGTTTCTTA
AGCTCACTGTCAATTTCTTGTGCTATCTGTGACATGTTTGTAAAGTATGTATTATTGATTCA
ATTTAGTAAAGAGCTCTGTAGATAGTTCTTTAATTTCCCATCTGCTCATCTGAGAAATTTT
TTCACTGTTACTTTTAAATGCTATATCTTTAAACTCATTCAATTTTCTTCAGAGAAAAAGA
AAAAAATTAAGGTAAAGGAAAAGGCTAAATAAGAACAAAACACTTGAAGGCAACGAAAC
CCTACAAAAGAGAATACGGAATGCTGCCATCATTAAAGGAAGGGATGCTTCATTGTGAATT
CCATAAGATTGAAACTGCCCCGATTCTACTCATTAAATGCCAGCCACTGGGGACAGACA
ACACGATTGAGAATAACACTCCTACGGAAACAAATAGATTGAGCAAAACTTCACAGAAGT
TTTGGGAAAAGGTGTCACTAAATAGGGATGTTGAGAAAGGAAAGATTGCTCTACAATTAG
ATGGCAGGACTATAAAAACTCCTCTAGGAAATGGAATTATAGTTGATAATGCAAGTCTC
TCTTAGCATACCTATTAAAACTGGAGTGGTCCCTATCCAGTCTTTCCATCAAAACTC
ACTCTTTGCCACTAACTTCATTAGTGGCAAGATGCATAGATTTACAAATGACAAATGAGC
CTGGCTGTGACCCTCAATTAGTTGCAAAGATTGGAGGCAACAGTGTATTATAAAAAATC
AGTTGTTAAGATATTTAGATACCGATCTTTATTGGTCTTTTCCCCTATGAATGAGTTTG
AAGGAAGATTACGCAATGCGCAAAATGAGTTATATATACCCATCATCAAAGGAATGGAAG
AGTTTTTACGCAACTTTTCATCCGAGTCTAATATTCGACTACAAATTTTAGATGCCGACA
TCCATGGGTTACGAGGCAATCAGCAGTCGGATATCGTTAAGAATGCAGCAAAAAAATATA
TGAGCAGCTTATCACCATGGGATCTTGCAATCTTGAAAAAACTGTATTAAACCACAAAGT
CCTTCATTGCGCGGTGCTATTATTAGAAAAATAAAAAAGATACTGCGAACTTAATTTCCC
CCTTGAAAACTGATATGGATAATATTGTACGTGCCGCCACCTTAGAAACAATCTTCCAAG
TTGAAAAGTGGGGAGAGGTTGAAGATACTCATGACGTTGACAAAAGAGACATCAGAAGAA
AAATTCATACTGCTGCGATTGCTGCTTTTAAGCAATAA

YJL180C, 325 aa (SEQ ID NO 154)

MLPSLRKGC FIVNSIRLKLPRFYS LNAQPLGTDNTIENNTPTETNRLSKTSQKFWEKVSL
NRDVEKGKIALQLDGRITIKTPLNGIIVDNAKSL LAYLLKLEWSSLSLSIKTHSLPLTS
LVARCIDLQMTNEPGCDPQLVAKIGNSDVIKNQLRLYLDTDLLVFSMPNEFEGRRLRNA
QNELYIPIIKGMEEFLRNFSSESNI RLQILDADIHGLRGNQQSDIVKNAAKKYMSSLS PW
DLAILEKTVLTTKSFICGVLLLENKKDTANLIPALKTMDNIVRAATLETIFQVEKWGEV
EDTHDVKRDIRRKIHTAAIAAFKQ

YJL181W, 2336 bp, CDS: 501-2336 (SEQ ID NO 155)

GCAAGTCAGTACGATGCATCCTTGGATCAAGAAGGTGAGTCTGGAAACGGTGCTTCTAAT
GGCGATGTTTACCATTATAATGAAGGGGACTTGGCTGCCTCCTTCAAGGGATGTAGATCA
AGAGGTACGTGTGCTAGTGAATAGGTCACATGTACCAGAAAATCAAGAAATCTTAGATG
TGTGTAACTTGAATTTAGTTTCAACAAGATCCTTGTATTTATATAAACAAGATATA
ATTTTTTAAAAAAATTAGAAAAAGCAATATAATTCAGGTCCCACTTGGAAATAATGGCA
CTGTATTGATGCATTTTCTTATGCTTAGTGACGCGTTTTTCGCGCGTCAGTTTCAAGTTT
TTCTTGGCTTTTTTTTTTTTTCATTTTCGTAAAGGGTCTTAAAGGATTAAAAATGCAGTA
TTGAAATAAAGAACAATTACGAACGGTGAAGCTGCTATTTTGGTTATTATACCCTTCCAG
GACAGTACGCGCAAATATTATGGAGATATCAAGGAAGAAGAAGAAGCTTTTTTCGG
CGATAGAAGGTATAATATATGCCCTGTGAGGTGTATGACCCGTACCCCGTCATTTACATA
AAAGCAAAACAAAGATCATCAATGCTGCTAAATTAATTTATAGAAACGCATCTTTTCATATT
ATACAATACTCAATAACATTTTCAGATATACAAGCCTATCTTTCTACTTGGCTTAGGGATC
TTGGAACGACAGGTCCATACCAACAATTTCTTCAGAAAGTATTTCTCTCATGTTTGACC
GCACTGTATCTATCTTCAGGAAATGTACGATAGAGGGAGGTTTTCCACATTTGATCGCAC
GTCPTTATCTCAGATTGAAAAGCTACCAGAAGCTCTTAAACGATGCAGGATTAAAGAATT
TTTTTTCAAGCTACGATTATGCTTTTCGGGGTTGCATACAACCTTGTAAATTGCTCTGAAT
ACAGGTATGACGAAGTTTCAATACATATCGAACGGCACTTACTCATTAGTTGCATCGATGA
AGATAGATCCTGCTGAAGTCATTAAAGGGAACATTTTAGGCTTACAATTCGAAATTTA
ACATATCTAATATATTAATTGAAATTTTTTCATTTGCTCGATGGATTAGCATTTTTTAAAGG
TGAACCTTGATAGTTTATCTATATCTACAGCTTCAGCAGAAACAATCTTTCGCAGTATCT
CCGAAGGTAATCATCAGGTCTTAGAATTGGGGAGAAGTTTAAATGTTTCCATTGTTGAGGA
CTGGAGATTTTGAAATCTGTCGTATTGACGACGCGGGAGCTGTCATAACATTTACAGAAG
CGAAGGATGTAAAAC TAGAAATAATCAGTCTGGATGAAGTTTCTGGGTAATGCAGTGGGA
AATCTTGTCTTCAAAATTATGAGAGAAGGGCAGCAATGACAGTTCATTTATCAAAACAC
ACCTACAATTTAAGAAGGCCAACAAATTTCAATGAAGATAATAATGGGCTAGGACTAATTG

TAGACAGAAATATTCCAACAGATGATTTTACGCTAGCTTCTACAAACCGTCAAAGTCCCC
CGCCTTCAAATACTGGTTGTTTATTACACAGGTCTAAACCTTGCATATCCCTTTATCAT
CTGTTATTTCGTGAAGACTTTTATGATAGCTCTCTAAATGAGCGTATATCTAAAGACGGAG
ATAGCAGTTGTGAATCCTTCAGTGGCGCCGAAAGTATCTTATCAGACTACGATTTTCATG
ATAATGAATTTTAAACAACAGTCACCTCATTATTTTTCAGAACACATAGACAATAACT
CGAGAGAGGTGGTAATAACAGATGAAAATACGATAATATCTTTGGAAAATACCCAAGTAA
GTCCGTGGTCAAATTACTCATGGCAAAAAATTTACCGCATCAATTACAGGTCTCTATTA
TCCAATGCGCATGGGAAACTTCATTGTGGCTTATGATTCTGATTATAACCTTCATCAGT
TCAAAATTCTGTTGTGTGACGATATAAAATGTATACAATCCACAGAGCAAGACATACAAA
TACGTGTCCCGCTCGGCGCAATAATGTGCAGCGTCACTGGTATCTTGAATATTAGGACGA
AGGACGCTGACAAGTTGCTTCGGGTATTAAGCTTTTATACCACTGACCACACGGAAGCTG
TATCGCACTCAACAATCAAGATGCTACTGCAAGTCCACTTTTCGTGAGTTTCATCAGCAA
TGGATCTCAAGCATTATTACAGAAATGTTCTCTACAATAATGCCCCAAGAGTTGACGC
AGGACGTATCGGTTCAAATCAGACCTAATCAGTAATATTTCGTCAAAAAATATAA

YJL181W, 611 aa (SEQ ID NO 156)

MEIFKEEEEEAFSAIEGIIYACEVYDPVPRHLHKSSTKIINAAKLIIETHLSYYTILNNI
SDIQAYLSTWLRDLGTTGPTYQILSEISLMFDRTVSIFRKCTIEGGFPHLIARLYLRLLK
SYQKLLNDAGLKNFFSSYDYAFGVAYNLVNCSEYRYDEVHYISNGTYSLVASMKIDPAEV
IKREHFRLTIPKFNISNILIEIFHLLDGLAFFKVNPDLSISASTASAEIFRSISEGNHQV
LELGRSLMFPLLRTGDFEICRIDDAGAVITFTEAKDVKLEIISLDEVSWVMQWKSCLQNY
ERRAANDSSFIKTHLQFKANNFNEDNNGLLIVDRNIPTDDFTLASTNRQSPPPSNTGC
SLHRSKPLHIPLSSVIREDFYDSSLNERISKDGDSSCESFSGAESILSDYDFHNEFFNN
QSPHYFSEHIDMNSREVITDENTIIISLENTQVSRWSNYSWQKISPHQLQVSIQLRMGN
FIVAYDSYDNLHQFKIRLCDDIKCIQSTEQDIQIRVPLGAIMCSVTGILNIRTKDADKLL
RVLSFYTTDHTTEAVSHSNQDATASPLSSVSAMDLKHSQKCSSTIMPQELTQDVGSK
SDLISNIRQKI

YJL187C, 2960 bp, CDS: 501-2960 (SEQ ID NO 157)

TCTTGCAACCATCGTCTCTAAGGAAAGAAATGTGGCACCTTTAAATAGGTTCCACCTCA
CAGATGCCAACATGTGGGAGATAGGGGGCTATTTCGCAATTTATTAACGTCTCTAGTACTG
GTAAGCCTTTCTAACATTCTTGTGGTCACGTGATGTGTATGTTCTTTTTTTTATTCCTC
CGGGTGATAACGACGCGAAAAATATTTTTTCATTTTTCTTTTAACCATCACAAATTTGCGA
CGCGACGCGAAAAAATGCAGAGAAGTAAAGAATGCTGGATAAGAAATCAACAACACAG
TTGAACATTGGCGTGCCCTGTGTATTAAAGTAAAGGTTGTCCAAGAGGCTCTTTTTGTGTA
TGTATGCGTGTGTTAACTATCCTGCACATCATCTTGCGCAGTTAGTCCAATAAAAAAGGA
TTACTACTGAACAGGTCTTACTATTTTTGATTGCGTAGTGCTGGGGAAAAGTAAACACAC
ACAGGCGCACACGAGAACAGATGAGTTCTTTGGACGAGGATGAAGAGGACTTCGAAATGC
TGGACACGGAGAACCTCCAGTTTATGGGGAAGAAGATGTTTGGCAAACAGGCCGCGGAAG
ACGAGAGTGATGATTTTGCTATAGGGGGTAGCACCCCGACCAATAAACTGAAATTTATC
CATATTGCAACAACAAATTGACAAGAAGTACGGGGACCTTGAACCTGTCAATTAAGTAATA
CAGCTTTGTGAGAGGCTAACTCCAAATTTCTTGGGAAAATTGAAGAAGAGGAAGAAGAGG
AGGAAGAAGGCAAGGATGAGGAAAGCGTGGATTCTCGTATTAAAGGTGGTCTCCGTTC
ATGAAATGAAAGTGTACTACTCTATTACAAAAAGATCTGCGGAAAAAACGAACAGTC
CTATTTCTCTCAACAATGGAACAGCGATGGTTTCCGAAAAATGATGCTCGCACTGAAA
ATACATCTCATCTCTTCTATATAGCGTCGCTAAACCTAACCAATCAGCCTTTACGTCTT
CGGGCTCGTATCTAAAATGTCTATGGACACTTCGTTATACCTGCGAAATTGAGGATAC
CAGAAACACCAGTGAAAAAATCACCTTAGTGGAGGGAAGAGACCATAAGCATGTCCACC
TTTCGAGTTTCGAAAAATGCATCGTCTTCTCTAAGTGTTTCCCTTTAAATTTTGTGTAAG
ACAATAATTTACAAGAAGACCTTTTATTTTCAGATTCTCCGTCTTCGAAAGCTTTACCTT
CCATCGTGATACCAACCATAGACTCATCCCCACTGAGCGAGGCAAAATATCATGCACATG
ATCGTCACAATAACCAGACAAACATCTGTCTCCCACTAATAGCTTGGTTACCAACAGCT
CTCCACAAACATTGCATTCTAACAAGTTCAAAAAATCAAAAGAGCAAGGAATTTCGGTTA
TTTTGAAAAATAGAGAGCTAACAAACAGTTTACAACAATTCAAAGATGATTTATACGGCA
CGGACGAGAATTTCCACCTCCAATCATAATATCAAGTCATCATTTCAACTAGAAAGAACC
CTCAACCTTATCAATTTTCGTGGACGCTATGACAATGACACTGACGAAGAGATCTCCACTC
CAACAAGACGAAAAATCTATTATTGGGGCAACATCTCAACACATAGAGAAAGCAGACCAT
TGTCACTTCTCTGCGCATCGTGACAAACACAAGTGCAGAGACGCATTCCATATCTT
CCACGATTCTTCGCGCTTAAATTCAAAAGGCGTCTAATCTCTTCAAATAAGTTATCAG
CAAATCCAGATTCCCATCTTTTCGAAAAATTTACGAATGTGCATTCCATTGGTAAAGGCC

AGTTTTCCACGGTCTACCAGGTTACGTTTGGCCAAACAAACAAAAAGTATGCAATCAAAG
CCATTAAACCAAACAAATATAATTCCTTGAAACGCATATTACTGGAAATTAAAATACTAA
ACGAGGTAACAAACCAAATTAACAATGGATCAAGAAGGGAAGGAATACATCATCGATTACA
TCAGTTCTCGGAAGTTTCAAAATTCATACTATATTATGACAGAATTGTGCGAAAATGGTA
ATTTGGATGGATTTTACAAAGAGCAAGTTATCGCAAAGAAAAAAGGTTGGAAGATTGGA
GAATTTGGAAAATCATCGTGGAAATTAAGCCTGGCTTTACGATTTCATCCATGATTTCTGTC
ACATTGTGCATCTGGACTTGAAACCCGCAACGTCATGATCACATTTGAAGGTAACCTAA
AACTAGGTGACTTTGGAATGGCTACTCATTTACCGTTGGAGGATAAAAGTTTGGAAAATG
AAGGTGACAGAGAATATATTCACCAGAAATCATTTCTGATTGTACGTACGATTACAAGG
CAGATATTTTTTCCCTGGGTCTGATGATTGTTGAAATTCAGCGAACGTTGTGTTACCTG
ACAAATGCAACGCATGGCATAAGTTGAGATCGGGTGATTTATCGGATGCAGGAAGATTAA
GTTCCACAGATATTCATTCTGAATCATTTATTTTCAGACATTACGAAAGTAGATACAAATG
ATTTATTTGATTTTGAAGAGACAATATCAGTGGTAATAGTAACAACGCTGGCACCTCCA
CTGTTCATAACAATAGTAATATCAACAACCTAATATGAATAATGGCAACGATAATAATA
ATGTCAATACTGCCGCTACCAAGAATCGTCTTATTTTGCATAAAAGTTCTAAAATTTCCCG
CATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACGATGGATGA
TAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGAGGAATGCC
TGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTTTGGACCTA
AGCCAAAATTTTTTATATGA

YJL187C, 819 aa (SEQ ID NO 158)

MSSLDEDEEDFEMLDTENLQFMGKKMFGKQAGEDESDDFAIGGSTPTNKLKFPYPSNNKL
TRSTGTLNLSLNTALSEANSKFLGKIEEEEEEEGKDEESVDSRIKRWSPFHENESVT
TPITKRSAEKTNSPIILKQWNQWFPKNDARTENTSSSSYSVAKPNQSAFTSSGLVSKM
SMDTSLYPAKLRIPEPVPKKSPLVEGRDHKHVHLSSSKNASSLSVSPLNFVEDNNLQED
LLFSDSPSSKALPSIHVPTIDSSPLSEAKYHAHDRHNNQTNILSPTNSLVTNSSPQTLHS
NKFKKIKRARNSVILKNRELNTSLQQFKDDLYGTDENFPPIIISSHHSTRKNPQPYQFR
GRYDNDTDEEISTPTRKSIIGATSQTHRESRPLSLSSAIVTNTTSAETHSISSTDSSPL
NSKRRLISSNKL SANPD SHLFEKFTNVHSIGKQFSTVYQVTFQAQTNKKYAIKAIKPNKY
NSLKRILLEIKILNEVTNQITMDQEGKEYIIDYISSWKFNQSYIIMTELCEGNLDGFLQ
EQVIAKKRLEDWRIWKIIVELSLALRFIHDSCHIVHLDLKPANVMITFEGNLKLGDFGM
ATHLPLEDKSFENEGDREYIAPEIISDCTYDYKADIFSLGLMIVEIAANVVLDPDGNNAWH
KLRSGLSDAGRLSSTDIHSESLFSDITKVDTNDLDFDERDNI SGNSNNAGTSTVHNNSN
INNPNMNNNGNDNNNVNTAATKNRLILHKSSKIPAWVPKFLIDGESLERIVRWMIEPNYER
RPTANQILQTEECLYVEMTRNAGAIQEDDFGPKPKFFI

YJL188C, 809 bp, CDS: 501-809 (SEQ ID NO 159)

AATTCCCGCATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACG
ATGGATGATAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGA
GGAATGCCTGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTT
TGGACCTAAGCCAAAATTTTTATATGATAAATGGAACAAAAAACCTTGTTTTATTTACA
TACTTTTTTCCACACGTGCTTATGGGCCGATTGTATAAATAATCCAATAACGAAAAAG
AGTGTAATTGCAGTCCGGTAGTAATACCATGTAAAACCTTAGATGAGTTTATTTTAAGTA
CAGCCGCTTCAAGCATTTTTATTTTTATTTTACAGATGTAGCAGATAACAACCGTTAAAT
TATATTATATATATATATATATATATATCAAATACGACGTATTACATATATATTGAGAAT
AAGGGAAGGATGGAAGACAAATGACAAAAAGTTTGAAGCATAAATATGTTCTTCGCTTAG
ATGTTTCATCTTGGTTCTTCTCAGTTTCTTCTCTTAGCGTTGTAACGGATAGTGTGTGTG
GTTCTCAATCTGATCCATTGTGGCAATGGTCTGTTTTGCTTCTTAGCCTTAGCCATTTTT
TGCTTGATTCTGAAAGACTTTTGAGCCTAATTAAGGGAACATATCGTGCACATACGA
AGTGTAATTTGTAATAAATGTTAGTAACAATGTTCAAACCTCATCAATATGATGCATTCA
CGGATCCAAGGCAATACCACCTGACATAA

YJL188C, 102 aa (SEQ ID NO 160)

MTKSLKHKYVLRDLVHLGSSPVSSLSVVTDSVVGSDPLWQWSVLLLSLSHFLDLSERL
LSLIKRETYRAHTKCTIVKNVSNVQTHQYDAFTDPRQYHLT

YJL189W, 1042 bp, exon1: 501-506, intron1: 507-892, exon2:
893-1042 (SEQ ID NO 161)

TATTCAAGAATTATTTACATCTTCCAGCGAGTAAACATGCCGCTGGTAATCGCGCGTCC
TCAATATTTGAGTTTTTCAAATAGTGAGGTGTGGATGTATAGAGGAATTACACACTTTTA

AGTATGTGATGTATGGGCGCACAGTACCAATTTAACTTTTTTTTTTTTTTTCATTTTTTAGC
TTGATTTTTCAAAAACTTATGGGCGTTTTAGGCTCCGGCTCAAACCTACCACCACCACGCG
GCAGGCCGAGGCAAACAGTACGCCTTGGCGGGGACGCCGAAGCGACTCCTTCTGTTCCAA
GCTCAATGGTCCCTTGCCTTACGCTCGCGCGTGGGCTAACTAACGCAATTCGGCTTTTGG
GCTGTGCGAACCAGAAATTTATCTTCGCTTGATAGATACTTTAAAACTTCTACTTAAT
ATACTTTCTACAAATTTTTGGTACATTCATATTATACTGAAAAATTCGAAAAAGACAAGCAA
ATAAACACAGATAGATCAACATGGCTGTATGTTAGAAAAGATATTATAAATCCCAGTTAGA
TGCTGAACCTGATCAATAGCAAATTTATAAACCACATCCATCTAAATGACCTTACCACCTAC
AATTTGGATTTGAAATAGAAGCAATGTGTAAATATAGGGAAAAGGATTAGGAGTGTAAAC
CATACTAAAAATTTTTCTTATCCGAAACAGAAATCTAAAGTCGCCACTACGCAGATTAAAA
TATGGTCATAAAGCTTATTTCTGAGAACTTTTGGTGGTCCAGCGTGGTTTATGTCAGGT
GCTATTTGCCCTTGGATCCGTGAATGCATCATATTGATGAGTTTGAACATTGTTACTAACAT
TTTTTACAATTTGTACACTTCGTATGTGCACGATATGTTTCCCTTTTAAATTAGGCTCAAAA
GTCTTTTCAGAAATCAAGCAAAAAATGGCTAAGGCTAAGAAGCAAAACAGACCATTGCCACA
ATGGATCAGATTGAGAACCAACAACACTATCCGTTACAACGCTAAGAGAAGAACTGGAG
AAGAACCAAGATGAACATCTAA

YJL189W, 51 aa (SEQ ID NO 162)

MAAQKSFRIKQKMAKAKKQNRPLPQWIRLRTNNTIRYNAKRRNWRRTKMNI

YJL190C, 893 bp, CDS: 501-893 (SEQ ID NO 163)

TCTCGACAGCCCAAAAGCCGAATTGCGTTAGTTAGCCACGCGGAGCGTAAACGCAAGG
ACCATTTAGCTTGAACAGAAGGAGTCGCTTCGGCGTCCCCGCCAAGGCGTACTGTTTGC
CTCGGCTTGCCTGGTGGTGGTAGTTTGAGCCGGAGCCTAAAAACGCCCATAAAGTTTPT
TGAAAAATCAAGCTAAAAAATGAAAAAAAAAAAAAGTTAAATTTGGTACTGTGCGCCCATAC
ATCACATACTTAAAAGTGTGTAATTCCTCTATACATCCACACCTCACTATTTGAAAACT
CAAATATTTGAGGACGCGGATTTACCAGCGCATGTTTACTCGCTGGAAGATGTGAAATAA
TTCTTGAATATGGGTTTGCAGTTAGTCAATTTCAATCTAAATAATCTTAATCGACTATTC
AATCTTAAATTTGAAGGTTTTTAAATGGCTTTTCAGTTCTAGTATTTTTTATAAAACAA
GACCAACATACATATCCAAGATGACCAGATCTTCCGTTTTAGCTGATGCTTTGAATGGCCA
TTAACAACGCTGAAAAGACCGGTAAGCGTCAAGTTTTAATCAGACCATCCTCCAAGGTCA
TTATCAAGTTTTTGAAGTTATGCAAAAGCACGGTTACATTGGTGAATTTGAATACATCG
ATGACCACAGATCTGGTAAGATTTGTTGTCAATTTGAACGGTAGATTGAACAAGTTGGTG
TTATTTCCCAAGATTCAACGTTAAGATTTGGTGACATTGAAAAATGGACTGCCAACTTGT
TGCCAGCCAGACAATTCGGTTACGTCATCTTGACCACCTCTGCTGGTATCATGGACCATG
AAGAAGCCAGAAGAAAGCACGTTTTCTGGTAAGATTTTGGGTTTCGTTTACTAA

YJL190C, 130 aa (SEQ ID NO 164)

MTRSSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLQVMQKHGYIGFEFYIDDHRSBK
IVVQLNGLRNLKCGVISPRFNVKIGDIEKWTPANLLPARQFGYVILTTTSAGIMDHEEARRH
VSGKILGFVY

YJL197W, 4265 bp, CDS: 501-4265 (SEQ ID NO 165)

CTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAGTAGATAGAAAGGGCGATCGCT
ATTTAAGTGTCACTGACTTTCTTAAACGAGAGGTGTTCCAGCTTCTATTTTTGGCTTTCCCTAT
GTGTCACTTACTCTAGGTTATGGTATCATGGCATCTGTTGTCAAGGGTAACGCAACCTCTG
CGTAAGAGATACGTCTACGATAGCATGTAACAGCGTATATATAATCTATATGTATTCGAT
TAATCCAACACTTCTGTTGTGTAGTCTAATGTTTCGAAAAAAGGTACGCTTCCCTGTTAT
AATCAGGTATATTTCTGTTATTTCTTATAAGCTAAAAGATTAAAAATTTTTCCACTTTCCCTT
GAAATTTGGTTCGGTTTCGTGAAAAATATTATTACGTATTGAAGAAGTGCATGAAGATAAA
AGATGGGATTACTGGAATAAAGGGAGGAAATCCTGCAGAACGTTGTTGTTTCAATC
GAAGGTTTCTTCATTCGAAAATGGGTTCTTCAGATGTTTCAAGTCGTGAATGTTTCAATG
TTTATAATGAAGATCCCGATTTACCGATGGCACAACACCATGTGATCGTTGGGAGTGG
ACTTGATGAATGTTCTAGATGACAAGGATGAAATAAAGCAAGAGTCTGTCCAGTCTCAG
ATCGTGAATTTGAGGATACGGAATCCGATGCTTCCGCTGTTTCTTCATTTGCTAGCGCTA
ATGAGTTAATAGCTGAGCCACACGCTGCAAGTGAACTAATCTTGGAACCTAATGGTCAAG
ATGGAAGAAATGTCTTGAACAACAAAGAGACGTGGTTGCTAGACTAATAGAAGAAAAACA
AGGAAACGCAAAAGAGGGTGATAAAGTCTGTATTGTCCCAAGGTTTGGTACGATAAAT
TTTTCGACCCGATGTTACCGATCTGAAGATATAGGCCCTATTAATACACGCGCATGTTT
GCAGAGACTTTGAAAAATTTTGTGCTTGAGGATTACAATAGATGTCCGATCTGTCTATTG

CAGAGCCTGTTTTCAATTTTCTATCAGAAATTTACGGCATGACAAGTGGCTCTTACCCAG
TGGTAAC TAATTTGGTTATCAACCAACCACAGGGGAGTTAGAGACAGAATACAATAAAT
GGTTTTTCAGACTACATTACCTGACCGAAAAACAAGACGGGAGGAAAAGGAGGCATGGCC
AGGACGATTCAATAATGTACCTCTCGATGCTGCGTTGAATTTAGTACGTGATTTGGTTG
AAAAGAGTATGAATCTGTTTTTTTGAGAAAAGCTGATCATCTAGACGTGAATGCGGTGGATT
TAAAAATTTGGTTTGTGTCAGAGGGATCTGATATTGCCACAGATAGCAATGTTAGTACTT
TTTTGAATTCCTCATATGAAATAACTCCGCTTCAATTTCTCGAACTACCGATAAAGAAAC
TACTAATACCAGACATGTTTGAAAACCGTTTAGACAAGATAACTTCAAATCCGAGTGACC
TTGTCATAGAAATTAACCTATAGAAGGGAATCACCATTGGCCCTCAAAC TATTTTGCTT
ATAATAAACTCGAACCAGCATCAGGTACTACTGGTTTGGTCAATTTGGGAAATACATGTT
ACATGAATTCGCGTTGCAATGCCCTGGTACACATTCCGCAGTTGCGTGATTAATTTCCCTTT
ATGATGGTTATGAAGACGAAATCAATGAAGAAAATCCTCTTGGGTACCACGGCTATGTGG
CTAGGGCATTTAGTGACTTGGTTTCAAGTTGTTTCAAAACAGGATGAGCATAATGCAAA
GAAATGCTGCTTTCCCCCTTCAATGTTCAAATCCACTATCGGGCAGCTTTAATTCGATGT
TTTCTGGTTATATGCAACAGGATTCTCAAGAAATTTTAGCCCTTCTGTTAGACAGTTTAC
ATGAAGATTTGAACAGGATAATAAAGAAAGAAATACACAGAAAAACCATCATTATCTCCTG
GTGATGACGTGAATGATTGGAATGTAGTCAAGAAACTGGCAGACGATCTTGGGAGATGAC
ATTTAAAGAGAAATGTTCCGTTATAACCGATTATTTTGTGCGGGATGTACAAATCAACGC
TATATTGTCCCGAATGTCAAATGTTTCTATAACGTTTGACCCGTATAATGATGTTACAT
TGCCGCTTCCGTTGATACAGTGTGGGATAAACTATAAAAAATTTTCCCATGAACCTCTC
CACCACCTCTTCTTGAAGTTGAGTTAAGCAAAATCGTCCACTTATATGGACTTGAAGAAAT
ATGTTGGTAAATGTGCGGCCCTAGATCCAAATACACTATTTGGCTGTGAGATTTTCAGTA
ATGTTGAATTTGAACAATATAAAGATATACTACAGTATACGTTCAATTTTAAAGGTGACGAG
AATTGATCAAACCTGCTGATGACGTTATTTTATGAATTACCAGTAACAAATGACAATG
AAGTAATTTGTTCCCGTATTGAATACTAGAAATGAAAAAGGCTACAAAAATGCAATGTTAT
TTGGAGTCCCTTTCTTTATTACGTTAAAGAGATGAATTGAATAATCCAGGTGCAATAA
GAATGAAATTGCAAAACAGGTTTGTCCATTTAAGTGGTGGGTATATCCCATTTCCCTGAAC
CTGTAGGAAATCGAACCAGTTTGTGCTGATGCTTTTCCATTATTAGTAGAAAAATATCCAG
ATGTTGAATTTGAACAATATAAAGATATACTACAGTATACGTTCAATTTTAAAGGTGACGAG
AGGATAAATCCTTTTTCATCAAGATTCTGTCTGTAGAAAAAGAGCAGCAATTTGCTA
GTAATAACCGAACAGGGCCTAATTTCTGGACCCCTATCTCCAGTTAAACCTTGACAAAG
CTACAGATATAGACGATAAACTTGAAGATGTGGTGAAGGATATCTACAAATATTCTATCCT
TAGTAGATTGTGCTGAAGGGGTCTTATGCAAGTGGATGATGAGGGAGATACCGAGGGTA
GTGAAGCAAAGAATTTTCCAGCCCTTCCAATCGGGAGATGATGAAGAAAAATAAGAAA
CTGTAACAAATAATGAAAAATGTAATAATACTAATGATCGGGATGAAGATATGGAAGCTAA
CAGATGATGTTGAAGAAGATGCAAGTACAGAGCCAGAATTAACAGATAAGCCAGAGGCGT
TAGATAAAATTAAGGATAGCTTGACTTCCACTCCGTTTGGCATTCTTTCTATGAATGATA
TTATTGTTTGTGAGTGGAGCGAATTTGGGTTCAAAATGAGGCATTTTCCGATGATAAAATAT
ATAACTGGGAAAATCCAGCTACTTTGCTTAACAAAGAGTTGGAGAACGCTAAGTTGGAAA
GATCTAACGCTAAGGAAAGAACCATAACCTTGGACGATTGTCTCCAATTAATTTCCCAAC
CAGAAATACATAGGATTAAACCGATTCCGTTGCTGCTACTGCCCTACATGCAAGGAACATCTCAGG
CTACCAAAACAAATACAACCTTGGAAATACACCAGATATTCTGCTAATTCACCTTAAAGGT
TTGAAAGTCAAAGGTCTTTTAGCGATAAAATTGATGCCACGGTTAATTTCCCATTTACAG
ATTTGGATCTGTGAGGTACGTTGTCTATAAAGATGATCCCAGAGGTTTAATCTATGACC
TGTATGCAGTAGATAACCACTATGGTGGTTTGGGTGGTGGGCACATATACCGCGTACGTAA
AGAATTTTGGCGACAATAAATGGTACTATTTTGTATGATTCTCGAGTAACTGAACTGCGC
CAGAAAAATAGTATAGCTGGATCGGCTTATTTGCTATTTTACATTCGCCGCTATAAAGATG
GCAATGGATTAGGCAGCTCTAAACTACAGGAAATAATCCAAAAGTCACGCCACGGATATG
ATGAGCGTATCAAAAAGATATACGATGAACAGATGAAGTTGTATGAATTTAATAAGACTG
ACGAGGAGGAAGATGTTTCTGATGATATGATAGAATGTAATGAAGATGTGACGGCCCCGTG
AATATAGTAATCGTAGTTTGGAGGTTGGGCATATTGAAACTCAGGACTGCAACGACGAAG
ATGACATGATGATGGTGAGAGGACAAATTCAGGTAGGAGAAAGTTAAGATTGTTGAAAA
AAGTCTACAAGAAATAATTCAGGCTTGGGTTTCATCGAGTACGTTCTGAAATATCTGAGGAT
GCCAGAAAAACGAAGTCGCTGATTTGAATTTAAAAAATGGTGTGACACTAGAATCGCCAG
AATAA

YJL197W, 1254 aa (SEQ ID NO 166)

MGSSDVSSRECSLVYNEDPDFDGTTPCDRLGVLDLMNVLDKDEIKQESVPVSDREIEDT
ESDASAVSSFASANELIAEPHAASETNLGTNGQDGRNVLEQQRDVVARLIEENKETQKEG
DKVCIVPKVWYDKFFDPDVPDIPINTRMICRDFENFVLEDYNRCPYLSIAEPVFNF

LSEIYGMTSGSYPPVVTNLVINQTTGELETEYNKWWFRLHYLTEKQDGRKRRHGQDDSIMY
LSMSALNLVRDLVEKSMNLFFEKADHLVDNAVDFKIWFVSEGSDIATDSNVSTFLNSSYE
ITPLQFLELPIKLLIPDMFENRLDKITSNPSDLVIEIKPIEGNHHPWSNYFAYNKLEPA
SGTTGLVNLGNTCYMNSALQCLVHIPQLRDYFLYDGYEDEINEENPLGYHGYVARAFSDL
VQKLFQNRMSIMQRNAFPSPSMFKSTIGHFNSMFSGYMQQDSQEFALFLDLSLHEDLNRI
IKKEYTEKPSLSPGDDVNDWNVVKLADDTWEMHLKRNC SVITDLFVGMKYKSTLYCPECQ
NVSITFDPYNDVTLPLPVDTVWDKTIKIFPMNSPPLLEVELSKSSTYMDLKNYVGKMSG
LDPNTLFGCEIFSNQIYVNYESTESNAQFLTQLQELIKPADDVIFYELPVTNDNEVIVPVL
NTRIEKGYKNAMLFQVPPFITLKEDELNNPGAIRMKLQNRVHLSGGYIPFPEPVGNRTD
FADAFPLLVEKYPDVEFEQYKDILQYTSIKVTDKDKSFFSIKILSVEKEQQFASNNRTGP
NFWTPISQLNLDKATDIDDKLEDVVKDIYNYSSLVDCAEGLVMQVDDDEGDTGSEAKNFS
KPFQSGDDEENKETVTNNENVNNTNDRDEDMELTDDVEEDASTEPELTDKPEALDKIKDS
LTSTPFAILSMNDIIVCEWSELGSNEAFSDDKIYNWENPATLPNKELENAKLERSNAKER
TITLDDCLQLFSKPEILGLTDSWYCPTCKEHRQATKQIQWLWNTPDILLIHLKRFESQRSF
SDKIDATVNFPIITDLDSRYVVYKDDPRGLIYDLYAVDNHYGGLGGGHYTAYVKNFADNK
WYFFDDSRVTETAPENSIAGSAYLLFYIRRHKDGNGLGSSKLQEI IQSRHGYDERIKKI
YDEQMKLYEFNKTDEEEDVSDDMI ECNEDVQAPEYSNRSLEVGH IETQDCNDEDDNDGDGE
RTNSGRRKLRLKKVYKNSGLGSSSTSEISEGCPENEVADLNLKNGVTLESPE

YJL198W, 3149 bp, CDS: 501-3149 (SEQ ID NO 167)

TGTCGTATTTCCACTGATTTGGATGTATGTTGCATGGTGCCTAGATTGTGAATAAATCATT
TCCACTGGTTTCTAGCAGAGGTAAGAAAATCAGTAGTAGCGGCAGCAGCCAAGAAAAATG
GCAGCCTGGCAAGCAGCGAAGGCCATCTGTGCTGCATTCCACACTCCTTGTATGACTGC
ATACGCATAAAGAGGTGCCTTGTCTGTAGGCGTATATGATCCTAAGCAACAGAGAAACAC
GGTTCCTCTCTCTCTTATTTCGTTATTGTCTTCCCTTTTTACTATGGGTAAAGTCGCCC
TAAAGCGGGCGCTCACAAATATCGCCGAGCTACAGCCGTTTTTTTTTTTTTTTTTTTTT
TTTGCGCTGCTTCTCGAAGAATGAATGGCTCACTGAAAAATTTTGATTTCATCGATATAAA
GAACACTGTTCACTTCGATGTCTCCGCCAATAAAGTTGTTTTTAGGATAAACAGAGTAA
GTGGTAGCTGGTACAGGATCATGAGATTTTACACTTCTTGAAGTACAATGCTGTGCCAG
AATGGCAAAACCATATATGGACTACAGCGAGCTGAAAAATCTTATTTACACGCTACAAA
CAGATGAACCTCAGGTTGGTGATAACGAAGAAGGATTTGGCGCAGGAAAGAGCTCTAACA
TTACAGATAGGTTCAAAAACAAGTTTTCTTTTAAAAATGCGAAGGAAGATACGTCTTCCG
GTATGAACAAAGATGCAGGCATCGTTGAGGAAACCATCGAGTTGCGAGAGTTGCCTACTG
CTCAGACGGTCGCTGCCAAACCTTCTCCTTTTCAAGAATGAAGGAAAAGATATTTTACA
AAAGAAGTTCGTCTTCCGCATCGTCCGTCTCCTCCACGGCCAACGAAAAATCTGCAATTAG
ACACTTATGATACGTTTTGTTGGTGATTTAACAGCTGAAAAACAGAAAGTAGATGATTTTT
ATAAGAGGACAGAAGCGAAGTTCTACGACAAATTTGACGCGCTGGTGAAGGACCTGAAGA
AAATCGGAGTTATAGAATACGATATCGACGATGATCTCTGTTTAAACGAACCGATTGCCA
GCACAAATGACGAAGTTCCCCCACTAGACTTGGATGATGACGAAGACGACGACGAATTTT
ACGATGATCAATCTAATATTGAAGATAATACTGCTTTGCTGCATCATTTCGCAGTATAACA
TTAAGTCTCAGAAAAAATCGCTGTTGAAGAAGTCGATCGTAAACCTATATATCGATCTTT
GCCAGTTGAAGTCGTTTCATCGAATTGAACCGCATTTGGGTTTGCAAAAAATTACAAAGAAAT
CAGACAAAGTTCTTCACTTGAATACAAGAACCGAAGTATCGAATCGGAGCAGTTTTTCA
AAGACACATATGCATTCCAGGCAGAAACGATCGAATTGCTAAATTTCCAAAATTTCCCAGC
TAGTCACATTTTATGCGCGCATCACTGACCGGCTCATAATATCTCGCATAGCAAGCAAG
AGTTGAAATCCTACCTGCATGACCACATTGTTTGGGAAAGAAGTAACACTTGGAAAGACA
TGTTGGGACTGCTATCGCAAGCTGACGAGTTGACACCAAAGGAAACAGAATATAATGCAA
ATAAGCTGGTAGGCAAGTTAGATTTGGAATACACAGATGGCCACTACCCAGACCGATAA
ACTTAAAATTCAGTAGTATAAACAACGTTGCACTACCGAAATTATTTTTTACCAAGAAAG
CATACAAGATTTACTTTATTATTCTAGTCACTGGACTCTTGTAGGAATAAAGACCTTCA
ACGACGCTGCTCAGCACCGCTGCATGGCCCTTGTGAGTGTGTGCGCTTTTTTGTGGGCTA
GTGAGGCCATCCCATACACATTACAGCATTCCTTGTACCACTACTTGTAGTCTTTTTCA
AAGTCTTAAAAACCTCCGACGGGGCTATAATGAGTGTGCAAGCGCTTCATCAGAAATTT
TGGCCGCCATGTGGTCTTCTACAATTATGATTCTGCTGGCAGGTTTTACTTTGGGTGAAG
TACTTGCACAATATAACATCGCCAAAGTTCTTGCTCGTGGTGTGGCCTTCGCTGGTT
GTAAACCCAGAAACGTTCTTTTAAATGGCAATGTGTGTCGTGTTCTTCCATCAATGTGGA
TTTCCAATGTGCGACACCTGTTCTAACATATTCGTTGTTATCTCCCTATTGGATGCCA
TGGATGCGATAGCCCATTTGCGCAAGCATTTGGTGTAGGTGTAGCGTTGGCTGCAATA
TCGGTGGTATGTCTTACCAATCTCTTCACTCAAAACATCATTTCCATGTGCTGATTTGA
AACCTATGGTATTGGCTGGGGCCAATTCTTTGCTGTTGCATTGCCATCTGGTATCTGG

CCATGCTTTTGGTTTGGATTTTATTGTTCACTACTTTCAAGATGAATAAGACCAAATTTGG
AAAAATTTAAGCCTATTAAAGACGAAATTCACAGTTAAGCAGTATTATATCATTTACTGTCA
CTGTGGCCACTATTTTGTGTGTGGTGTGTGGAAAGCCAGATTGAAGGTGCTTTTGGGTGTCAT
CAGGTCAAATTTGCAATCATTTCCCATCGTTTGTMTTGTGGTACCGGATTACTATCAACAC
AAGATTTAAATGCCTTTCCGTGGTCAATCGTTATTTTGGCAATGGGAGGTATTGCTTTTGG
GGAAGGCCGTCTCATCCTCGGGTTTGTCTATCAACCATTGCAAAAGCATTACAAAAGAAAA
TTGAGAATGATGGTGTMTTGTGCCATTCTATGTATTTTCCGTATCCTGATGTTGGTGTGTGG
GTACTTTTCGTCTCGCATACAGTATCCGCTATTATCATCATTTCCCTTGGTGCAAGAAGTTG
GTGACAAAGCTTGGCAACCCCAAAGCTGCTCCTATCCTTGTMTTGTGGTGTGTGCAATTATGT
CATCCTGTGGTATGGGACTAGCTTCTTCCGGGGTTCCCAATGTCACTGCCATCTCTAAAG
TAGATAGAAAGGGCGATCGCTATTTAAGTGTATGACTTTCTTAACGAGAGGTGTTCCAG
CTTCTATTTTGGCTTTTCTATGTGTCTATTACTCTAGGTTATGGTATCATGGCATCTGTTG
TCAAGGGTAACGCAACCTCTGCGTAA

YJL198W, 881 aa (SEQ ID NO 168)

MRFSHFLKYNAVPEWQNHMYDSELKNLIYTLQTDDELQVGDNEEGFGAGKSSNITDRFKN
KFSFKNAKEDTSSGMNKDAGIVEETIELRELPTAQTVAAKPSPFRRMKEKIFYKRRSSSA
SSVSSTANENLQLDYDTFVGDLTAEKQKVDDFYKRTEAKFYDKFDALVKDLKKIGVIEY
DIDDDTLFNEPIASTNDEVPLDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIKSQKKS
LLKKSIVNLYIDLQKLSFIELNRIGFAKITKSKDKVLHLNTRTELI ESEQFFKDTYAFQ
AETIELLNSKISQLVTFYARITDRPHNISHSKQELKSYLHDHIVWERSNTWKDMLGLLSQ
ADELTPKETEYNANKLVGKLDLEYRWPPLRPINLKFTSINNVALPKLFFTKKAYKIYFI
ILVTGLLLGIKTFNDAAQHRCMALVECVAFWASEAIPLHITAFVLVPLLVLFKVLKTS
GAIMSAASASSEILAAMWSSSTIMILLAGFTLGEVLAQYNIKVLASWLLAFAGCKPRNVL
LMAMCVVFFLSMWISNVAAPVLTYSLLSPLLDAMDADSPFAQALVLGVALAANIGGMSSP
ISSPQNIISMSYKPYGIGWGQFFAVALPSGILAMLLVWILLFTTFKMNKTKLEKFKPIK
TKFTVKQYIIITVTATILLWCVESQIEGAFSSSGQIAIPIVLFFGTGLLSTQDLNAFP
WSIVILAMGGIALGKAVSSSGLLSTIAKALQKKIENDGVFAILCIFGILMLVVGTFVSH
VSAIIIPLVQEVGDKLGNPKAAPILVFGCALLSSCGMGLASSGFPNVTASIKVDRKGDR
YLSVMTFLTRGVFASILAFLCVITLGYGIMASVVKGNATSA

YJR049C, 2093 bp, CDS: 501-2093 (SEQ ID NO 169)

ACTGCCATCTCTTCCATTCTTTGAAAAGATTATTAAGTTCGTCGTTAAGTTCCGCAATCT
GCATTTTCATTTAAAGACGGATCATATATTCTTGTGCTTTTGTGTTTATCTCTTTACTTA
CTPTTCGCTTCCATTTCGTTGGCCTCTTTTATGGATTTTACCTTAGACACGTTCCCTGGGCC
TCTGGTAACGTGAATAATCCTTGTATCCACCTGCCGACTCTGCTTGCTGCTCTTGAAATC
GTACCAGAACTGAGTTGGCCTTATCTACATTTCTACTCATTTTGAATGCACAGGTATCTG
ATTACTGATGTGGTGCGCCCTTGCATATAACGGTGTGTCACTTTTATTTGCTCTTTTCATG
CATCCTGAAATTAATTTACCCGCACTACGCAAAGAGAACGGAGAAAAAGGTATAATAGGGC
AAATGATCATTTGACATCGTGATCGTAAGCCAAAAAATAACAATAGGCTCCCTAAATAA
GTAGAGTAAAGCTCTTGAGATGAAGGAGAAATGACATGAATAATGGCGTAGAATAATGGG
TAAATGAGGAAGATGGTTCGAAATGATCATCATAACAACAATAAATACTTGATGAAGAAG
CCATGATGAACAATGAGCAAATTGATAGAACTCAGGATATCGACAACGCCAAAGAAATGT
TGAGGAAAAATATCAAGTGAAAGCAGCTCGCGCAGAAAGCTCCCTGTTGAATAAAGATT
CATCTCTGTAACGGCAATGCAAACAGTGGCGGTGGTACGAGCATTAACGGAACAAGAGGAA
GTTCTAAGAGTAGTAATACACACTTTTCAGTATGCCCTCCACGGCGTATGGTGTAAAGAA
TGAGTAAAGATATATCTAATACCAAAGTGGAACTGGATGTGGAAAATTTGATGATTGTTA
CGAAACTCAACGATGTCTCACTGTATTTCTTAACAAGAGAGTTGGTAGAATGGGTTTGG
TACATTTTCCACGTGTGACTGTTTATGTGGATTCCGAATTGAAAAACAGCAAAAAATTTG
CCGCTGGCGAGTTATGTGAAGATAGTAAATGTAGAGAATCAAGGATCAAGTATTGGACAA
AGGATTTTCATCAGGGAACATGATGTTTTCTTCGATTTGGTAGTGACTTTGGGTGGCGACG
GTACTGTTCTTTTGTAAAGTTCCATTTTTCAGAGACATGTACCACCCGTTATGTCGTTT
CATTAGGGTCTCTAGGATTTTAAACAAATTTTAAAGTTTGAACATTTTCAGGGAGGATTTAC
CTCGGATTATGAATCATAAATCAAGACAAATTTACGGTTGAGGTTGGAGTGCACAATTT
ATCGTAGACACCGCCCTGAAGTAGACCCAAACACGGGGAAGAAAATATGTGTGGTGGAAA
AACTAAGCACACACCACATTTTGAACGAAGTGACCATCGATCGTGGTCCAAGTCTTTTC
TATCCATGTTAGAATTGTATGGTGACGGCTCATTAATGACCGTTGCGCAGGCGGACGGAC
TGATTGCTGCTACTCCGACTGGGTCCACGGCTTATCTTTGAGTGCAGGTGGGTGATTGG
TATGCCCAACCGTCAATGCAATCGCTTTAACACCCATTTGTCCACATGCATGTAGTTTCA
GACCCATCATCTTACCAGAAAGTATAAATTTAAAAGTGAAGTCTCGATGAAGTCAAGG

CTCCAGCATGGGCGGCTTTTGATGGGAAAGATAGAATTGAATTGCAAAAAGGTGATTTTA
TAACCATATGCGCCAGCCCATATGCTTTTCCAACCGTGGAAGCCTCGCCCGATGAGTTTA
TTAACAGTATCAGTCGACAACCTAACTGGAATGTGAGGGAACAACAAAAGTCCTTTACGC
ATATTTTGTCCCAAAAGAACCAAGAAAAATATGCACATGAGGCGAACAAGTCAGAAATC
AAGCAGAACCTTTAGAGGTAATAAGAGATAAAATACTCTCTGGAAGCAGACGCTACTAAGG
AAAACAACAACGGAAGCGATGATGAGAGCGACGATGAGAGTGTAACCTGCGAAGCTTGCA
AATTAAAGCCTTCGAGCGTCCCAAAACCTTCTCAAGCAAGGTTTTTCAGTATAA

YJR049C, 530 aa (SEQ ID NO 170)

MKENDMNNGVNDKWNNEEDGRNDHNNNNNNLMKKAMMNEQIDRTQDIDNAKEMLRKISSE
SSSRSSLLNKDSSLVNGNANSGGGTSINGTRGSSKSSNTHFQYASTAYGVRMLSKDISN
TKVELDVENLMIVTKLNDVSLYFLTRVELVWLVHFPRTVYVDSSELKNSKKFAAGELCE
DSKRESRIKYWTKDFIREHVDVFFDLVVTLLGGDGTFLVSSIFQRHVPPVMSFSLGSLGF
LTNFKFEHFREDLPRIMNHKIKTNLRRLLECTIYRRHRPEVDPNTGKKICVVEKLSTHHI
LNEVTIDRGSPSFLSMLLEYGDGSLMTVAQADGLIAATPTGSTAYSLSAGGSLVCPTVNA
IALTPICPHALSFRPIILPESINLKVKVSMKSRAPAWAAFDDGKDRIELQKGFITICASP
YAFPTVEASPDDEFINSISRQLNWNVREQQSFTHILSQKNQEKYAHEANKVRNQAEPLEV
IRDKYSLEADATKENNNGSDDESDESVCNCEACKLKPSSVPKPSQARFSV

YKR094C, 1255 bp, exon1: 501-508, intron1: 509-876, exon2:
877-1255 (SEQ ID NO 171)

AGGTTGTGTTCTTCAATGATGGGCAATGCAATTTGGCGTTAAGCGCCTGAGCAATAAGGT
AACAGCGAAATTTATGACATATTATTTTGAACCTTTTACAACTAGTAGATTTAGTGATT
TATTACCTATTGGCATTCTTTGTGTTCTATATGTGGATGAGGATAGCCGCCTTTCTTCT
CATCGGAGGCCATATCATCTTTGACAATCCTTTTTAAATACTATTTCCATCCGTGCCTC
TAATAGATTTGTGTAGTTGTCTGGGTGCAATCTTTCCATTTTGTGTAACCTTTTTTTTT
TTTTTCATGTTTTTCAGATTCTGAAGTACCGCAATAGGATATGGCGGATAATCCGCCATAT
GATCCGCCTCATACTAGCCATTACCCATCTATCCCAGGCATTATGGGTATGCAACTCATA
ATCTCAAATACACAAATAAGAGCAACCTTATATATCACTTTTTCCCGTTTCAGCAAGAGGT
AAAGCCACCAAAGGTTCAAATGCAATGTATGTTACGGCGAATACAGAATACTATGTTC
GAAATAATATGAGGATTATACGATAGCAAAAAAGCCATAAACGAAAGACATAAATGGAAA
ATGATTGACAAGCTCACAATTTATTAACAAGTAGCAATTGAGAAAACTATTACTCGCG
GCAAGCTTCTGAGTTTACATTAATCTGTAGAGCAAAATGAAAATGTCGCATATGTGCTG
AAGGTTTGTGTTTCCATCTTATTTTGCATAACATAGTTATATTTACTTGGTCGCATAA
AAATATTTTTTACTAACGTGAAGTTTCTTTCTTTATGATGTACGCACGCACGTCTGTGC
TTACTCCATAAATGAACCTATTCCAATTTGTACAGCTTCGTTAAGACTTTGACTGGTAA
GACCATCACTTTGGAAGTTGAATCTTCTGACACCATGACAATGTCAAGTCCAAGATCCA
AGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGA
AGACGGTAGAAGCTCTATCTGACTACAACATCCAAAAGGAATCCACTTTACATTTGGTCTT
GAGATTAAGAGGTGGTATCATTGAACCATCTTTGAAAGCCTTGGCTTCCAAATACAAGT
TGACAAATCTGTTTGTGCTGTAATGTTACGCCAGATTACCACCAAGAGCTACCAACTGTAG
AAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTGAAATAA

YKR094C, 128 aa (SEQ ID NO 172)

MQIFVKLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQRLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGGIIEPSLKALASKYNCDSVCRKCYARLP PRATNCRKRKCGHTNQ
LRPKKKLK

YLR040C, 1175 bp, CDS: 501-1175 (SEQ ID NO 173)

AGCTCTCAAACAACTAATACTATAAGTTCAAGTACAAGCACAGGAGGTGTAGGTTTCAGTC
AAGCCATGTCTTTACTTCGTTTTAATGTTAGAAACAATCGCTTATTTGTTTTCTTAAACA
AATATATTAGGTTCAAGGTCTTCGAGGTGTAAGAAAAACCGTGGTCTCCATATCTTAA
GTATGATAAATAAAAAAACTTAATAAATTAATTAATGCTTCAAACCTTTTCTTTTTT
TAGTTTTTAATATTTCAAACGTTATCTTCATTGAACGCCCAAATAGGGAAAAATCCTGGC
AAATTTTTTATTGCTGTCTATCCAAGGCTATGCTAGAAAATTCAGAGCTTGGATGATTTA
AAAAGACACTCTCAATCGAGAAAGTTTATCTTTGTTATTCTGCTTTACCTGATCATATT
CCGGCGTATTGTTTCTAATCAAGTGATTTGATATCCAGTTACGAACCATTTACAACATT
CCTGAAAATATTGCGTATCAATGATATTGCTCCTTCTTTCTCCCTCATTAATAATATTC
TCCTGGTAAGCTTTCTAATCAGCCACAGTTTGTGCTGCCAAAACCTTTAACGTCTAGTTCCA
ATGACGATACACTTGCCAGGTCCGCAGCTGCAGATGCAGACATGGCATTCTTCATGGAGT

TTTTAAACGATTTTCGACACCGCTTTTCCACAGTATACCTCATACATGATGCAAAACCATT
TAACCTTACCTCAACCTGTTGCTGACTACTACTATCACATGGTTGATTTGGCCTCAACAG
CAGATTTACAATCTGATATTGCTCAGAGTTTTCGGTTCACTCAATTCCAAACATTCATTA
CGGCTTTTCCATGGTATACCTCTTTGCTAAACAAAGCCTCCGCCACCACCATATACCTTC
CCCAACACTTCATAACAGGTGAGACAGAAGCTACCATGACTAACTCATCTTATGCCAGCC
AAAAAACTCCGTTTCCAATTCTGTTCCCTTTCTCGACAGCGAACGCAGGCCAGTCCATGA
TTTCCATGGCTAATGAAGAAAACAGTACAACAGCACTTATATCCGCATCAAACTCTTCTT
CAACATCCAGAACTAGTCAATCACAGAATGGTGCCCATGCCAAAAGCTTATATTTCCCA
TGGCGTTGTTCCGAATCTTTGCAGTTGCCCTTTAA

YLR040C, 224 aa (SEQ ID NO 174)
MIFAPSFSLIKNILLVSFLISHSFAAKTLTSSSNDLARSAAAADADMAFFMEFLNDFDT
AFFQYTSYMMQNHLTLQPVDYHHMVDLASTADLQSDIAQSFPFTQFQTFITAFPWYT
SLLNKASATTIYLPQHFITGETEATMTNSSYASQKNSVNSVPFSTANAGQSMISMANEE
NSTTALISASNSSSTSRTSQSQNGAHAKSLYFPMALFGIFAVAL

YLR048W, 1618 bp, exon1: 501-590, intron1: 591-949, exon2:
950-1618 (SEQ ID NO 175)

GCACCTTTTCTTTTCAATAACAAAAAGAGCTTGGGCATTACGTTTTCAACACTTTT
AATATTTCCCTTTTACATCCGTACATATAAAATGTAAACCCATGCATTCATGACAATTT
TACCTATTTCTTAAAGGCCCTTTGTCACTTCTTTATGGGAATGGCGCTACTTTAATTTTCC
GCCTACTTTGAAAAATTTACCAAGGCCGAAATTGAGTGCCTAGGCGGAAGTTCCAGGGCA
CGGTACCCGAACCTTTGTGCTGTTTGAACGAGGGTCCCGCTGGAGGTTGACGGACGCGG
GAGGAGCTGGAAAGATGGAATGGAAGGACTGCAACACTCAGTAAGAAGGTTCTGTTAGG
GAACATCACCTTCTCTAGTTCTGTAAAAATAATATGATCAAGTTTGAATCCTCGTATTG
AAAAATCGCGAGTTATTAAAGTGTGTAATTTAGAATACCGAAATAGCACAAAGAAGAGATAA
GATAAGATACTGATAGGATAATGTCTTTACCAGCTACTTTTGATTTGACTCCAGAGGATG
CCCAACTTTTGTGGCCGCTAACACCCATTTAGGTGCTAGAAACGTTCAAGTATGTACAC
ATATCCCATACGATTATGTTCTATAGATGATAATAGGTCTCGAAAAGAATATGTCCCCGA
TTTAATCATATTTGGAGGTCAGAGGACCAAAGGTAATTTAGAGGAATTTTGAACACGCC
GGGTTTAGAAGAGTTAGAATTTCACTTCTTAGTGAGGGTAAGGAGAAGAACTCAATAAG
AATATACATCCTCGACTGTGTCAAAGATTATGAACTCCGATGAAACAGTAAACGTCAAA
AAATTCACGGGATATAATTCGGTACTTTATTGGATATGGAAGAAAACATTATATATGCA
CAAATGAACGCTCTTACTAACATAATTTATCTTTCTCTCTTTTATAGGTCCACCAAGA
ACCATACGTTTTCAATGCTAGACCAGATGGTGTTCAGGTTATCAATGTTGGTAAGACCTG
GGAAAAGTTGGTTTTGGCTGCTAGAATTATTGCTGCCATTCCAAACCCAGAAGATGTTGT
TGCCATCTCTTCCAGAACCTACGGTCAAAGAGCTGTCTTGAAATTTGCTGCTCACACTGG
TGCTACTCCAATCGCCGGTAGATTCACTCCAGGTTCTTTCACTAATTACATCACCCGTTT
TTTCAAGGAACCAAGATTGGTTATTGTTACCGACCCAAGATTAGACGCTCAGGCCATTAA
GGAAGCTTCTTACGTTAACATTCCAGTCAATTGCTTTGACTGATTGGACTCCCCATCTGA
ATTTGTTGATGTCGCCATCCCATGTAACAACAGAGGTAAGCACTCCATCGGTTAATCTG
GTACTTGTGGCTAGAGAAGTTTTGAGACTAAGAGGTGCTTTGGTTCGACAGAACTCAACC
ATGGTCCATCATGCCAGATTTGTACTTCTACAGAAACCCAGAAGAAGTTGAGCAAGTTGC
TGAAGAAGCTGCTGCCGCTGAAGAAGGTGAAGAAGAAGAAGTTAAGGAAGAAGTCACTGA
AGGTCAAGCTGAAGCTACTGAATGGGCTGAAGAAAATGCAGACAACGTTGAATGGTAA

YLR048W, 252 aa (SEQ ID NO 176)
MSLPATFDLTPEDAQLLLAANTHLGARNVQVHQEPYVFNARPDGVHVINVGKTWEKLVLA
ARIIAAIPNPEDVVAISSRTYGQRAVLKFAAHTGATPIAGRFTPGSFTNYITRSFKEPRL
VIVTDPRLDAQAIKEASYVNIPVIALTDLDSPSEFVDVAIPCNNRGKHSIGLIWYLLARE
VLRLRGALVDRTPWFSIMPDLYFYRNPEEVEQVAEEAAAAEEGEEEEVEKEEVTGQAEAT
EWAEENADNVEW

YLR088W, 2345 bp, CDS: 501-2345 (SEQ ID NO 177)
CTTCCCATGTAGAATATCATTGTCAAACATACTACTACCGTGAGAATCCAATCTACTAAA
AAGACCCAGCTAAAGTCCTTTTGGTGTGTCAATGGAACACCACGTAATTGTGAAATAGCT
TCCATGCTTGCTAACTTATTACCGTCAATAGAAGACTTGAGTCAGGTGGCTTTAATGAGT
ACTATTCTTTTTTTTTTTTCCAAAGAGCACTATGTTGATAATACCGCAGTAATTTTTTTTG
AGTATCTGTAGCCTAGAAAGGTTGAAGCTTATAAAACCGTGCCAACAGCTTTATAGTGG

GGAGTTTGGCTTCCCTCTATTTGTATATTGATCGCCATCCCTACGAAGTTATTGGGAACG
CATCGTGAACCTCTCACTTTAATGCCAGCGGTAGAAAAAAGTCATAAACAATACACGC
CGGCTACACTTAGAAAGAAATGACATTTGCTGTCTTATAAAAGGACTTGACAGACCAAAG
ACGCGTATAATACACCAAGAATGGCCTTATTGGAGAAGTTGCATCGAAGGATTGTTGATA
TGGGGCTTGTCCCGGTATAATCGCCTTATTACCAGTTATTTCCATGCTATGCGCTCTAT
TTGGGTTTATTTCTATAGCTATTCTGCCTATGGATGGACAGTACAGAAGAACATACATTT
CTGAGAATGCATTGATGCCTTCACAAGCGTATAGTTACTTTAGAGAATCTGAATGGAACA
TTTTGAGGGGCTATCGATCTCAAATTAAAGAAATGGTAAACATGACTTCTATGGAAAGAA
ACAATTGATGGGTTCTTGGTTACAAGAATTTGGTACTAAGACTGCTATTTACGAAAATG
AACAAATATGGAGAAACATTGTACGGTGTAAATGCACGCTCCTAGGGGTGATGGAACAGAAG
CGATGGTGCCTTGGCGTTCCATGGTTTAATTCAGATGATGAATTCAATATTGGCGGCGCAG
CTTTGGGTGTATCTTTAGCAAGATTTTTCTCACGTTGGCCAGTATGGTCCAAGAATATAA
TTGTTGTCTTCAGCGAAAATCCTCGTGCAGCATTAAAGATCATGGGTTGAGGCATACCATA
CTTCCTTAGATTTGACTGGTGGTTCCATTGAAGCTGCTGTTGTGTTGGATTATTTCGAGTA
CGGAAGATTTCTTCGAGTATGTAGAAATCTCATACGACGGTCTGAATGGTGAGCTGCCCA
ATTTGGATCTTGTCAACATCGCTATATCCATTACGGAACATGAAGGTATGAAAGTTTCTT
TGCACGGTCTACCCAGTGTACAGTTAACTAATAATAATTTCTGGTCAAGATTAAAAATAT
TATGCCCTGGGAATAAGGGATTGGGCGTTGTCCGGTGTAAAAAGCCCCATGGTAACGAGG
CATTTAGCGGCTGGAGGATTCAATCTGTAACATTGAAAGCACATGGAAACAGTGGTCATG
ATATTACTACATTTGGACGTATACCCGAAGCAATGTTTCGCTCTATTAATAACCTTTTGG
AAAAATTTACCAATCGTTCCTTTTATTGTTATTAGCACCCAGTCAAGTTCGTATCCA
TTAGTAGTTATTTGCCAAGCGCTGTGGCTTTATCTATAGCATTCCGCCATAAGTTCATTAA
ATGCATTTATAAACAATGCTTATGCAAAATATATCCTTATTTTCCGAGTATAATTTGGTAG
CGTTGTGGTTTGGTTTCGTGTCAATTGGTGATATCAATTTGTTGTTTCAACAAGCGTTTCTTC
TAATACCTTCATCGGGATTATTGATGACAATTAGCATGGCATCTTGTTTTTTACCTTTGA
TACTTTCCAGAAAAATTCACATCTCAGAACCACTATCATACAGGTTGAAAAATGTTGCTT
TTTTATATTTCAAGTTTGGTTTCAACATCTTTGCTAATGATAAACTTTGCAATGGCTTTAC
TGATCGGCACATTGGCATTTCCTATGACATTTGTGAAGACCATTGTTGAAAGTTCTAGCG
AACATGAGGTGACAACTCAATCCTCTAACCCAAATAAAAACTGAGCCGAAAGATGAGATAG
AGCTCGTCGAGAATCACATGGATACAACGCCAGCAACCCCCCAACAACAGAAACAAAAAC
TAAAAAATTTAGTACTATTAATTTTGACAAATCCATTTATTTCAATAACCTTTATTCGGAC
TATTTTTTGTATGATGAATTTTCATGGATTGATATAATAAACAACCTGGTTTCAGCATGGT
TGGATTGAAATGTTGGAGTTGGTTTGTACTTTGTATAGGTTGGCTTCCATGTTGGCTAT
TGATATTAGCGTCATCGTTTGAATCTAAATCTGTCTAGTAAGGTTCGAAAGAAAAGCAAA
GTTAG

YLR088W, 614 aa (SEQ ID NO 178)

MALLEKLHRRIVDMGLVPRIIALLPVISMLCALFGFISIAILLPMDGQYRRTYISENALMP
SQAYSFYRESEWNILRGYRSQIKEMVNMTSMERNNLMGSQLQEFGKTAIYENEQYGETL
YGVMHAPRGDTEAMVLAVPWFNSDDEFNIGGAALGVSLARFFSRWPVWSKNIIIVFSEN
PRAALRSWVEAYHTSLDLTGGSIEAAVLDYSSTEDFEYVEISYDGLNGLPNLIDLUNI
AISITEHEGMKVS LHGLPSDQLTNNFWSRLKILCLGIRDWALSGVKKPHGNEAFSGWRI
QSVTLKAHGNSGHDITTFGRIPeamFRSINNLEKFHQSF FFYLLAPRQFVSISSYLPS
AVALSIAFAISSLNAFINNAYANISLFSEYNLVALLVWFVSLVISFVVSQAFLLIPSSGL
LMTISMASCFLPLILSRKIHISEPLSYRLKNVAFLYFSLVSTSLLMINFAMALLIGTLAF
PMTFVKTIIVESSEHEVTTQSSNPIKTEPKDEIELVENHMDTTPATPQQQKQKLNVLVLL
ILTNPFIISITLFGLFDFDEFHGFDIINKLVS AWL DLKWSWFLCIGWLPCWLLILASSF
ESKSVVVRSEKQs

YLR159W, 845 bp, CDS: 501-845 (SEQ ID NO 179)

TCCGTCCCAAAGATAGCTTGATCATCCTAAGCGGGTCGCATTTTACTATCCCCAGTTCGG
AAGAATAACAAGGCTCAATGCATATGCTGTTTATCGTGCTCAACAAGGCGGTATGACGTTT
TAGCAATTGTAATATATATAAAGATCTTTAGTCACTATGAGTGGTTGATTGCCCCATA
GAGAGCTATAAGCCGACGTGAAAGCTGCTGGTTCAGCTTGGCTCATGTCGTCACCAGTC
ACTAGTCACTTGGTCGCATTTCATTGCTACTCATCTGCGAGTGAGCATATTTGAGATCTGA
CTTGCCAAGGGATTAGAAATCACGTAAGACTCTTGATCCTTAGAAGATATTTCTGACAAAG
AACCACCTAAGCCATGCAAGTTTTTTTTTTCATTTGGTGGCGAAACAAAGGTGATGAAAG
TTTCTTCTGTACAAACGCCAAGCCCGATAGGTGAGACAAATCTTGAAGTAATGGACCTC
TGAGTAAGCATATCAGTCAATGAAGTTCCAATATGCGTTGGCCAAGGAACAGCTAGGCCA
GCAACTCGCGCAGTGGCGTCAAAAACTAATAAGTAAACACCACTGGCTTCCGGAATACT

ATTTCTCTGATCTCTCATTCTTCTGTTGTACAGCAGTGGGACAGTAGAGCCATTGAAAAAA
CTACAATCATATCTTTGTATGCGGCCGCAAACCAAGAGATTTATCCTTTGAGACATTGTG
AGACCTCCGTTTCGCAACCGTGCTCTCTGTTTTTCATCACTATATGCACGCTCTTTCCAAA
GCTCCTGCACCTTGCACGTGGCGGAGCCATCGCCCGGCTTCCATATGTACGGCTGCCACA
CCTAA

YLR159W, 114 aa (SEQ ID NO 180)

MKFQYALAKEQLGSNSRSGVKKLISKHHWLPEYFSDLSFSVQWDSRAIEKTTIISCM
RPNQEIYPLRHCETLRSQPCSLFSSLYARSFQSSCTLHVAEPSPGFHMYGCHT

YLR167W, 959 bp, CDS: 501-959 (SEQ ID NO 181)

ATCAAAAAGAGTGTTCAGTAAGTAAAAACATTTGAGCCTCCCCATTTGTTGAAAGGAGA
GAAATTAAACTTGGTTGGGGTTAATTATTTGATGGGTATATTAATTTGCAACCGCAAGGT
ATCGATAATAAATATCTACAAAACCTTTATCAATAGTGGTGAAGTCTTTAGTGCGATCT
ACCTGGGGTTAATGAACGAGAAGTTCTTGAGATATCTTTCCTGTTTACCTCCGTGCATCC
TGTAAGGAATTGGGTTTATCATTTATCATTTATTTTAGTACAACTTTTTTTTTTTGGCCC
GGCGCAGCTTTTCAAGCGGTGGGAACCTCATCAAAATGAAAACTAGATACTTTTAGACT
TATTAAATGGTTTAAATATTTTGAGATGTTTCGTTATATCAGAACTTCTTACTTCTATC
TTTTATTCCAATACAAAGAAGTCACAAGATTACTTGGTAAGAAAGAAGCAGTTAATTTTT
AATTTTGCCGACAAGCCAAGATGCAATTTTCGTCAGACTTTAACCGGTAAGACTATTA
CCCTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCCAAGATCCAAGACAAGG
AAGGTATTCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGAAGATGGTA
GACTTTGTCCGACTACAACATCCAAAAGGAATCTACTCTACACTTGGTCTTGAGATTGA
GAGGTGGTGGTAAGAAGAGAAAGAAGAAGGTCTACACCACCCCAAAGAAGATCAAGCACA
AGCACAAGAAGGTCAAGTTGGCTGTCTTGTCTACTACAAGGTCGATGCTGAAGGTAAGG
TTACCAAATTGAGAAGAGAATGTAGCAACCCAACCTTGTGGTGTGTTTCTTGGCTA
ACCACAAGGACAGATTGTACTGTGGTAAGTGTCAATTCGCTCTACAAGGTTAACGCTTAA

YLR167W, 152 aa (SEQ ID NO 182)

MQIFVKTLTGKTTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGGGKKRKKKVYTPPKIKHKHKVKLAVLSYKVD AEGKVTKLRRE
CSNPTCGAGVFLANHKDRLYCGKCHSVYKVNA

YLR232W, 848 bp, CDS: 501-848 (SEQ ID NO 183)

AGCCACCAATTCCACGAGGCCCGGCATTCAAGTACTTGTAAGAACACCAACAGGCAAAGT
CAACACCCCAATCATGAAGTTGCAATGGGACGTTCCCTACAGCGTGTGCTAAATCCCATC
CAACCAATATGTGCGGGAATTGGTGGGCAATGAGGTGATTGCGCCAATATCGAAATATT
GCCCCGTGTAATACTGAACACCTGACAAACAGACCAGCGCCAATTCATCTTGATTTACCT
CTATGGTATCCAGGATATCTTGAGTCTGATATAAGTCTCTCCCTCGCGTGGCTCGATCT
GAATAAAAACATTCTCAGGTTCCGAAATTCATGAATTTGCACTGGTTGTAGAAAGCAT
AATAGTCTGATGGAAAGGAGCCCTTTTCAAAAAGGATCTTGAATCTTTTCTCAGTAGGTT
TATAAAACGTAATTAACAATGAATTCAAATTTGCAGTGAGACTATTCAATTACTGCAACTT
CATTTTCTTGAGCACCCACGATGGGGGCTAGTAGTGGAAGAATAGGTAAGTCAATGCTGA
CCCAAGGCACCTTTCTCTGGCTTCTTCAGGATGTTTGAAATGCGATTCCACAGCACAAT
CGCTCCACGCATCTAGCTCAGCATTAATTGAATTCCTAGTTGACTTCGGCATCAAACCTA
AAGAATTCCCGCATAAGTACGTCACAGGCTTATCGTCGGACGATAGTCCCATGGATTTAA
ATGTAGGGATGTTGAATTCATCCCTCAGAGATTCCGGATATTCTCCGTCTAATTCCAAAG
CTTTCTCCATAATTACCAGTTTGTCTTTTTCACAGAATATTTAGGCTTAATATGTA
CGTATTGA

YLR232W, 115 aa (SEQ ID NO 184)

MGASSGRIGKSMLTQGTFFLASSGCLKCDSTAQSLHASSSALIEFLVDFGIKPKEFPHKY
VTGLSSDDSPMDLNVGMLNSSLRDSGYSPSNSKAFSIITSLFLFSTEYLGICTY

YLR233C, 2600 bp, CDS: 501-2600 (SEQ ID NO 185)

GCGCATTTTCCCCACCCATGCGAATCATGGCTGAAATCAATGCCTGTTAGGTGCCCTGCA
ACACTAGTCATGGTAACTTCGCAGTTAGCCCCATTTCTGGCAAACGGGAACCCACTAAAC
ATGAAATCATAGTTCTTTACATACATGTAGCCGGAATCCCTTGAAGTTGATCTGCCTCCT
CCTAGGATCTGTGAACTGCCTTCGCTATAGAATTTTCTCTGCGACACATAGCACTTTC
ATTATTGTCTATAATACACCTTTACGTAGCTGAAGCGAGCGCACAGACGAAGGTGCTTTC

AAAAGCGATGCECTCTTTATTGACAGTTACTAATTCGCCAAACTGCTTTTTTTTATCAAT
GTGATTTTCGCGTTTCACGCCATTATCCAATGTCAAAAAGGATAATGGAAATGTTAACATG
CCTGTATGATCCGACCGTTTTCAGCAAACCTTATCAGGGGAAAAAGTATATTCCATTAAAT
GACACATGCCACCATAGATAATGGATAATGAAGAAGTTAACGAAGAATGTATGAGATTAT
TTTTCAAGAACGCTCGTGCGCATCTGGATAAACATCTAACATCAAGGTTGACATCGCATG
AAAATGCATATATCAGTTTCAGATGCTTCCTGGATGGAATACATCGCAAATCTACTAGGT
TTCTCGAAGAGCTACTTTTGAAACAAGAAAAATATGTACCATAATAACAATTACGAACGCA
TAAATGATTCCGTGATACCATTTGGTCTGAAACTTTTATGGCTTCAAATTCACGAACCTA
CACTCCAATGGTTTGAGCACTGGTTCATGATATCATGCGACTAAGTAACAGAAGAAAGT
TCAGAGTTTTTAGAATTTTTCAAAAAAATGATTCAATTTTTCAAATTAACACACAGGT
ATTATGTGACATCATCGAACACCTATGCGCAAAGTACGATATGAATTCGGTTATTTCAA
ATGCTCTCTTCGCGAAGTTGAATTTAATGCAATACACAGATGGACTTTCAACTCATGAGA
AAATTATCTTAAACACGAGTAATCCACTGACGTTTTCCATTGTAATCTCACTACAAAGAT
GCGTGATTAATCTAGGTTCCACACATTTTATAAAACACTACTAAACAAGCCGTCTAACA
AACCCAAGAGTGTGGAAGGTTTGAAGAAGTCTATTAGGTACTTGAATATTGCCTCACTCT
ATCTCCCAGCCGTTGGAGATACTTATTTTCAACGAGCGAAAATTTACTTGATCACTGGGA
AATTCTCACTGTATTTCTTTGAATTAGTAAGAGGAGCATTGGTAAGGATTCCGTCTAAAT
GTGCGTTAAACAATTTGAAAGATTTTCATTTTGACTCCTGATTTTCCGGAAGAAGACGTC
TGATGAAAAAATTGGCAATTTCTGTGTCAAAAGATCTCAAAGGTGAGAAATCATTCTTTG
AAGGTCAAATTTGTTTGAATTTCTATCGATAGTAGAACACACTTTGGTTCCACAGTCAT
GGAACGCATCACGTGCTTCTAATTGTTGGTTATTGAAAGAGCATTACAAATGGCTGCAT
TAAAGTATCATTACAGGTAATATTAATGTTATACTTGAAAACCTGGCTGCCACAATGGGAA
GTTTCGATCTTATGTTTACAACCTCGAAAAAGTAAGGAACAAAAGAACAACCTCAAATATG
CAGATTTGAGTGAGCGCCAGGTTTTTTTTTTAGACTTGAGCTTTGATTTTATTGCTAATA
TCATAGACGTCGTCATCAAACCTCCTGGCAAAAAAATGGAAGACTTTGATATCTAG
CCATTATTCGTTTGCTTATGTGCTGGATTAAGTCATATAGATCTATTTTGCAGTACACTC
ACAGACACAGGAAGTTTTGCACTTCATTTCGCTTGTGCTGAACGACTTGATAAATAGTC
CACTGAATTGTTTCAGGAAATATATATAGCCACAGGCCGAAAAGAAGCTATCTTTTTAGAG
AAGATATTATTTTCAGGGAATTTCTTGCATTAACTTTGCACTAACAGATTTAATGACG
ATTATGTGTATGATTCTCCCGACATGATTAATAATATAAATTGGATGCCCTACATTGACTA
AAGTGCTTTCTCCAAAAGAAGAATGTGTTCTGCGAATTAGATCAATAATATTTTCTGGCA
TGAAATTTTTAGAGAAAAATGACACCGCGTCATATGGAATGCCAGCAAATATAAGTTTG
ATTTAATAAGCCCAAATATTAAATAAAACGCCAAATAGCATTATCGGAAATTTCTCTCCA
AAATAAATGTAAAAACACAACAGGAAAGAGTAGTCTCTTCGAGAAAAGTTGAGGCCAAAA
GAGATGAAACAACAGCGCAAAAGAGCCGGGAAAATAGCTGTGACAGAAGTGGAAAAACAAT
TTGCAAATGTCCGGAGAACAAAAAATTTGCTCCGCTCCAGAAAAAGATGGCGTTTCTT
CTGAGTTGGTAAAACATGCTGCTTACGAGGGAGAAAAACTATCACTGGCCCACTATCCT
CTGATTTTCTCTCATATCCAGACGAAGCAATTGATGCTGATGAGGACATCACCGTCCAAG
TGCCAGATACTCCTACTTGA

YLR233C, 699 aa (SEQ ID NO 186)

MDNEEVNEECMRLFFKNARALDKHLTSRLTCDENAYITFRCLDGIHRKSTRFLEELL
KQENMYHNNNYERINDSVIPLVLKLLWLQIHEPTLQWFEHWFHDIMRLSNRRKFRVFRIF
QKKMIQFFKITHRYYYDIIIEHLCAKYDMNSVISNALFAKLNLMQYTDGLSTHEKIIILNTS
NPLTFISIVISLQRCVINLGSTHFYKTLNKPNSKPKSVEGFESIRYLNIAISLYLPAVGD
TYFQRAKIYILITGKFSLYFFELVRGALVRIPSKCALNNLKDFILTPDFPERRRLMKKLAI
LVSKDLKGEKSFFEGQIVLQFLSIVEHTLVPSQSWNASRASNCWLLKEHLQMAALKYHSGN
INVILENLAATMGSFDMFTTRKSKEQKNKLYADLSERQVFFLDLSFDFIANIIDVVIK
PSWQKNMEDFRYLAIIRLLMCWIKSYRSILOQYTHRRHKFCTSFALLNNDLINSPLNCSGN
IYSHRPKRSYLFREDIIFREFSCINFALTDNFDDYVYDSPDMINNIIGCPTLTKVLSPE
ECVLRIRSIIFSGMKFLEKNDTGVINWASKYKFDLISPNIKIKRQIALSEISSKINVKTQ
QERVVSSRKVEAKRDEQQRKRAGKIAVTELEKQFANVRRTKKLSPLPEKDGVSSELVKHA
ASRGRKTIITGPLSSDFLSYPDEAIDADEDITVQVPDPT

YLR234W, 2471 bp, CDS: 501-2471 (SEQ ID NO 187)

AATGGTATCACGGAATCATTTATGCGTTTCGTAATTGTTATTATGGTACATATTTCTTGT
TTCAAAAGTAGCTCTTCGAGAAACCTAGTAGATTGCGATGTATTCCATCCAGGAAGCAT
CTGAACGATGATATGCAATTTTCATCGCATGTCAACCTTGATGTTAGATGTTTATCCAGA
TGCGCACGAGCGTTCTTGAAAAATAATCTCATACATTCTTCGTTAACTTCTTCACTATCC
ATTATCTATGGTGGCATGTGTCATTTAATGGAATATACTTTTTCCCTGATAAGTTTGCT

AAAAACGGTCGGATCATAACAGGCATGTTAACATTTCCATTATCCTTTTTGACATTGGATA
ATGGCGTGAACCGGAAAATCACATTGATAAAAAAGCAGTTTGGCGAATTAGTAACTGT
CAATAAAGAGGGCATCGCTTTTGAAAGCACCTTCGTCTGTGCGCTCGCTTCAGCTACGTA
AAGGTGTATTATAGACAATAATGAAAGTGCTATGTGTCGCAGAGAAAAATCTATAGCGA
AGGCAGTTTCACAGATCCTAGGAGGAGGCAGATCAACTTCAAGGGATTCCGGCTACATGT
ATGTAAAGAACATATGATTTTCATGTTTGTAGTGGGTTCCTGTTTGCAGAAATGGGGCTAACT
GCGAAGTTTACCATGACTAGTGTGTCAGGGCACCTAACAGGCATTGATTTTCAGCCATGATT
CGCATGGGTGGGAAAATGCGCCATCCAAGAGTTATTTGATGCGCCACTGAACGAGATTA
TGAATAACAACCAAAAAAGATAGCAAGCAACATCAAGCGAGAAGCGAGGAATGCAGACT
ATCTGATGATATGGACAGATTGCGACCGGGAAGGAGAGTACATCGGTTGGGAGATATGGC
AGGAGGCCAAGAGAGGCAACAGGCTCATACAAAATGATCAAGTATACCGGGCAGTCTTTT
CGCATCTCGAAAGACAACACATATTAATGCAGCACGAAACCAAGTCGATTGGATATGA
AGAGTGTGCACGCTGTAGGCACGCGGATTTGAAATCGATCTTCGAGCAGGTGTTTACATTTCA
CCAGACTCTTAACAGAAACGCTACGAAATAAACTGAGAAACCAAGCCACCATGACCAAGG
ATGGTGCAAAACACCGCGGTGGTAACAAGAACGACTCACAAGTCGTATCGTATGGTACAT
GCCAGTTTCCAACGCTCGGCTTTGTAGTAGACAGGTTTGAAAGAATACGAAATTTTGTTC
CCGAAGAGTTCTGGTATATCCAATTGGTAGTCGAAAAACAAAGACAACGGCGGAACAACAA
CGTTCCAGTGGGACAGGGGCCACTTGTTCGACCGGCTGAGCGTGTAAACGTTTACGAGA
CATGCATCGAAACCGCCGGCAATGTTGCTCAAGTAGTAGACTTGAAATCAAAGCCAACAA
CGAAATACAGACCTTTACCTCTGACCACAGTGGAGCTACAAAAAACTGCGCCCGGTACC
TGCGTCTGAACGCCAAACAATCACTAGACGACGAGAAAAGCTATACCAAAAGGGGTTC
TATCGTATCCAAGAACAGAGACTGATACTTTCCACACGCAATGGACCTAAAATCCTTGG
TCGAAAAGCAAGCTCAATTGGACCAACTCGCTGCAGGCGGCAGAACCGCCTGGGCATCGT
ACGCGGCTCGCTGCTCCAACCCGAAAACACAAGTAACAATAACAAGTTTCAAGTTTCCAC
GAAGCGGCTCCCATGACGACAAAGCGCATCCACCAATCCACCCCATCGTAAGTCTGGGGC
CTGAAGCAAATGTTTCGCCAGTGGAAAGAAGAGTATACGAGTACGTGGCCAGGCATTTT
TGGCATGCTGCTCAGAGGACGCCAAGGGCCAATCGATGACCTTGTGTTGGACTGGGCGG
TTGAACGTTTCTCAGCTTCAGGTCTCGTAGTCTAGAGAGAAATTTCTCGATGTTTACC
CTTGGGCCCGATGGGAAACCACCAAGCAGTTACCGCGCTTGAAATGAATGCCCTCGTAG
ACATCGCGAAGGCCGAAATGAAGGCGGGCACTACGGCGCGCCCAAGCCGATGACTGAGA
GTGAACCTCATTTCTCATGGATACAAACGGCATTTGGCACAGACGCCACCATTGCGGAGC
ACATAGACAAGATCCAAGTACGTAATTACGTTAGGAGCGAGAAAGTAGGCAAGGAAACCT
ACTTACAACCCACGACCCTGGGTGTCTCACTAGTGCACGGCTTCGAGGCCATCGGCCTCG
AAGACTCCTTTGCAAAAGCCCTTCCAGCGCAGAGAAATGGAGCAAGACCTCAAGAAAATCT
GCGAAGGTTCATGCCTCCAAGACTGATGTTGTAAAGGACATAGTCGAGAAGTATAGGAAGT
ACTGGCACAAGCAATGCCTGCAAGAATACTCTCTTGCAAGTTTATGACCGTGTCAAGG
CATCCATGTAA

YLR234W, 656 aa (SEQ ID NO 188)

MKVLCAEKNISIAKAVSQILGGGRSTSRDSGYMVKNYDFMFSGFPPFARNGANCEVTMTS
VAGHLTGIDFSHDSHWGKCAIQELFDAPLNEIMNMNQKIASNIKREARNADYLMITWD
CDREGEYIGWEIWQEAQRNRLIQNDQVYRAVFSHLERQHILNAARNPSRLDMKSVHVG
TRIEIDLRAGVTFTRLLTETLRNKLNRQATMTFKDGAKHRGGNKNDSSQVVSYGTCQFPTLG
FVVDREFIRNFVPEEFWYIQLVVENKDNNGTTTFQWDRGHLFDRLSVLTFYETCIETAG
NVAQVVDLKSPTTKYRPLPLTVELQKNCARYLRLNAKQSLDAAEKLYQKGFISYPRTE
TDTFFPHAMDLKSLVEKQAQLDQLAAGGRTAWASYAASLLQPENTSNMNFKFPKPRSGSHDD
KAHPPIHPIVSLGPEANVSPVERRVYEVVARHFLACSEDAKGQSMTLVLDWAVERFSAS
GLVVLERNFLDVYPWARWETTKQLPRLEMNALVDIAKAEMKAGTTAPPKPMTESELILLM
DTNGIGTDATIAEHIDKIQVRNYVRSEKVGKETYLQPTTLGVSLVHGFEAIGLEDSFAKP
FQRREMEQDLKKICEGHASKTDVVKDIVEKYRKYWHKTNACKNTLLQVYDRVKASM

YLR238W, 1937 bp, CDS: 501-1937 (SEQ ID NO 189)

CTTCGTTACACTTAATATTAATAACAGCTCTTCTTAATAATAACATATACACTAGAT
ATATAATACCAATAAATTAATAAAAAAGAAAAACAAAAATAACGTAGCTTTGTTACAG
TCGTAAAAAAGAACAAATAAACCAATCTTATTGCCAGCGTCTAACTAGTCCTATTATAT
TCCAATATATTAAGGGGTAAGGACTACTATTATTCGCCCTGAATTGAAATCTTTTAGAAA
GCACCTGTTCTCTCTGTTGTTCTTTTTTCTCATCTATTATCTAATTTCTTCAACCTT
CGTTATTTGTTGTTATTCCGTAATCGTGGTGCTCAACTTTTGAAATTTCACTTGTFTTACC
ATAACGGAACATAATTAATAATTTGTTCTTGAAAGTCACAAGCACTACGTGAACACAAAA
TTAAGGCAAGAGTGACAAAGTAACCCCTACAAGGAGCCTGTCGTTGGTTATATTGGAAGC

TATAGATATAATCGAATCCAATGACTGGTCTCGGACCTGAAATAAATAAGGAGGAGCACC
CCAGTTCTCCGGGCAAGAAACAGATAACATATAATAGTATACCCAAGAATGCAAATCTAA
TTGATGGATCTACGAATTCATCGAAGAGGCCAATTGAAAAGTATGACAAGAGAATAGCCG
ACCCAACAAAAAGCTATTTTCCACATAGCATATCAAGAACACCAAGGAGAAAAATATACTT
ACATTTCTAGTCCTCACATCACTAAATGGAACCTTTTGAGAGCAAACATGTGGTGATACCAT
TTAAACCAGATGGTTTGAAATTGGGAAGGCCTGTTGCTAATAGTAATAGCAGCTCCAGTT
CATCGCTCAGGGGCGGTAAAAGAGTGGATTACACACTTTTTTCCCAAGTAAGGTCCGATA
ATGGTAATTTTCGATTCAAGAGTACTCTCCAGGAATCATGCATTGTTAAGTTGCGACCCGC
TCACGGGTAAAGTATATATACGAGACTTAAAATCCAGTAATGGTACGTTTATTAACGGTC
AAAGAATTGGCTCAAATGACGTAGAAATCAAAGTTGGCGATGTGATAGACTTGGGAACAG
ATATAGATACGAAAATTGAGCATCGAAAAATAAGTGCCACAGTTGAAGAACTATTTGTAC
AACCTTTATTAGAATCACCGATTTTTTGAAAATGAAGATAGTGATGATTGCCATACAATTA
CAGAAAAAGAGGAGGCTGCTGCCATAACAAGTCACATATATGGTGATTCCAACAACCTAG
AATTGGGAAGAAGTTATCCTGGGCTCTGATACAGAAATACTGAGTGGAATTTTTTATTAATA
ATTGTATTGGTACGAGCCCGACTTTATCTAATATCATCAAAACCCTGGCAATTGGAAATTC
CATTTTTCCAAATGCGATAATTTTAAATTACAGTCGATGGAGAATTTCTTAATTAATTATA
CGACACATCTAGAATACACGAACAACTTTTAGTGGAaaaaaATGATCAGCAACTGGTAA
AGCTGCAAAATGGATTAAGAAGGAACTGTGCGGGGAAATACGAAAAGATTATCGAACAAA
ACAGAAATCAAGTAAAACAGTTGGAAAGGGACCATATGTTTTTCAAAAAGTCATTTGAAG
TGAAGAAAAGAAGAAATAATGAAAAGCAAAAAGCATGGAAGGGAAATAGAAGACTTGA
AACTAGGTTAGAAGTGAACGATATAAGAATTCACAAATGATGAAGAAGAACAAACAGA
AAGAACAAGAACTCTCAACTGCATCTAAAAAAAAGACTACCGAACATGACACTAGAGGCG
TCCCGGGCATGAATCCTAAGGGTACTGACAAATTTAGCATCAAGAACACGCTATGTAATC
ATTTACACTATTAACATTTGGAACATTTCCATCGGGATTATAGCTATTGTCTTCAAGA
TCCTTTCCCCCACTAG

YLR238W, 478 aa (SEQ ID NO 190)

MTGPGPEINKEEHPSSPGKKQITYNSIPKNANLIDGSTNSSKRPIEKYDKRIADPTKSYF
PHSISRTPRRKTYIILVLTSLNGTFESKHVVIIPFKPDGLKLRPVANSNSSSSSSLRGGK
RVDSTFSQVRSDNGNFDNRVLSRNHALLSCDPLTGKVYIRDLKSSNGTFINGQRIGSND
VEIKVGDVIDLGTIDITKIEHRKISATVEELFVQPLLESPIFENEDSDDCHTITEKEEAA
AITSHIYGDSNNLEEVILGSDTEILSGIFINNCIGTSPTLSNIIKTLAMEIPFSKCDN
FKLQSMENFLINYTTHLEYTNKLLVEKNDQQLVKLQNLRRKLSGKYEKIIEQNRNQVKQ
LERDHMFKKSFVKKRRNNEKQKSMEREIEDLKRLEVERYKNSQMMKKNQKEQELST
ASKKKTTEHDTRGVPGMNPKGTDKFSIKNTLCNHFTLLTFTGISIGIIAIVFKILSPN

YLR241W, 2849 bp, CDS: 501-2849 (SEQ ID NO 191)

CGAACATACCTGATATCAGAATAGATCCCAATGGTGCTATATTACGTGTAAGAGAGAGAT
TTAATTTGAATATGTCCGAAGAAGATGCCACAGTGCATTTTCAGAATCTAATCAATGATA
GTGTAAATGCTTTGCTGCCTATCGTGATTGATCATTTACATAATCTGGCACAATACTGGC
GGACCTGATTGGTTGATAATTGGTGCTTCAAAATTTAAATTTTCGTCACTCTAATTATACT
TAACATATAAATGGTACCTTCAATATATCTTCTTAGTAAAAAGTAGCATGATTTTGTGTT
AATTTGCACTTTTTTTATTTAAAAATAAAAATCACAGTTAATTTTTTCATGATCTTGCAAA
GACACGCCTCCCCCTAATGTGGCATATATAACAATTGTGAATCAGAAAAACTCAACACTT
TAACATAATGGCGGGCACGAAGGCTAAACAAACAAGATTAGCATTTGAATGCCTTTTTTGG
GTACAATAGAACAGTACTGAATGACATCATATATCGAAAGGCTCAAGTCGGCAGCATCGT
ATCTTGATACAGTTCCAGATGAGCATCATGATTTTCAGAAAACCCACCGCCAAGGTTGTAA
CGACGCAACTGACTATTGCTACTTCACTAGGTATTTTTGCTTTGCTTTTCGTTCTCAATTC
TACTAAAAAAGTGGCCTAGATTATACGCAAGCAGACGATATAAAGATGACGGGAACCTTC
GCTTACCGTCTCGGAATCAGTCAAGTTTATTCGGCTGGTTAACAGTGTTGTATAAGATAC
GGGACGAACAGATTCTGGAATATGCAGGTTTAGATGCGTATGTGTTTTTGAGTTTTTTCA
AAATGTGCATCAAATTACTTTCTATTTTTTGTCTTCTCTGTGTGCGTTATATCTCCAG
TAAGATATCATTTTTACTGGAAAAATTGATGACGGCAACGATGATGATGACAGTGAAAGTT
CTTTAATACATCTGGTAAAAAGAATTGTGGAGGGAAGTGGCGATGGTGACAATCATTCAG
CTCCCGAACGTACAAATGTGTACCTCTGGATGTATGTTCTCTTACATATTTCTTCCACT
TCTACGAATTAATAATGGCAGTTGCGGAACAAAGCACGTCGTAAGTACTAGGCAAGCTT
ATCTTGGGAAGCAAAATACGATTACTGATAGAACGATAAGGCTCTCAGGCATCCCGATAG
AGCTTCGTGATTCCGAAGCCTTAAAGACCAGAATTGAACAATTAATAATCGGCACCGTTT
CATCAATCACTATTTGTGAGAGTGGGGTCTTTGAACAAGCTATTTTCATTGTGCGGAAGA
AAATACTCAAAAACCTGGAATTAATAATTTTCAAGATGTCCAAGGGAGCTCCGTACTCGAC

AACCATATTTCGGAGAACTATCATTATTGTTGGGAAACGAGCAATCAGGCGCAGTTACACATG
GAGAAAATGTTCCATCAAGCAATAATAATGACGAGGATACTATACTATATTCTCAAATTT
CTCTTTGGAGAGAGACCAAAAATGAAAATTGGATATCGTGGTATCTTTGGGAAGGAAGTAG
ATGCCATAGAGTACCTGGAGCAGCAATTAATAATTTATTGATGCTGAAAATTATTGAAGCGA
GGAACAACACTACTCCGCAACACCTACGGCATTTCGTTACGATGGATTCTGTTGCTAATG
CGCAATTCGAGCTCAGGCGGTATTAGATCCTAGAGTACATTACTTCATAACCAGATTGG
CTCCTGCACCTCACGATATCAAGTGGGATCATGTTTGTCTTTCTAGAAAAGGACCGGTAA
CAAAAGTTTATTCTACTACCGTATTTATAGGCCTTTCAAGTTTGTCTTTTAGTCATTCTCTG
TATCATACTTAGCCACATTGCTAAATTTGAAAACACTTTTCGAAATTCTGGCCAAGCGTAG
GGCAGCTACTAAAAGATCACCAGTGGGCCGCTAACATTGTAACGGGGCTATTACCAACCT
ATCTCTTCACATTGCTTAACTTTGGAAATCCCTATTTTACGAGTATTTGACTTCTTATC
AAGGATTGGTATCATACAGCGAAGAGGAAATCTCACTTGTCTCAAAAAATTTCTTTTATA
TTTTTGTCAACCTTTTCTTAGTTTTCACATTGGCAGGTACAGCATCTAATTACTGGGCGT
ACCTCAGCGATACCACCAAAATTGCTTATCAACTTGTCTACATCTGTGAAGGAGTTCTCCT
TATTCTATGTCGATTGATTATATTGCAAGGTATTGGTATGTTCCCGTTTAAGTTGTTAT
TAGTTGGTAGTTTGTATCGGCTTTCTCTAGTGAATAATCAAGGCTAAGACACCTAGGCAAC
GGAATGAACTTTACAATCCACCGATATTTAACTTTGGACTACAATTACCACAGCCAAATC
TGATTTGATTATAACGTTGATCTACAGTGTAAATGAGCAGCAAAAATTTGACTTCAGGGC
TGGCGTACTTTATTTATTTGGGTTTTACGCTCTATAAATATCAATTGATTTTGGCCACAGATC
ATTTGCCCATTTCTACAGGAAAAGTATGGCCATTAATTTTTAGAGAATCATCGTTGGAT
TGCTATTGTTTCAATTAACAATGACAGGAACACTGGCAGGATTCGAAGGAGGATGGGTTT
TGTCATCTTGCCCTTTTCCCGCTTCCAGTAGTGACATTATGTTTCTTATATGATTTGAGA
AGAACTATTTGCCGTTGTCAAATATATCGCATTGAGTTCAATTCGCGAGTACGAAAGAG
ACAATTCACGGTGAATTCGCCAATGAGGAAGAGTCGTATGCATACCTTACGCTGTGA
GTGAATTAGAGGGTCCGATGTTGGATTGA

YLR241W, 782 aa (SEQ ID NO 192)

MTSYIERLKSAASYLDTVPDEHDFRKPTAKVVTTQTLTIATSLGIFALLSFSILLKKWPR
LYASRRYKDDGNLRLPSWNQSSLFGLTVLYKIRDEQILEYAGLDAYVFLSFFKMCIKLL
SIFCFFSVCVISPVRYHFTGKIDGNDSSLIHLVKRIVEGSGDGNHSAPERTNV
YLWYVLFYFFTFIAIKMAVAETKHVVSTROAYLGKQNTITDRTIRLSGPIELRDSEA
LKTRIEQLKIGTVSSITICREWGPLNKLPHCRKILKNLELKYSECPRELRTROPYSENY
HLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPKMKIGYRGIFGKEVDAIEYLE
QQLKFIDAEIIEARKQHYSATPTAFVTMDSVANAQMAAQAVALDPRVHYFITRLAPAPHDI
KWDHVCLSRKDRLTKVYSTTVFIGLSSFLVIPVSYLATLLNLKTLKSFVPSVGQLKLDH
QWAANIVTGLLPYLEFTLLNFGIPYFYEYLTSYQGLVSYSEEEISLVSKNFFYIFVNLFL
VFTLAGTASNYWAYLSDTTKIAYQLATSVKEFSLFYVDLIILQGIGMFPFKLLLVGLIG
FPLVKIKAKTTPQRNELYNPPIFNFGQLPQPILILITLIYSVMSTKILTSGLAYFIIG
FYVYKYQLIFATDHLPHSTGKVWPLIFRRIIVGLLLFQLTMTGTLAGFEGGWVLSCLFP
LPVVTLCFLYDFEKNYLPLSKYIALSSIREYERDNSTVNSANEEESYAYPYAVSELEGPM
LD

YLR321C, 1781 bp, CDS: 501-1781 (SEQ ID NO 193)

TTCAAGTGCACCTCTTTGTAAGGAAGATTACAAGTCTCCAGTGGTCACAACTGTGGCCAT
TATTTTTGTGGATCGTGTCTTTCGCAAGATATGAAAAAGGGCACCAATGCTTTATATGC
CACAAGGAGACCCACGGCAGTGCAAAAGTAGCATCTGACTTACAGAAGATGCTAAATAAA
AGGAAAAGTTGATGGAGAATGCCATATCACCCCAAAATACACGCACCCGATGCTAATG
TACAGGAATTATAGAGCACATGACCCATAGATTATTCGAGCATTTGTTGCAATTTTCGAAAG
ACTCTTTACATAATAAAGTATGTAACTATATAGATAGAAGATGTCCCGTGTCTTTTG
TCTACTAAATGATGATCTGCTCATTTAAAGTCGCCGCGACTACTTTGACAAAAA
ACTTAGAAAATACGACAAATAGAGATTATTGAATGAAGTACATTGAAAAAGAAAGA
AAGGCACATAGCAGCACACAATGTCGCACCAAAACCAGCTTATCCACAAGCTTATATTT
CTAACTTTTCATAACAGATTGACAAACGAAGATGATGGTATCCCCATCTTTACAATGGCTC
AACAAAACAAGGCAGCATAAAAGGGCTAAAGTGGTCAACTATGCGGAATATGACAACGATC
TCTTTGATGAATTCAATATGAACGGTTCTAATTTCAACAATGCTGATACACATATAAAG
ATAATGCAGTGTCTCATGAAAATACTCCGGCACTTACAAATGGTGTACCATGGACGGTT
CCGAATACAATGTCTAGAGAACATGAATGGAGCTGATAGTATTATCTTAACAACAAAT
ACGATGCGGGTTCAAACATGGTTGTGGAATCTTTATCCGGTTTGAATAGCAATAACAACG
CCAGCAATGGTCCGAGCAACAAAGCGCAGGCACAGGATATTGGAAACGCCGTTCTACCGG
ATCTGCAAGACCAACACCACAACCCCTTCAACATATTGAGATACCTAAAATAAGAGATA

CTTTCATTAACGGAAAAGTGGTGTCTCCATATAGACTCAACACTGATCAAGAAACGAAGG
CAAACGCCAATTCTGGAGAGGCAATCATGATACCAATTACTTTGGATATAGAACATATGG
GTCATACCATAAAAAGACCAGTTTCTCTGGAACATAATGACGACTCCATATCTCCGGAGG
AATTTGCCTCTATATACTGTAAAGATCTTGATATGACTTCCGCTACCTTACAACTCAAA
TTGCGAATATAATAAAAAGAGCAGTTGAAAGACCTCGAAAATATTGCAGCCACTGAGATAA
TGTCTGACCTCCACGTGATAATCAACCTAACCTGCAACTTACAAGACAGATTTTGAAG
ATAACTTCCAGTGGAACCTGAACGACAAATCACTTACTCCAGAAAGATTTGCTACATCCA
TTGTACAGGACCTTGGCTTAACAAGAGAGTTCATCCCCTTAATATCTCAATCGCTTCATG
AACTATCTTGAAGATAAAGAAGGACTGGGTAGATGGCCACTTGATTTCAGGACCATGTCC
CAAACGATGCCGCATTTGGGTACTTATCTGGTATAAGGCTGGATATTGATGAACTGGGCT
CCAATTGGTGCCCAAGGTTGAAATATTAACAAAAGAAGAAATACAAAAGAGAGAAATTG
AAAAAGAAAGAACTTAAGAAGATTGAAAAGAGAACTGATAGATTATCTAGAAGGGGCA
GGAGAAGATTAGATGACTTAGAAACCACAATGAGAATGTAG

YLR321C, 426 aa (SEQ ID NO 194)

MSHQQLIPQAYISNHNRLTNEDDGIPIFTMAQQTRQHKRAKVVNVAEYDNDLFDEFNM
NGSNFNNADTHYKDNVSHENTPALTNVMTMDGSEYNVLENMNGADSIISNNKYDAGSNM
VVESLSGLNSNNNASNGPSNKAQAQDIGNAVLPDLQDQHNPFNILRYPKIRDTFINGKV
VSPYRLNTDQETKANANSGEAIMIPITLDIEHMGHTIKDQFLWYNDDSIISPEEFASIYC
KDLDMTSATLQTQIANIIKEQLKDLENIAATEIMSDLHVIINLTCNLQDRFFEDNFQWNL
NDKSLTPERFATSIVQDLGLTREFIPLISQSLHETILKIKDWVDGHLIQDHPNDAAFG
YLSGIRLDIDELGSNWCPRVEILTKEEIQKREIEKERNLRLKRETDRLSRRGRRRLDDL
ETTMRM

YLR322W, 815 bp, CDS: 501-815 (SEQ ID NO 195)

GTCATATCAAGATCTTTACAGTATATAGAGGCAAATTCCTCCGGAGATATGGAGTCGTCA
TTGTAGTTCCAGAGAAACTGGTCTTTTATGGTATGACCCATATGTTCTATATCCAAAGTA
ATTGGTATCATGATTGCCCTCTCCAGAATTGGCGTTTGGCTTCGTTTCTTGATCAGTGTTG
AGTCTATATGGAGACACCACCTTTCCGTTAATGAAAGTATCTCTTATTTTAGGGTATCTC
AATATGTTGAAGGGGTTGTGGTGTGGTCTTGCAGATCCGGTAGAACGGCGTTTCCATA
TCCTGTGCCCTGCCCTTTGTGTGCTCGGACCATGTGCTGGCGTTGTTATTGCTATTCAAACCG
GATAAAGATTCCACAACCATGTTTGAACCCGCATCGTATTGTTGTTAGAGATAATACTA
TCAGCTCCATTCTATGTTCTTAGGACATTGTATTCCGGAACCGTCCATGGTAACACCATTT
GTAAGTGCCGGAGTATTTTCATGAGACACTGCATTATCTTTATAGTGTGTATCAGCATTG
TTGAAATTAGAACCGTTTCATATTGAATTCATCAAAGAGATCGTTGTCATATTCGCCATAG
TTGACCACTTTAGCCCTTTTATGCTGCCCTTGTGTTGTTGAGCCATTGTAAAGATGGGGATA
CCATCATCTTCGTTTGTCAATCTGTTATGAAAGTTAGAAATATAAGCTTGTGGAATAAGC
TGGTTTGGTGCGACATTGTGTGCTGCTATGTGCCCTTCTTCTTTCTTTTCAATGTAC
TTCATTCAATAATCTCTATTGTCGTATTTTCTAA

YLR322W, 104 aa (SEQ ID NO 196)

MRHCIIIFIVCISIVEIRTVHIEFIKEIVVIFRIVDHFSPFMLPCLLSHCKDGDIIIFVCQ
SVMKVRNISLWNKLVLRHCVLLCAFLLSFFNVLSIISICRIF

YLR325C, 737 bp, CDS: 501-737 (SEQ ID NO 197)

CCACATGTCACAACTACTTTGTGAAGTTGCAATGCGTGATTAGTATTATAAAACATCATA
GCCTTGCCAAATAAACTCGCTTCCCAGAAAAGACGCCAAATTAAGTCCGCTGTATGTG
ACAAAACAGGGCATCTCACATATTCCGCTACTGGTGTCTTTTAGCTCATTCGGATATTA
TTCCAAGACGGAATTTTCATCTAGAGAAAATGCATCCGTGCATTTTCATAAACCCACACA
ATTAAAATGCCTTGCGAAAAGGAGGACTCGTCCGTGCAACTGTTGAAAAAATAGACGGA
GCATCATACGTTTCGAGTGGAATAATATGAGAGATTTTCCAAGCTCTATGGCATGTAGAGT
CGTGATTGCTGCTGTACGCTTTTGACAATATTGAATCTTCAATCTAAAGAATTAAATTT
TCTAATTTCAATGTAGAAATATTTCACTGTAGTTTATTTTATTTTCAGGTTGAATATAGTA
CGACAAAATATCAAGGAAAAATGGCTAGAGAAAATCACCGACATCAAAACAATTTTGGAAAT
TGACCAGAAGAGCTGACGTTAAGACCGCCACTGTTAAGATTAAACAAAAAATTGAACAAGG
CCGGTAAGCCATTTCAGACAAACCAAGTTCAAGGTTAGAGGCTCTTCTTCTTTGTACACTT
TGGTTATCAACGATGCTGTAAGGCTAAGAAATTGATCCAATCTTTGCCACCAACTTTGA
AGGTTAACAGATTATAA

YLR325C, 78 aa (SEQ ID NO 198)

MAREITDIKQFLELTRRADVKATVKINKKLNKAGKPFRTKFKVRGSSSLYTLVINDAG
KAKKLIQSLPPTLKVNRL

YLR344W, 1331 bp, exon1: 501-519, intron1: 520-966, exon2:
967-1331 (SEQ ID NO 199)

TAAGGGCTGTCAATTTTTCATTTCCCTCAAAGTTAATGCGCAAGAGTTAGGATGATCTTG
ATTATTAGTTATTTGTTTGTTCATCAATTATGCCGACGTCCATGAATGCTATTGAAGTA
TCGATTACTTATGCTATTCTATTGTATTGAGCCGGCGGCTAGTAAACAAGACAGCATAC
CTTTCCAACATCCGTACATATTGATTATTGTATCTATGATTTTCATGTAATGTATGGGTT
AACTAATCCTTTCTCTCTTTTTTTTTTCTGAAAATCAGTAGCTAGAGGAACCTGTTTC
GTGAAAGATATGGAATATTCCGTCTAGGGAAGAGCCGAGAGCTGAGAGCAGTATCCATCG
GATGGAATCTTGCCTGGATGCGTAACGACGACAGCTTGTCTAGAAGGCGAAGTACAAGAT
ACTAAGAAGACTATAACAACAGAAGACAATTTTGTAGTGCGATTCTATATTATTGACGTA
ACCAACAAAAAAGTATCAGAATGGCTAAACAATCATTAGGTATGTGCACAAATGCTAAAT
CACTGAAACCCTGTAGAGCTGGAATTGAAAATATAGTTTGTACCTTTTGCCTGAGGGCAG
AATGACTCAATGTTATCTTAATTCGATTAGAAAAAGAAGGTGCGTTATCCAAGGTTGAAA
CTTGTAAGTATTTAGGTGATGTCTCATAACTGCAACCACTGGAATGACGCAATATC
AAAATAATAGGGAGATAAAGTCTCAGCATGAAAAATCATAGAATTATTGTTCAATTT
ATCTAGCCGTATCTTACCTTATGGAAAAAGTGTGAATATGTTTTCTAAATCGAGCTTCC
CGGAAATTACACTATATTATGCATCCGTGATACATCTGAAATTCATACTTTCTCCAAGG
TCCTGCTTACTAAGAGGGTAAGATTTGTTGAAACTCGAAATACTAACATTATTTTCATTA
TTTTAGACGTTTCTCCGACAGAAGAAAGGCTAGAAAGGCTTATTTACCGCCCCATCCT
CCCAACGTCGTGTTTTGCTATCTGCTCCATTATCTAAGGAGTTGAGAGCTCAATACGGTA
TCAAGGCCTTGCCAATCAGAAGAGATGATGAAGTTTGGTTGTTGTTGTTTCCAAGAAGG
GTCAAGAAGGTAAGATTTTCTGTTTACAGATTGAAATTTGCCGTTCAAGTTGACAAGG
TTACCAAGGAAAAGGTCAACGGTGCTTCCGTTCCAATTAACCTGCACCCATCCAAGCTTG
TCATTACTAAATTACATTTGGACAAGGACAGAAAAGCTTTGATCCAAAGAAAGGGCGGTA
AGTTGGAATAA

YLR344W, 127 aa (SEQ ID NO 200)

MAKQSLDVSSDRRKARKAYFTAPSSQRRVLLSAPLSKELRAQYGIKALPIRRDDEVLVVR
GSKKGQEGKISSVYRLKFAVQVDKVTKEKVGASVPINLHPSKLVITKLHLDKDRKALIQ
RKGGKLE

YLR367W, 1376 bp, exon1: 501-633 intron1: 634-1116, exon2:
1117-1376 (SEQ ID NO 201)

ACTTTTGTCTGCTGCTGGTCTGTTTGTCTTTCTGTTTAAATGCGCTAGACAAGTAAAC
AGGGATTGCTTAAGAATCAAAGTAGCTTAACTCTAAAGTATTATTTTCTCAGTTGTGGG
CCCATGTGTTGGAGGGAAGGAATATATTGAAATGTAAATGTTCTTAAGTTCCGTTGAACT
TGGATATTGTTACAAGAGTTCTAGTCTTTGATACCATTTTACGCAATTACAACCGCATT
ATTTACCTTTTCATCTTCAGTTTACGGTTCAGTTTATTCTGTTACGAAAGAATATGGT
GATTCAAAGGCGAAGTGCGTAGGATTGTAACCTCTATATCTTTAGGATACTTACAATTTT
GTACTGTTTTCAAGACCCTGTAACCGATAATAAACCGGAGGACACATTTTAACCCACTA
TTTTTTTTCAGAAGATCAGATGCGAGAGCTCGAAGCATAAGTATAATACTAACGTTTCAAA
ACATAGTAATTAGGTAAAAAATGACTCGCTCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAATAACGCCGAAAAGACCGGTAACGTCAGGTTCTATTGAGACCTTCTTCCAAGGTTA
TCATCAAGTTTTTACAAGTTATGCAAAAGCATGGTATGTTCCAATATTTTCAATATTT
TCACATGTGTTTTCAATTTCTGCTTATTTTTTAAATGTTACCACGAGGTTTGTCCAAGTTCA
ATGTTGCGCAACTCTAACGAAGAAATAATTATTGCCATTGTTTTTACTCCGGGCTGATA
ACTAGATGGTGTGATCGGGCAGTATACTAATTTTACTGGACAAAGACTCGTAAAAGATG
TTCTTTGTGCTTAGTCCCATACGTTTTTTAAGTGTCCGGGATATTTAATCCCATGTGGA
AATGCTTCTTACACGGTTATGGATTACACCTCATGTGTAGCTACTATATCCATTACCGTT
TACTTTTCTCATAAATCTCACCTTAAATTTTCAATGGCAAAATCTTCCGCAACAAT
AGACAACATTTTCTGTTTTTATGAAGTAAGCAAAAATTTTCAATCAACAACGCTCCAT
GAGATTCTTCAATACTAACATTTACTCCTTATTTAGGTTACATTGGCGAATTCCAATACA
TTGACGACCACAGATCTGGTAAGATTGTCGTCCAACCTGAACGGTAGATTGAACAAATGTG
GTGTTATTTCCCAAGATTTAACGTTAAGATTGGTGACATTGAAAAATGGACCGCCAAC
TATTGCCAGCCAGACAATTCGGTTACGTTATTTTACTACTTCTGCGGGTATTATGGACC
ATGAGGAAGCTAGAAGAAAGCACGTTTCCGGTAAATCTTGGGTTTTGTCTATTAA

YLR367W, 130 aa (SEQ ID NO 202)

MTRSSVLADALNAINNAEKTGKRQVLLRPSSKVIKFLQVMQKHGYIGEFEYIDDHRSRK
IVVQLNGLRNKCGVISPRFNVKIGDIEKWTANLLPARQFGYVILTTSAGIMDHEEARRKH
VSGKILGFVY

YLR393W, 1340 bp, CDS: 501-1340 (SEQ ID NO 203)

CCCTCAACCCGCATTTTGTGAGAATTTTCACCAAGGCCCTAGGTGATATTAGATTCCAC
CTGACTAATTGCATTACAGCCGACCCAAGGCAATATCAGTTTAATAAAATATCATGTATC
TCACCCTCTTCTTGGTATTAGTAAAGAGACGCCTGATCTTGTAAACAGTGGTGAAGATTGT
ACTAGAGCAGAATCAAGAATTTAAAAAGTGTAAGGCAAGGCAGAGGCGATGTACATAAA
ACTTCGAAGTAAGAAATATTTAATAGTTCTCGCCACATCACTATGCAGCTATATAAAAAC
TACTATAAACGTTTGTTTTGTTCCTTACGCACAATATCCTTGCCTAGAAATCGTTTTTGA
AATTTAAATTTTTATTACCATTTATTTGATTGCGCTTCAGAAAAATATGGAAGAGTGCAT
ATTTAAAAAGGACTATTTTACGATATAGTAAAGTCAGGTTATTTGTTTTATTTGCGATAT
CAGAGTAACTTAACTAACTATGCAGGGCACTTTAAAAAGGTTTACCATCCCACGCTTA
CGCGGATGTCCTTCTTGGATAAATTCCTCAAGCCTATGATGGCAACGGCTTCCCCAAAGG
AATACCAGATCAAACAACCTGGTCAAGCCAATAGGCTTAACACAAGCACCAAGGAAAAAGCA
CCAAATACTCCCAGGGGAACCTCTTTGAGGGATATGTTTGATTGCGAAAAGACAAACCACA
GAGTTAAAGAGTTGGCCGTTGAATTCAGCAAATCTGGACTTTATGACGTGCAAGTCTTCC
AAAAGACAAAGGGGAATTTGTTTATAGCTCCAGTTTCATATTGGAAAGAAGATAAAGCTT
TGTTTTTTCCTCATTTGATAGGAACGGCAATGGATGGTACGAAACAACAGAATATCGAGG
ATATGTTAAGGGGTAAAACAGTATAGTGAGGTTATTTAGTACAGCATCTGGCGATAAGT
TGAGTAGTTTCATACTTCCAAGGAATCGTAGACGATAACAAAAAACTGACTACTTGACTG
AAGCTGATGCGCGTTTAAAGTTTAAATGACAGTAACGTCCAAATCATCGAGGTCAATCTTG
TAGAAAACGCTGTGAAAAGTGCTCTAGTGAACGCTTGCTCGTTGGGCCAATCGCGTTC
CATCCTGGCGCCAGCCATTTTATTTTCAATGTTCTAGAGGCCAATGGCCATTTTCCGTCA
GGGAAGAGCTCTTTTGCAATAATGTCCTTTCTGGATACGTCTTTCTTGTTGGACCAGCAGT
TAAAAATTAGGTGGGCAGCTTGGGGGAGGCTACTCCATCTGAAAAGGAAGCATTGTGGA
AGTTTGCCAAACGCTCTGTGA

YLR393W, 279 aa (SEQ ID NO 204)

MQGTFKRPHYHTLTRMSFLDKFLKPMMATASPKYQIKQLVKPIGLTQAPRKSTKYSQGN
SLRDMFDESEKTNHRVKELAVEFSKSGLYDVQVFQKTGKGLFIAPVSYWKEDKALFFPHLI
GTAMDGTQQNIEDMLRGKTSIVRLFSTASGDKLSSSYFQGIIDDNKKTDYLTADARLS
LNDNSNVQIIIEVNLVENAVKSALVKTLARWANRVPSWRQPFYFECRSRQWPFVREELFCN
NVFSGYVFLVDQQLKIRWAACGEATPSEKEALWKFARL

YLR423C, 1754 bp, CDS: 501-1754 (SEQ ID NO 205)

TTCTATTGGTGTAGTTATACCAGAACCATCCTTCCCAAGGCCCTTTCCCGCAACATATCC
CATACTCGAAAGTAACCTTCGCACCAATACCATATGCTTTCGTTAATTTTGAGATCGTTGG
GGCATTGCCGCTACTAGTTTTCAGGCATCATTAGTGATGTGATGTCATGCTACTATTCATGCT
TGAATTATTATCTTCTCATCGCTATAATTATAGGAATCGATTCTTCTTTTTTTGAAAAA
GAACTTTTTATCTGTGTTGGAGTCCGAATCCTCCATGTTTTGGCGTACTGAAGGCTTAAG
TTCTTCGACCTCTCTCGGTTGTACTATTTGCAAAATTTGGATTTTGTATTGTTTTGAC
ATAATGTAAATACTAGATGCGCGCTCTAAGGCCTCAGTATTAAAAATTGCAAGATATCCC
TAACTTGATAAATTATTTGAAAGTCGCATAACGTACGATAAATTCGATACTGCGAGGATAT
TATCAACGTTATTTAACACCTATGAACGAAGCAGATGTTACAAAATTTGTTAATAATGCCA
GGAAAACGCTGACCGATGCTCAACTTTTATGTTCAAGTGCTAATTTAAGGATTGTAGATA
TTAAGAAAAAATTGTCATCTTGGCAGTTGAGTATTTCAAACTCAATTTTCTAATAGTTG
GCTTGAGACAGCAAGGAAAGTTTCTTTACACTATTTTAAAGGAAGGCATTGGGACAAAGC
TAATCCAGAAACAATGGAATCAAGCTGTCTTAGTGGTCTTAGTTGATGAGATGAAGTACT
GGCAATATGAAATCACTTCTAAAGTACAAAGGTTGGATGTTATAGTAAATGAATTGAGCA
TATCAGAAAAAGATGATACCGATCCCTCTAAACTAGGAGATTACATCTCGAGAGACAAAG
TTAACTTATTGAATGACAACTGAAAGAAGTGCCAGTAATTGAGCGTCAAATTGAAAAACA
TTAAGCTTCAATACGAAAAATATGGTCAGAAAAAGTTAACAAAGAACTGATTGATACCAAGT
TGACGGACGTAACCTCAAAAATTCAAAAGTAAATTTGGTATAGATAACCTGATGGAAACAA
ATGTTGTCAGAGCAGTTTAGCAGGGAACTAACGGACCTTGAAAAAGATTTAGCAGAGATAA
TGAATTCATGTGACACAGCACTTTGATAAGACATTGCTGTTACAAGATAAAAAAATTGATA
ACGATGAACGTGAGGAGCTGTTTAAAGGTGGTACAAGGCGACGACAAAGAACTATACAACA
TTTTCAAACTCTGCATGAGGTAATTGATGACGTGGACAAAACAATTTTAACTTGGGTC

AATTTTTGCAGGCAAAAATAAAGGAAAAGACAGAACTACACAGCGAAGTTTCTGAAATAA
TAAACGATTTCAATAGAAAATTTGGAATATCTATTAATCTTTAAAGATATTTCCAATCTGA
TTGATAGCTTCAAAAATTCCTGTACACAAGATATTTCAAACTAAGGAAGTTTGTGAAT
TTTATGATAATTTTGAAGAAAGCTACGGTAAGTTAGTTCTAGAAGCAAAGAGGAGAAAGG
ATGTGGCAAACAGAATGAAAATATATTTGAAAGATTTGTGAAAAGCAGTTGCAGAATTTAG
ATGCTCAGGACCAGGAAGAACGTGAGAATTTTATAGCGGAAAATGGAAGTTATCTTCCTG
AGACAATCTGGCCCGGTAAAATTGACGATTTTCTTCCCTGTACACTTTAAATTACAACG
TGAAGAATCCTTAG

YLR423C, 417 aa (SEQ ID NO 206)

MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKKLSSWQLSISKLNFLIVGLRQQGK
FLYTILKEGIGTKLIQKQWNAVLVVLVDEMKYWQYEITSKVQRLDGIVNELSISEKDDT
DPSKLGDIYSRDNVNLNDKLKEVPVIERQIENIKLQYENMVRKVNKELIDTKLTDVTDQK
FQSKFGIDNLMETNVAEQFSRELTDLEKDLAEIMNSLTQHFDKTLLLQDKKIDNDEREEL
FKVVQGGDDKELYNIFKTLHEVIDDVDTILNLGQFLQAKIKEKTELHSEVSEIINDFNRN
LEYLLIFKDISNLDISFKNSCTQDIQTTKELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDCQKQLQNLDAQDQEERQNFIAENGTYPETIWPBKIDDFSSLYTLNYNVKNP

YML026C, 1342 bp, exon1: 501-547, intron1: 548-948, exon2:
949-1342 (SEQ ID NO 207)

ATCTGTAAATAAAGCCCATGAAATATCAATCTCACAATGAAAGAATTGTATAATTCAG
AATGATTTGACGTAAAAGCAAGTCTCATTCAAGAACTGTAAAATCCGTACACACTACTG
AATTTTACATCCATACATTTTTTTTGAATTTTCATGTTTTTTTGAAGAAATTTGGAAGGGC
TAAATTATCCGTCGGGGTGTCTCTCTAGCTCGGCTCAACCTAGGCAAATGCGTTTACTGG
GGCCATCCAAGCTCATCCTTCCAGAGATTCGCCTTTCAGAGGCAAAGAACTCGTCTCCGC
AGGCCTCTTGTTCGGGAGGAGGAGAATTCTTGC CGGAACTGGTTGATGCCTGGGCTA
TGGTAATTCTGACACCTTTGCTATCCTAACTGGAAAAGGTCCTTAGTAATAACAATATCA
GGTACTTTAACATTGTAAAGATATACTATTAGTGAAAAACCGATCTTACGAAAAGCCAA
TAGAGCAGAAAGTGGTAAAGATGTCTTTAGTTGTACAAGAACAAGGTTCTTCCAACACA
TTTTACGGTATGTTTTACGAGTACAGTGCAGATATGTTGAGAGAGTTTACATTACATGG
GATAATAGCTTAATATTGCGATTGAAAATATGTGAGTGCCTCCGATGGAATAATAAAGC
TCACGGGTTACCAAATACGAGGCCGAATTAACCTACGCTACTATAAAAAATTATCCTAG
ATTTTAAAGTAATACACAGTTTATTGGAATAACAATATATGACTCAATGCGAATTTAAA
AATTTTCAGTCAATACAGCTTGACAAATTCATATTTATCGTCCCTCCATGTTCTGACGCCA
TTCCAAAATGATGCGCCATGTTGAAAATTTCTCGAAGAACCTAGCAGTGGTGTGAAATAA
ATTACTAACAATAAGATGTACAATTTTTTGTGCGCCCATTAACAATCAGTTTGTGTAACAC
CAATGTGCGATGGTAACATTAAAATTGTTTACGCTTTGACCACTATTAAGGGTGTGTTGGT
TCGTTACTCCAACCTGGTCTGTGAAGAAGGCTGATGTTGATTTGCACAAGAGAGCTGGTGA
ATTGACCCAAGAAGAATTGGAAGAATTGTCCAATCATGCAAAACCCAACCTATTACAA
GATCCCAGCCTGGTCTTAAACCGTCAAACGACATTACTGATGGTAAGGACTACCACAC
TTTGGCTAACAACGTGCAATCCAAGTTGAGAGATGACTTGGAAAGATTAAAGAAGATCAG
AGCCCACCGTGGTATTAGACACTTCTGGGGTTTACGTGTTAGAGGTCAACACACCAAGAC
CACTGGTAGAAGAAGAGCTTAA

YML026C, 146 aa (SEQ ID NO 208)

MSLVVQEQGSFQHILRLNTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPHTYKI PAWFLNRQNDITDGKDYHTLANNVESKLRDDLRLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YML063W, 1268 bp, CDS: 501-1268 (SEQ ID NO 209)

TATATTATTTTTTCCCTTCTGGGTCTTTTCTTCTTTCTTGTTTACCTTTTTTGCTTT
TTCATAAAATAATTTCTCTAGATTTGAAGACAGCATTTTTGTACATCCATACACCATACA
CCATACACCATAGCACCAGTACACTATTTTTTATGAATTTTACTAAGAATTATTCCTGC
AGGAGCTCCACTGAAAAAAAAGAGCAGCATGGATGTCCGGTAGAAGTGCTACTGAGTAA
ATGGGAAGGACGCGGTAGATCCAGTGTGGAATCAAGGTGGTGCCGGTGTGAAGCCGCCTC
GGCCGGCTGGACTCTCCAGGCCGGAGTGATGATTGCCACGCTGAACGTAACACAGTTTCA
CAATACCAGTGTCTCATTAGTGAGTTCCAATGTATAGTTAGTAGTGGTATTTTGATATA
TGTGAGTGGTAGCAGATTTGAAGTTAGTTAGTTGTATTGCGCTTTGAGGAAACCAAGCAA
AAAACCGATCTAGACTAATCATGGCTGTTGGTAAGAATAAGAGACTATCCAGAGGTAAAGA
AGGGTTTGAAGAAGAAGGTCGTTGACCCATTTACCAGAAAGGAATGGTTCGATATTAAAG

CCCCATCCACTTTTGAAAAACAGAAATGTTGGTAAGACTTTAGTTAACAAGTCCACTGGTT
TGAAGAATGCTTCCGATGCTTTGAAGGGTAGAGTTGTCGAAGTTTGTGGCTGACTTGC
AAGGTTCTGAAGACCATTCTTTAGAAAGGTCAAGTTGAGAGTCGATGAAGTTCAAGGTA
AGAACTTGTGACCAACTTCCACGGTATGGACTTCACTACCGACAAATTGAGATCAATGG
TCAGAAATGGCAAACTTTGATCGAAGCTAATGTTACCGTTAAGACTTCCGATGATTACG
TTTTGAGAATCTTTGCTATTGCCTTCACCAGAAAGCAAGCTAACCAAGTTAAGAGACACT
CTTACGCTCAATCTTCCACATCAGAGCTATCAGAAAAGTTATTTCTGAAATCTTGACCA
GAGAAGTTCAAACTCTACTTTGGCTCAATTGACCTCCAAATTGATTCCAGAAGTTATCA
ACAAGGAAATCGAAAATGCTACCAAGGACATCTTCCACTACAAAACATCCACGTTAGAA
AGGTTAAGTTATTGAAACAACCAAGGTCGACGTTGGTGCTTTGATGGCTTTGCATGGTG
AAGGTTCCGGTGAAGAAAAGGGTAAGAAGGTTTCTGGTTTCAAGGATGAAGTCTTGAAA
CTGTGTAA

YML063W, 255 aa (SEQ ID NO 210)

MAVGKNKRLSRGKKGLKKKVDPFTRKEWFDIKAPSTFENRVGKTLVKNSTGLKNASDA
LKGRVVEVCLADLQGSSEHDFSRKVKLRVDEVQGNLLTNFHGMDFTTDKLRSMVRKWQTL
IEANVTVKTSDDYVLRIFAIAFTRKQANQVKRHSYAQSSHIRAIRKVISEILTREVQNST
LAQLTSKLIPEVINKEIENATKDIFLQNIHVRKVLLKQPKFDVGALMALHGEESGEEK
GKKVSGFKDEVLETV

YML128C, 2042 bp, CDS: 501-2042 (SEQ ID NO 211)

TTAATAGGGTTAGCCACCATTGTCTCGAACATGTTACAGGCTCGGAGCTTGTGGCGGGT
GCCTCGCTTACTGGAGTACCATTAGCGGTGTGTTTGAAGCTAACGAGTTTCTTCAAT
CTTTATTTCCACTTCTTACAAGCTTTCTGCCTTTCTCTATGACGCTTTTCCCAAAACAC
TACCTCTTGACACGACTTGTGTTTTTCGTTTTTCTCTAAGAATATCACTATTTTCACTTT
TTTCACTTTTCCACCATTACGTCGGTAAGCAACAGCATTACGCCGGCCTCACCTTAGAG
GGGAAGAATAAGGGATCTTTGGAAGTGAAGGAAAATAAGGGAGAGGGAGGAAACAAGGAG
GCGGTGAAAGGGGATCGACAGGGTATTTAAAGCCACTCATGGAGTCGTATTCTTAGCATG
ATTAGATTACCGGAGTTTGAAGAGGATCTGCAATAGAAGAGGAGACAACACTACAAAAGAA
CTGTTAATTAAAGAGAAGAAGTGAAGCAATTCAAGTTGGTTAATGCGGTTTCCGCATCAT
TTGTGCTTATTGGCTTAGTGTTGGCCAATTTCAGATTCAAGTGTTCGACAAGTGGACGAGG
AAGACCTGGCCGATTATTTACGTGATAATAAGAAGAGCTTGGAAAAGTACGCTACAGACT
CCATTGAGGACTTGAAAACGGAGGCATCGCAGGTATGGGACAAACACGCGCAGCCCAAC
CATGGTGGCAGGTGTGGTCTAGTGACAGCAGTAGCGTGAGCAACAGTAACCCCGGATGGT
TTGGTTATACTGGTCTTTCGGATCACCCAGTTTCTGACTGGCTCTTTGACACCTGGTCCA
CAGACAGTCTACGTAACTTCTTGAAGAAAACGGCGTGGATGTTGACGACGCTTAAGGCTT
CCAAGGACTCGCTGGTGAAGACTGCTAAGGAGAACTTCAACAAGATTTCCAAATCTTTGA
AGTCGTCGGGATACTATCCTTCTAGCTCTTACTTTGATAGCTGGTCAACCAAAGATTTGC
AAAAGTGGTTGAATGACAATGGTATCGACTACGACAAGGCAGTTCAAAGCAAGGACGAGC
TAGTTTCAGAAAGTCAAGGAAAACATCTACCGAATTCAGAAAAGGCAGAACAGCAGCGTC
TGGGTTTGCTAGAAAGCTTGGATTGGCTCACCACAAATATTAGACACATCGGGACAAA
TAAAAGACTGATGTTTGAACAAGTGGTCTAGTGATCAGTTAACCAATTGGTTGGAGAGCC
ACAAGGTCAATATTGACAAGAATCATGGCCAAGAAAACACGACTATTTGGTTAGAATGGCCA
AAGAAAATTCTGCCAATTTGAAAGATGATATCTACTGGTACCTGGACTATATGAAAAGAG
AGTCTTCTCCATTTTTGACCAAGACCCAGAATACGTTGGTTCCGTTTGGGACTCTTCTA
AAAATTTCTCTACAAATTTGTACTCCAAGTTCAAGAGGTAAGACTGACAATGTGATCAATG
ATACTTTTTTGGTTGGCCTAGACTCTTGGCCAAAGGACAAATTGAAAATGTTTTTAGATG
CTCGTGGTATTAAGTACTCAATGCTGTCTACTGAACATCAATTGAGAGAATTAGTCAAAA
AATCCAGAAACGAAAACTCAAGATCTGCCAAAAGACTACCAAAAATACTTTGACAACA
GTAAGTGGTCTTTGGATGACATAAAGGGTTGGTTTGTGACAAAAGGACGACTTCCAAG
ATTCTCAGACTTACTCCACAATTATGCAGGATTTTGAACAAGTTTCCAAAAACACAAATG
ATGCTAAGGACCAATCGCTAAGACCTGGTCAATACCTTTCAAGAGCTGGTCTCAAGAAG
ACCTATTGCAGTACCTAAAATCATTCGGTGTTCGGTTAAACAGACTTCTACGAAGGACG
ACTTAATCAACTTGGCCAAGCAGAATACGCAATGGTTGTTCCGGCACTGTTAAGGAGCCTG
CTTACAAGAGGTACCTACATAACGTTAAAACTGGTCAAAAAGCATATTAGGGTTCAACT
AA

YML128C, 513 aa (SEQ ID NO 212)

MKQFKLVNAVSAFVLIGLVLANSDSVFDKWTQEDLADYLRDNKKSLEKYATDSIEDLKT
EASQVWDKHAQPKPWWQVWSSDSSSVNSNPNPGWFGYTGSSDHPVSDWLFDTWSTDLSLRF

LKKNQVDDDAKASKDSLVTAKENFNKISKSLKSSGYYPSSSYFDSWSTKDLQNLNDN
GIDYDKAVQSKDELQVQVKENIYRTSEKAEQRLGLESLLDLAHQQILDTSQGIKDTVFD
KWSSDQLTNWLESHKVNIDKNMAKKHDYLVMAKENSANLKDDIYWYLDYMKRESSPFLT
KTPEYVGSVWDSKKNFLTNLYSKFRGKTDNVINDTFLVGLDSWPKDKLKMFLDARGIKYS
MLSTEHLRELKVKSRNEKLKILPKDYQKYFDNSNWSLDDIKGWFADKKDDFQDSQTYST
IMQDFDKVSKNTNDAKDQIAKTWSNTFQSWSQEDLLQYLKSFVGVKQTSTKDDLINLAK
QNTQWLFGTVKEPAYKRYLHNVNKNSKSLGFN

YML130C, 2192 bp, CDS: 501-2192 (SEQ ID NO 213)

ACGAGATCATTTTCTTATCTATCTATTGAGTAATGCTTACTTTTCATATTTTCAATGAAC
AATAGGATATGTAGGAGAATTGATATATTCCTGCGTATCAGAGAAAAGGTCTACTGACA
TTTTATGGCAAATGTATCTACACAAATCGAGAATACCACAGACAATGGTACAAGACATA
CACAAAGAGAAAGACTGTTCTAATTAAACAAATAATATTGAGTACCTGCTAAGTGTCTC
TTTTCCCTTTGTCTTTGGTTTCTCTTATAGAAGACCCTGGAAATTTTCGCAATTTTCC
GGCTTTGGGCGTTAGTAAGAACAAAAAGAAAGAGAACAAAAAGAAACGATACGGA
GTACGTGTCATAAAAACTTGTTCATCATCTTGAAGCTAAGTATAAAGAGCTTGAAAG
GTTTACCACTTAACTGGTTATACTATTTCAAGAGTGTAACATTTTATTGCAATATACCA
CAGTAACGTGCAGGTAAACATGAGATTAAGAACCCTGCTTGCACACTGTGCCTCACGG
CTTTTACATCTGCAACTTCAAACAATAGCTACATCGCCACCGACCAACACAAATGCCT
TTAATGACACTCACTTTTGTAAAGGTCGACAGGAATGATCAGTTAGTCCCAGTTGTAACG
TAACATTTCAATGAATTAAATGCCATAAATGAAAACATTAGAGATGATCTTTCGGCGTTAT
TAAATCTGATTTCTTCAAATACTTTTCGGCTGGATTTATACAAGCAATGTTCAATTTGGG
ACGCCAACGATGGTCTGTGCTTAAACCGCGCTTGTCTGTGTTGATGTCGTAGAGGACTGGG
ATACACTGCTGAGTACTGGCAGCCTGAGATCTTGGGTAGTTTCAATAATGATACAAATGA
AGGAAGCGGATGATAGCGATGACGAATGTAAGTTCTTAGATCAACTATGTCAAACCAAGTA
AAAAACCTGTAGATATCGAAGACACCATCAACTACTGTGATGTAAATGACTTTAACGGTA
AAAACGCCGTTCTGATTGATTTAACAGCAAATCCGGAACGATTTACAGGTTATGGTGGTA
AGCAAGCTGGTCAAATTTGGTCTACTATCTACCAAGACAACCTGTTTACAATTTGGCGAAA
CTGGTGAATCATTGGCCAAAGATGCATTTTATAGACTTGTATCCGGTTTCCATGCCTCTA
TCGGTACTCACTTATCAAAGGAATATTTGAACACGAAAACCTGGTAAATGGGAGCCCAATC
TGGATTGTGTTTATGGCAAGAATCGGGAACCTTCTGTAGAGTGACAAACATGATTTTCA
ATTATGCTGTTGTAGCTAAGGCTCTCTGGAATAATCAACCATATTTACCAGAAATTTTCAT
TCTGTGATCTAGTCAATAAAGAAATCAAAAACAAAATGGATAACGTTATTTCCAGCTGG
ACACAAAAATTTTTAACGAAGACTTAGTTTTCGCAACGACCTAAGTTTGAAGG
ACGAATTGATCTCGCTTCAAGAATGTCACGAAGATTATGGATTGTGTGCAATGTGATA
GATGTAGATTGTGGGCAAAATTCAACTACCGGTTACGCAACTGCCTTGAAAATTTTGT
TTGAAATCAACGACGCTGATGAATTCACCAAAACATATTTGTTGGTAAGTTAACCAGAT
ATGAGTTGATTGCACTATTACAGACTTTCCGTAGATTATCTGAATCTATTGAATCTGTTA
ACATGTTTCGAAAAATGTACGGGAAAAGGTTAAACGGTTCTGAAAACAGGTTAAGCTCAT
TCTTCCAAAATAACTTCTTCAACATTTTGAAGGAGGCAGGCAAATCGATTTCGTACACCA
TAGAGAATCAATTCCTAAAGAAGGAAAGAAAAAGACTAACAATTCCTCAATCACATG
TATTTGATGATTTAAAAATGCCCAAGCAGAAATAGTTCCAAGGCCCTCTAACGGTACAG
TAAATAAATGGAAGAAAGCTTGAATACTGAAGTTAACAACGTTTTAGAAGCATTGAGAT
TTATTTATAGAAGCTATTTGGATTTACCCAGGAACATCTGGGAATTATCTTTGATGAAGG
TATACAAATTTTGAATAAATTCATCGGTGTTGCTGATTACGTTAGTGAGGAGACACGAG
AGCCTATTTCTATAAGCTAGATATACAATAA

YML130C, 563 aa (SEQ ID NO 214)

MRLRTAIATLCLTAFTSATSNNYSIATDQTNQAFNDTHFCVKVDRNDHVSFSCNVTFNELN
AINENIRDDLSALLKSDFKYFRLDLYKQCSFWDANDGLCLNRACSVDDVVDWDTLPEYW
QPEILGSFNNDTMKEADDSDECKFLDQLCQTSKKPVDIEDTINYCDVNDNFNGKNAVLI
LTANPERFTGYGGKQAGQIWSTIYQDNCFTIGETGESLAKDAFYRLVSGFHASIGTHLSK
EYLNKTGKWEPNLDFMARIGNFPDRVTNMYFNAYVAVAKALWKIOPYLPEFSFCDLVNK
EIKNKMNDVSIQLDKIFNEDLVFANDLSLTCLKDEFRRFKNVTKIMDCVQCDRCRLWGK
IQTTGYATALKILFEINDADEFTKQIHVGLTKYELIALLOTFGRLSESIESVNMFEKMY
GKRLNGSENRLSSFFQNNFFNILKEAGKSIRYTIENINSTKEGKKKTNNNSQSHVFDDLM
PKAEIVPRPSNGTVNKKWKAWNTEVNNVLEAFRFIYRSYLDLPRNIWELSLMKVYKFWNK
FIGVADYVSEETREPISYKLDIQ

YMR022W, 998 bp, CDS: 501-998 (SEQ ID NO 215)

AACAGTATTGGCTGTTGATTTCATTGCGCTGCAGCAGTCACCTTCAATTTGTGCACCATTT
TCGTATTCTGTACTTTGCGATGTAGAGTCTACTAAAATAGCGTCTCTGATAGCCATGGGT
GAAGGTCTTCCCTCTAGTTCTCACCTTAATTAGCATTTCGGTGAGAATGCCTGCATGTTGAA
GAGCGATGCCCTCTGATGCACGATGCACACGCATATTTGTTCCCATTAATATTATCATC
TCTGATAGAGCTTGAAGAACTTACCAGACTGTTTCAAGTTTAAAACAAGGCGCCTCATCG
CATCTACCTCACGAAGATGCAGCAGCTTATTGTCTCGAGATCCTTCTTATAACTCCTTTT
CGCCATTACCCGAAAACGAGATTACAGCCTCTAAACCAAGAGCTCGAAAAGCGCCAAAGT
AAACTCTGGCGTTTAGCGTACGAAGGAGATTATCCTAAAAGGAACTTCCCTAGTAATAGT
GTAATTTGGAAGGGCATAGCATGTGAAAACCGCTCAGAAACGTCTCCTCAAGGAGCTTC
AACAGTTAATTAAAGATTCTCCACCTGGTATAGTGGCTGGTCCCAAATCGGAGAATAACA
TATTCATTTGGGACTGCCTAATTCAAGGGCCTCCAGATACGCCATACGCTGATGGTGT
TTAATGCTAAGCTAGAGTTTCTTAAAGACTATCCGTTATCTCCACCTAAACTTACTTCA
CACCAGCATACTACATCCAAATATTTATCCAAATGGGGAAGTGTGCATATCCATTCTAC
ACTCCCTGGTGTATGATCCTAACATGTACGAATTAGCGGAAGAAAGATGGTCCGAGTGC
AAAGTGTAGAAAAAATTCTATTAAGTGTATGAGCATGTTGAGTGAGCCCAATATCGAAA
GTGGTGCCAACATTGATGCTTGCATCTTGTGGAGAGATAATAGACCTGAATTTGAGAGAC
AGGTAAAGTTATCCATTTTGAAATCATTAGGATTCTGA

YMR022W, 165 aa (SEQ ID NO 216)

MSKTAQKRLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQPPDTPYADGVFNAKLEF
PKDYPLSPPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKIL
LSVMSMLSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF

YMR118C, 1091 bp, CDS: 501-1091 (SEQ ID NO 217)

GTCTTTCGCTTTATATGTTTCGTTATCCTATCACATTATCAAATGACTTTGTGCCACTG
TGTTTTGACAAAATTACTGTAATATAATCAATAGTATTTACATGTTTGTACCAGAAGTAC
TTGCATCGCATCCAGTTCTCATGCAATATAGTTGTATACCATGTGTTGAAAGGAACCAG
AGTAAACACTTCTACCAGTATTTCTTTACGGTTCGGATCAAAACCATCACTCATTCGGTC
ATCTTACCCTACGATAAAACCAAATTACAAGGAAAAGTATCCCTAATTAGAGATCACTGC
ATCCGTAATAGTTTTTTTTTCTATTTTGGACTTTTGTAAAAAAGGGATTAGGGATATCTTG
CTCATAAAAAAATTGACGAAGATTTTAGATAATGGCAAATAAAAAATGAAATAGTATCAAT
ATACCGAAAAATTAATCACACTCAATGCGACTGTGATAGCTGATAAGTGGAGCTCAGAAA
TATTCAGAAGCGTAAGAATAATGAAAGCAACCATTCAAAGAGTAACATCTGTATTTGGAG
TTCCCCGAGCATCTGTATTCGTGCCAAGAATCAGCACACCATTTATTTTGCATAATTATA
TCTCTAATGGCAGAATGGACCTTTTTTCCAAGAATTCACAATGGCCGCGTATCCAAT
CTGATCTTTGGTCAAGCAACAAGGAAGAGGAGCTCTTAGTATCTCAAAGGAAAAAAGAC
CGATCTCTCCTCATTTAACTGTTTACGAACCTGAAATGAGCTGGTATCTTTCTCTTTAC
ATCGTATATCTGGCGTTTTACTGGCTCTTGGATTCTATGCTTTCACAATTACTTTGGGTG
TGACGACAATAATGGGAATGGATACGACTTTTCAGGATCTAAACAAGTGGTATCACGAAA
AGATGCCTAAGTGGTCCCAATGGGTGGCCAAAGGCTCTGCAGCATATCTGTTTGCATTCC
ATTTTGGTAACGGTATAAGGCATCTCATCTGGGATATGGGCTACGAATTGACCAACCGTG
GGGTATATAAAAACCGGATCAATCGTTTTAGCCGGCACACTCGTCTTAGGAACGTATTTAC
TGGCTCAGTAA

YMR118C, 196 aa (SEQ ID NO 218)

MKATIQRVTSVFGVPRASVFPRISTPFILHNYISNGRMDLFSKEFHNGRVSKSDLWSSN
KEEELLVSQRKRPISPHLTVYEPMSWYLSLHRI SGVLLALGFYAFTITLGVTTIMGM
DTTFQDLNKWYHEKMPKWSQWVAKGSAAYLFAFHFGNGIRHLIWDMGYELTNRGVIKTGS
IVLAGTLVLGTYLLAQ

YMR143W, 1121 bp, exon1: 501-524, intron1: 525-713, exon2:
714-1121 (SEQ ID NO 219)

CCGCTTAGCGCAAACATATCGTGAACCTCGTGCAACAACCTGAGAGGGCAAGGATATACATA
AAAATAGCCTACAAATTCTGAACCTCTGTAAAGGAAGCCTCAATAATAAGGTAGATAGTA
AAGTATACAAGAGAAGAATCCCAAGATGTCAGCTGTCCCAAGTGTTCAGTATGTTTCA
GTTCTGCAGAATGATGTTTGATAGTATCGATAATGGAGTGAGATCAAGAGAAAAAATG
AATATGTCAGCCAACCAAGTTCTGAGTAGGCAGTAAATGAGTACGCATAGTGTATTTATC
CAAAGGAAAGAATTGTTATTTTACAAGCCGAATTGAGATCCAATTAGGCAATGTTTGG
GGAGAGTATTTTGACAAGATTGGTTAAACTACTACGGTCAGTTCCGTAACCAAGTACGATT
GTACACATAAGGAAACAACCTGTAAAGATAAACAATAAGGGCTTCCAATGCCATTGTAAGA

TATCATATTCTTAAACAAAAATGTACAGCGAATATAAAGCCAGCGTCAGTGTCTTCCTGG
AAGGTTGCGCAACTAAAGAAGTTGAAATTAAATGGCAAGCGCTACATTTTCATCCATTT
TCACTCATCAGATGTCCAAGATTTTCGAAAAATAAATATTCTCATTTTCTCTCAATGAA
ATAATTGTTACTAACATTGAATTTCTCTCGTAACTAATTGCATTACTTCTTTAGACTTTTG
GTAAGAAGAAATCAGCTACTGCTGTTGCCATGTCAAGGCCGGTAAGGGTTTGATCAAGG
TTAATGGTTCTCCAATCACTTTGGTTGAACCAGAAATCTTAAGATTCAAGGTTTACGAAC
CATTATTGTTAGTTGGTTTGGACAAATTCTCCAACATCGATATTAGAGTTAGAGTTACTG
GTGGTGGTCATGTTTCCAAGTTTACGCCATCAGACAAGCTATTGCTAAAGGTTTGTGTTG
CTTACCATCAAAAAATATGTGATGAACAATCCAAGAACGAATTGAAGAAGGCTTTCACTT
CTTACGACAGAACCTTGTGATTGCTGATTCTAGAAGACCAGAACCAAGAAATTCGGTG
GTAAGGGTGCTCGTTCAGATTCCAAAAATCTTACCGTTAA

YMR143W, 143 aa (SEQ ID NO 220)

MYSEYKASTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEQSKNELKKAFTSYDRLLIAD
SRRPEPKKFGGKGARSRFQKSYR

YMR174C, 707 bp, CDS: 501-707 (SEQ ID NO 221)

GTCCCATCATTCTTTACACCTCGTACTGTATTTCATGATCATCTATCCATTTTACATACCG
CTCCCTTTAAGATACGTTTATTCGTAACCTCCATTTACCAATCACTATGAGCCGTCACG
TTTCCAAAAAACCTAAACATATGATGCAACCTCCAATGAGACTCAACGTAACATGCAA
GTAAATACAGAAGGTTAAGAGATAGTTGTCTTAAAGGGGTACCGAAAGCATTTAGGGGAG
GCTTAAGGGAGGGTGCCGATCCTATGAAGTATTAATACGTAATGCCAAAAGGAATTGTTG
AACATCTGAAGTGGATAGATTAAATCGTACAGTAATCGTACAGTACTATGTCTTACTGATG
TCGGGAATCTCAGGGGCGACCGCCCCGGCTAGAATTATCTATATAACGGTAAAAAGAAAT
AAAACCTCTATTCTAGTTCTCGCCATTTACCTTGACTTTAATGAACCAATAAAAGAAATTT
CTACAACCAAGACATCCAGAATGAATACAGACCAACAAAAAGTGAGCGAAATATTTTCTAGA
GCTCAAAGGAAAAATTCAGGGCGATGCAAAGGTAGTGAGTGACGCTTTTAAAGAAAAATGG
CTAGTCAAGACAAGGACGGCAAGACTACCGATGCTGATGAAAGTGAACCAACAACTATC
AAGAGCAATACAACAAGCTCAAAGGGGCGGGGCATAAGAAGGAGTAG

YMR174C, 68 aa (SEQ ID NO 222)

MNTDQQKVSEIFQSSKEKLQGDQKVVSDAFKQMASQDKDGKTTDADESEKHNYQEYQYNKL
KGAGHKKE

YMR191W, 1877 bp, CDS: 501-1877 (SEQ ID NO 223)

GGTTCGATACAACACTTGTGCTGGCTGGTATATCAACCATGGGTACGTCAGCATATTGAT
TCGATGTGGCAGTGACGAGAGCCATTCTGTATCGTTCGACAAAGTTTGCATGACTTCAT
GTTGTTTTCGTAGCAGTATTCGTTGGTCCAGATGCAGGAATGCTGGTTATAAAGTTTGTG
TTCTGGTCCACATTCATCTTTGGATGGCGTTGTTGGTGGCGAATTTGTCTTAGGCCTTT
TGTTCCGATGTGCTTTTGGATAGCCTGGAATACGAAATCTTTGTCTTCTGTAAAGTCG
CCGTTTCTTTTAAACATTTGTGCTCCCTTCTTAAGTTATGTGACGGCTTCGTCACCATTA
CCGCTTGTGTGTACGTGTATGATTTTTTAAATATATACAACAATAATCTGTATTTTTTC
CTTTCCTCTAGCCAATGACTCCAAGCTGGCTGATAAAAAACAACTAAACGGTAAAGCCAC
AAATCCGAAATGTATCACCATGATCACCAGCCTGCTAAGTGCCCTCTATTGATCCGTA
TATCAGCTTTTAGATCAGGCTCGAGTTTCTTGTATATGTGCATTGCAAAAGCATAAACA
AATCCTGGCAGCCGAAGCCGGGCAATCCACTTCGAAACGCACGGCTGAACATATAAATA
TAAAGGACATGTGGAGAGAAGCTTCTCTTCTTACATTTTCGATTTTCATGATCTAAAGT
GGTTCTTTTACAATAGAAGAGCACCAACACGAAATATGGCTGTGGTGGTAATAACTGGA
GCATGTGGCTGCGAATGTACGGGTCCACCTCAGGCAGATCACGAAGTCTCTGGACCGAA
CGCTGATCAGTTTGAGCCATGGGAATTTTTCCCAACCAATATAATCGCAATATTTTTGTCA
CTTGGTGGAAAGAGCCTATTTGAGGCTTCTACAGCTTTTAGGAGGGCAAGTGGTTTAAACGG
TATCTCCTCTCAGGAGGAGGAATCGCAAGGTTTGACCATTTTACAGCTGTTCCCAATG
TCAGTAATTTTGCTTCTTTTCCAGAGTGCCCAAGGAGCCCCAAGGGGCTTTTACCA
ACTGGAATATGACTACATCAAAGAGATTATTAGGGCAGAGAGCTTATTCGACTTCCAGTA
TCAAATTTACCAAGAAGCCGTGAATAACATGACTATATCTTTGAGGTGTTTTTCAACT
CACTAGGCGGATTAAATCAGTGCTCCCACTCTAATTCCTGCAAAGCTTATCAGAATGCGT
CTAATGTTACCTCTAAACAGGATCACGTCCAACCAGTTGCCCTTAAAGAAGTTATCTCAAA
AGGATATCAATTTTCAATTCGTAATTTAGAATTTTAAAGATAATGAAGACCCAGAATGAAG
TCGTTGATGAAACAAGCGCATATTACATGGAAAAACCAGGTTTCTATATTGAATTTACCA

TTTCAGAATTTAACGTTAATGGGACATTCTCCGCACCTTTGTCATTTTTAGATCCTTCTT
TGTTAGCGGATTTGGATGAAATGATTAGAAATTACAAATACGAATTAAAATCAATATACA
GTAGTGTGACATGATCTTGCAGAATTATGGATCATTGCCGATAACTTTTCATCGAAATA
AGATTCTGAATACATTTTCCAACTCAACTGTGGTGGAAACAGAAAACTAATTGCAGGTC
TGAATATTGCTACGGGTGTTATTTACGCAGATACGTCTCCCGATATCAGTCTAGAAGGTA
CAAATTTGAATGCTCTGGTTAATGTTGACAATTCAGGAAGCGTATGGTCTTTTGTTAAGG
AGCCCTCGTTTCCCTCTAGGAGCGCTTTTTCACCTATTTTATCAGATGCATCCTATGATA
CTTATGAATTGGTCTAG

YMR191W, 458 aa (SEQ ID NO 224)

MITQPAKCPLLIRISAFRSGSSFLLYVHCKSINKSWQPKPGNPLRNARLNYINIKDMWRE
ASLPSHFADFHLKWWFFHNRRAPTRNMAVGNNWSMWLRMSRVHLRQITKSLDRTLISLSH
GNFSHQYNRNIFVTWWSLFEASTAFRRASGLTVSPLTRRGIAFRDHFPRVFNVSASF
PRVPKGAPRGLFTNWNMTTSKRLLGQRAYSTSSIKFTQEAVERNMTISLRFFNSLGGNLQ
CSHSNSCKAYQNASNVTSKQDHVQPVALKKLSQKDINFIRNLELFKIMKTQNEVVDETS
YYMEKPGSYIEFTISEFNVTGTFAPLSFLDPSLLADLDEMIRNYKYLKSIYSSVDMIL
QNYGSLPITFHRNKIRIHFNSTVVEKLIAGLNATGVIYADTSPDISLEGTNLNALV
NVDNSGSVSVFVKEPSFSPRSASFSPILSDASYDTYELV

YMR230W, 1228 bp, exon1: 501-552, intron1: 553-962, exon2:
963-1228 (SEQ ID NO 225)

ATCAAATATTGATCGAGTTCATATAAAGCTAAAGAGTAGGAAATATACCATCAATGGTGA
GCACCTATTTTTTTTTGGATTTAGATGTGAGACATACTAAAAAAGTTGCTATCAAGCC
TATAATTTGGCTACGTTGTCTTCCGGTGTTTTTCAATTGATTTAAGTTACAACACTCAA
TCTGGGTAATTTGATCTTTTTTAATAATTATTTAGTGACATATAGTTCTTAGAGTTCGC
AGATTTATTTTGTCTATTTTTGGATCGGCGTCTTATAAAATCAAGACATAATACATCCGC
ACATCGCGCATGTGTGGGTGTATATGCCCTTTTCACGATTTTAAAGTTGCGTCTCAAAT
AGTTTCCGAGTTGGAAGCCTGAGTTTTTCAAACAATATAGGAATTAAAGGTATACGTCT
TTGGATACATGTTATTTGAAATGGGGTAGAACTAGCACAACTGAAACCAAGAAAACACAG
ATCATAACTAACCGTTCAAGATGTTGATGCCAAAGCAAGAAAGAAAACAAATTCACCAAT
ACTTGTTTCAAGGTATGTTTGCATTTTTTAGGTGAAATATGCAGTGATATGCTCCGAAAT
GGATAGCAAAGATGATAAATGAAATACAATTAAATTGAACTTGAATATCATTAAAGTG
GTAGAAAACCGATTGTTTCAAAAAGATCTTTGTGGACAAGTACGGCAGTGCATGAATCCG
AAAGAAAAGTGCAACCTAAGCAGAATTCATTATTTACGCGTCCATTTTTATAATGTTT
GAACTTTTGAGTCTTATAGAAATGCTAATATTATGATCAAAGCGATTATATCATTACT
TTACAGTTTTCCGGAGTTTCCGTATTATTGCAAAAGGACCACAAACAATTGAAATCATGAT
ATCGTAAGAAATATTATTACTAACAAGGAAGATCATTGAATTACGATCGCATATCGAAAT
AGAAGGTGTTGTCGTCGCTAAGAAGGATTTCAACCAAGCTAAGCACGAAGAAATTGATAC
CAAGAATTGTATGTTATCAAGGCTTTGCAATCCTTGACTTCTAAGGGTTACGTTAAGAC
TCAATTCTCATGGCAATACTACTATTACACTTTGACTGAAGAAGGTGTTGAATACTTGAG
AGAATACTTGAACCTTGCTGAACACATTGTCCAGGTACCTACATTCAAGAAAGAAACCC
ATCCCAAAGACCTCAAAGAAGATACTAA

YMR230W, 105 aa (SEQ ID NO 226)

MLMPKQERNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLREYLNLPFHIVPGTYIQERNPSQRPQRRY

YNL054W, 3998 bp, CDS: 501-3998 (SEQ ID NO 227)

CCCTTCGCTAAATCATTAAAGAGGTCAATTCATGAAGTTAATTCAGCACCAAAGTTGGACTG
TTAGACACGAGATACACATTGCAGTCCAAATGTGCAGATTTTTCAGATAATTGTCGTCGC
ACAAGACTGCCCCCTCCCGTCTCAGACAGACACAAAATTAGATTTTACGTTTACATAAAG
ATGTACATAACTTGAAAAAACGTTAATCCCTCTTAAATTTAGACCTTGTAAGTCTTCTCG
GCCACTCTTTGTGATATATTGTAGTGCAATATATTGATTCTGTTCTTCTTATTTCTTTGT
CTTAGGCATTTCCGCTTTAGAAAATTCGTTGGGTGGTTTCTGCGACGGGTATCCCCCTTCG
ATTTTGCATAATGATCTTCAATTCTACAATAAAATCAAGTAGATACAGGAAAATATTCC
ATAAATTATAGTGAAATCGCCCTGTATACACCTTATCGTTTCATCTCAGGCAAGTTAAA
GCATTTGGGAAACGTGCTAGATGACAGAAGAAGATAGAAAGCTCACTGTAGAGACAGAAA
CAGTTGAGGCACCCGTGGCAAATAATCTTTTATTGTGCAATAACAGTAATGTAGTAGCAC
CTAATCCTTCTATTCCCTCTGCCTCCACATCTACCTCTCCGCTACACAGGGAATAGTTG
ATGATTCTGTGCTACTGCTAACACCACCAGCAACGTTGTACAGCATAATTTGCCACCA

TAGATAACAATTTAATGGATTCCGATGCCACGTACATAATCAAGATCATTGGCATTTCAG
ACATAAACAGGGCAGGAACATCAATGTCAACGAGTGATATCCCAACAGATTTACATTTAG
AACATATCGGCTCTGTTCATCAACTAATAATAATAGTAACAATGCCCTAATCAACCACA
ACCTCTGTGCATCTCATCTTTCCAATCCGTCATCTTCATTACGAAACAAGAAGAGCTCTT
TGTTGGTAGCTTCTAACCCTGCGTTTGCTTCAGATGTTGAACTCTCGAAGAAGAAACCTG
CCGTCATCTCCAATAATATGCCCTACAAGTAACATTGCCCTTTATCAAACAGCGAGATCGG
CGAATATTCATGGTCCATCATCAACTTCGCGATCTAAAGCGTTTCAGAAAGGCTTCGGCCT
TCTCCAATAACACGGCACCCAGCACTAGTAATAACATCGGCTCGAATACACCTCCAGCTC
CTCTTTTACCTCTACCTTCACTATCACAACAAAATAAGCCAAAAATAATAGAGAGGCCCA
CAATGCACGTCACTAATTCAAGAGAAATACTTTTAGGTGAAAACCTGTTAGATGATACAA
AGGCGAAGAATGCTCCCGGAATTCACCACACACGATAATGGTCCAGTAGCAAAATGATG
GGCTGCGTATACCGAATCACTCGAACGAGATGATAATGAAAATAACAACAAAATGAAGA
AGAATAAAAAACATTAATAGTGGGAAAAATGAACGTAATGATGACACCAGCAAAATATGCA
CTACATCTACTAAAACAGCGCCTTCAACCGCACCTTTGGGCAGTACAGACAATACTCAGG
CTCTCACTGCTAGTGTCTCCAGCAGTAATGCTGACAATCACAATAATAACAAGAAGAAAA
CCAGCAGCAACAACAACGGCAATAACAGTAATAGTGCATCCAATAAAACCAATGCCGATA
TCAAGAATTCTAACGCCGACTTGAGCGCTTCTACCTCTAACAATAATGCAATAAATGACG
ACTCAGATGAGAGTAATTCAGAAAAACCAAAAGGCGGATTTTTCGCTGCAAGGCTGG
CTACAGCTGTAGGTGAAAAATGAAATTAGTGATTCTGAGGAAACATTTGTTTATGAATCGG
CAGCTAATTCGACTAAAAACCTAATATTTCTGACTCCTCCAGCCAGCAGCAGCAGCAGC
AACAGCAACCTCCAAAACAACAGCAACAGCAACAAAATCATGGAATAACCTCAAAGATAA
GCGCCCCATTGCTAAACAATAACAAAAAATTATTAAGCCGACTGAAAAATTCAAGACATA
TTAGCACTGGTGCCATATTGAATAACACAATCGCGACTATAAGCACAAATCCGAACCTGA
ATTCTAATGTGATGCAGAACAATAACAATCTGATGTCGGGACACAATCACCTGGACGAGT
TGAGCAGTATAAAACAGGAGCCACCGCATCAATTGCAGCAGCAGCAACCACCAATGGATG
TACAATCGGTAGATTCTGTATACCTCTGACAACCCAGACAGCAATGTTATTGCCAAGTCGC
CTGATAAGAGGTCAAGCTTAGTATCCCTATCTAAAGTTTCTCCACATTTACTTTCATCCA
CATCAAGCAACGGTAACACAATATCGTGTCCCAATGTTGCCACAAATTTCGAGGAATTGG
AACCAAAACAATGATATTTCAACGAAGAAATCTCTTTCCAATTCTACTTTGAGACATTCCT
CTGCTAATAGAAATTTCTAATTATGGTGACAACAAGGCCCTCTTAGAACAACAGTGTCAA
AGATATTTGATTCAAACCCTAATGGAGCTCCTTTACGGAGATACTCTGGGGTACCGGATC
ACGTTAATCTAGAAGATTACATCGAACAGCCGCATAATTATCCAACAATGCAAAATAGTG
TGAAAAAGGATGAATTTTATAACAGCAGGAACAATAAGTTTCCCATGGTTTAACTTTT
ATGGTGATAACAATGTTATTGAAGAGGAAAATAATGGTGACTCGTCTAATGTAAATCGAC
CGCAACACACTAACCTTCAGCATGAGTTTATTCCAGAAGATAACGAAAGTGATGAAAACG
ATATTCACCTCCATGTTTTATTATAATCATAAGAACGATTTAGAAACAAAACCGCTAATAT
CCGATTATGGTGAAGATGAAGACGTAGATGATTATGATCGCCCAAATGCTACTTTCAACA
GTTACTATGGCTCAGCATCCAACACGCACGAACCTCCATTACATGGAAGGATGCCTTCAA
GATCAAATAATGATTACTACGATTTTATGGTTGGCAACAATACTGGCAATAACAACCAAT
TGAATGAATATACCCCTTAAGAATGAAACGTGGTCAAAGACACCTATCAAGAACAACA
ATAGCATAATGAATGGTAGCATCCATATGAATGGTAACGATGACGTTACCCATTCCAATA
TCAATAATAACGATATTGTTGGTTACTCACCGACAACCTTTTACTCAAGGAAGTCCCAT
TTGTGAAAGTAAAGAATTTTCTTTATCTTGCATTTGTTATATCATCACTATTGATGACAG
GATTCATTCTGGGATTTTTATTGGCCACTAATAAAGAACTACAAGATGTAGACGTGGTAG
TGATGGATAATGTGATTTCAAGTTTCGGACGAGTTGATCTTCGACATCACAGTAAGTGCTT
TTAATCCAGGATTCCTCAGTATAAGCGTTTCCCAAGTCGATTTGGACATTTTTCGAAAAA
GTTCTTACCTGAAGTGCGATTCTAATGGTGACTGTACAGTAATGGAACAGGAACGGAAAA
TTTTACAAATAACGACAAATCTTTTCGTTAGTTGAAGAGAGTGCTAATAATGATATTAGTG
GTGGGAACATAGAGACGGTATTACTAGGAACCGCTAAAAAAGTACAGACACCATTAAGT
TCCAGGGCGGCGCATTTAATAGGAACTACGATGTGTCACTCTCGAGTGTCAAGCTTTTAA
GTCCTGGGTCTCGTGAAGCCAAGCACGAAAACGACGATGATGACGATGATGATGGCGACG
ATGGTGACGATGAAAACAATACTAATGAAAGACAATACAAAAGCAAACCAAATGCTAGAG
ATGACAAAGAAGATGATACTAAAAAATGGAAGCTACTAATCAAGCATGATTACGAATTGA
TAGTCCGTGGAAGCATGAAGTATGAGGTGCCCTTTTTCATAACGCAAAAATCTACGGCTA
TTCAAAAGGATTCCATGGTCCATCTCGGTAAGAAGTGA

YNL054W, 1165 aa (SEQ ID NO 228)

MTEEDRKLTVETETVEAPVANLLLSNNSNVVAPNPSIPSASTSTSPLHREIVDDSVATA
NTTSNVVQHNLPTIDNNLMSDATSHNQDHWHSIDINRAGTSMSTSDIPTDLHLEHIGSVS
STNNNSNNALINHNPLSSHLSNPSSSLRNKSSLLVASNPFAFASDVELSKKKPAVISNNM

PTSNIALYQTARSANIHGPSSTSASKAFRKASAFSNNTAPSTSNNIGSNTPPAPLLPLPS
LSQQNKPKIIERPTMHVTNSREILLGENLLDDTKAKNAPANSTTHDNGPVANDGLRIENH
SNADDNENNNMKKNKNINSNGKNERNDTSTKICTTSTKTAPSTAPLGSTDNTOALTASVS
SSNADNHNNNKKKTSNNNGNNSNSASNKTNADIKNSNADLSASTSNNAINDDSHESNS
EKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSQQQQQQQPPKQ
QQQQQNHGITSKISAPLLNNKKLLSRLKNSRHISTGAILNNTIATISTNPNLNSNVMQN
NNNLMSGHNHLDELSSIKQEPHQLQQQQPPMDVQSVDSYTSNDPDSNVIKSPDKRSSL
VLSKVSPhLLSSTSSNGNTISCPNVATNSQELEPNNDISTKKSLSNSTLRHSSANRNSN
YGDNRKPLRTTVSKI FDSNPNGAPLRRYSVGPVDHVNLEDYIEQPHNYPTMQNSVKKDEFY
NSRNNKFPHGLNFYGDNNVIEENNGDSSNVNRPQHTNLQHEFI PEDNESDENDIHSMFY
YNHKNLETKPLISDYGEDEDVDDYDRPNATFNSYGSASNTHELPLHGRMPRSRNNNDY
DFMVGNNNTGNNNQLNEYTFLRMKRGQRHLSRTNNSIMNGSIHMNGNDDVTHSNINNNDIV
GYSPHNFYSRKSPFVKVKNFLYLAFVISSLLMTGFILGFLLATNKLQDQDQVMDNIVIS
SSDELIFDITVSAFNPGFSSISVSQVDLDIFAKSSYLKCDSDNGDCTVMEQERKILQITTN
LSLVEESANNDISGGNIETVLLGTAKKLETPLKFQGGAFNRNYDVS SVSSVKLLSPGSREA
KHENDDDDDDGDDGDDENNTNERQYKSKPNARDDKEDDTKKWKLLIKHDIYELIVRGS MK
YEVFFNTQKSTAIQKDSMVHPGKK

YNL067W, 1076 bp, CDS: 501-1076 (SEQ ID NO 229)

GACGACTATTGATGCCAGGCAAATTTTGGATTTACTGCTCCTCTTTTAAGAAGACAAGTG
TGTGATATCGTAGCGGTAGGAACCAATTTTGCAATCGATTTACTTACAGCCAAGAAAATC
TATTTTCATGTTTAGCATTGCCATTTCTTCTGTGTACACGTTGTGCTTGCCAGGAAC TA
TAGGAGAGACGTATACAAGCATCAATGTTACGAATGTACGATCCCGTTTGCATCTGATGT
GTAAACTCATGTGGTGCCTGGTGTGTTTCCAAGACTGCACTATTAAGTGGGAATTTT
TTTTTCTTCTAGTGAATTTTAAAGCGACGCACAGGAAAAGTGAAAATTATTTAA
ACGGACGGCAAACATGAAAAAATTAACCAACCATATTTCTATTTCTTTCCCTTTAC
CTATTCTCTTTTGAATAGTTTCTTCTCTCTGAAACGACAATAAACCAAACTCTA
GCCTCCAATAGTCACTAAAGATGAAGTACATTCAAACCGAACAAATGAAATCCAG
AAGGTGTACTGTGTCAGCATTAAGTCCAGAATCGTCAAGGTGTGCGGTCCAAGAGGTACTT
TGACCAAGAAGTTGAAGCATATTGATGTTACCTTCAACAGGTCAACAACCAATTGATCA
AGGTTGCTGTTTCAACCGGTGACAGAAAGCACGTTGCCGCTTTGAGAACCGTTAAATCTT
TGGTTGACAACATGATCACTGGTGTACCAAGGGTTACAAGTACAAGATGAGATACGTCT
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGCTAAATTCATTGAAG
TCAGAACTTTTGGGTGACAAGAAGATCAGAAACGTCCAGTTAGAGATGGTGTACTA
TCGAATCTCTACTAACGTAAAGGACGAAATCGTCTTATCTGGTAACTCTGTTGAAGACG
TTTCCCAAAATGCCGCTGACTTGCAACAAATCTGTCGTGTTAGAAACAAGGATATCCGTA
AGTTTTTGGATGGTATCTACGTTTCCCAACAAGGGTTTCATTGTGCGAAGACATGTAA

YNL067W, 191 aa (SEQ ID NO 230)

MKYIQTEQQIEIPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVFTTKVNNQLIKVAVHNG
DRKHVAALRTVKS LVDNMITGVTKGYKYMRYVYAHFPINVNIVEKDGAKFIEVRNFLGD
KKIRNVPVRDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQICRVNRNKDIRKFLDGIY
VSHKGFIVEDM

YNL075W, 1373 bp, CDS: 501-1373 (SEQ ID NO 231)

TCGATGGATATCCCATCCAAGAACAGGAATACTGGGTTTTTGAAGACCAGAATGGAGATC
TCTGAGGAAGAAAAGATGGTACGTACAATATCACGGCTTGACAATACGAGTATTGCAAC
AGTAATGGAATGGTAATGATGACACCTTAATCAGAGAACGGAAGCACTGGGGCGTAAG
ACGAGTAATGGAGGGCGAATATGATTACTAAGTTAAATAAATCAGATACGATATTTAAAG
TTCTTTCAAAAAAGATAATGTCATATATTTTACTATCTACGCAGTGAAAGAGTTCCTTC
TAATGACACACTATTTCACTTCGGGTAACGGATATTGTGTACTGAAAAATATAAAAAATTT
TATCCCGGAAATGCGATGAGATGAAAATGCATGAAGTAGCGTATATATTGATTGCATGAG
GTTGGACTTGAAAGGGCATATATACTCGGTTTTATCATTGATTCAAGTGTTCCTATAAT
AATAAAACAGTTAAATCGAAATGCTAAGAAGACAAGCCCGTGAAAGGAGAGAATATCTAT
ACAGAAAAGCGCAAGAATTACAAGATTCTCAACTGCAACAAAAACGTCAAATAATTAAC
AAGCGCTAGCTCAGGGGAAGCCATTGCCAAAGGAAGTAGCAGAAGATGAGAGTTTACAAA
AGGATTTTCAGATATGACCAAAGTTTAAAGGAGAGCGAAGAAGCAGATGATCTACAGGTTG
ATGATGAATATGCTGCCACAAGTGGTATAATGGATCCAAGAATCATCGTCACAACATCTC
GTGACCCAAGCACTCGTCTCTCGCAATTTGCCAAAGAAATTAAGTGTATTTCCAAATG
CTGTCAGGCTGAACAGAGGTAATTATGTGATGCCAAATCTAGTGGATGCTTGTAATAAAT

CCGGTACTACAGATTTGGTGGTATTACATGAACATAGAGGTGTTCCAACCTCTTTTGACCA
TATCACATTTTCCACATGGACCCACTGCACAGTTTAGTTTACACAATGTTGTTATGAGAC
ATGATATTATAAATGCTGGTAACCAAAGCGAAGTGAATCCACATCTAATATTTGATAACT
TTACTACCGCTTTAGGGAAAAGAGTAGTCTGTATTTTAAAGCACTTGTTCATGCGGGGC
CCAAAAAGATTCCGAAAGAGTAATCACTTTTGCGAATAGGGGTGATTTCAATTAGCGTTA
GACAGCATGTATATGTGAGAACAAAGAGAGGGAGTAGAGATTGCCGAAGTTGGTCTTAGAT
TTGAGATGAGGTTGTTTGAACGTAGGTTGGGAACTTTAGAAAAAAGGACGCTGATGTTG
AGTGGCAGTTGAGAAGATTCATAAGGACTGCCAATAAAAAAGACTATTTGTGA

YNL075W, 290 aa (SEQ ID NO 232)

MLRRQARERREYLRYKAQELQDSQLQKQRIIKQALAQKPLPKELAEDESLOKDFRYDQ
SLKESEEADDLQVDDEYAATSGIMDPRIIVTTSRDPSTRLSQFAKEIKLLFPNAVRLNRG
NYVMPNLVDACKKSGTTDLVVLHEHRGVPTSLTISHFPHGPTAQFSLHNVVMRHDIIINAG
NQSEVNPHLIFDNFTTALGKRVCILKHLFNAGPKKDSERVITFANRGDFISVRQHVVYR
TREGVEIAEVGPRFEMRLFELRLGLTENKDADVEWQLRRFIRITANKKDYL

YNL096C, 1418 bp, exon1: 501-644, intron1: 645-989, exon2:
990-1418 (SEQ ID NO 233)

AAACACCTACTTATAGACACGACCAAACTTTCCACAACCTTTCATCAGAGAGAAATGTTG
ATCAAGTTGAATGCGTGAAAGTAGCAATTCGAAACAACAACCTACCTGTCATTCTGCATAG
TAGTAGTTACGAAAGGCACAGAAAAATAACAAAAAAGTCAATTTTCTACGGT
CTCCATCCGTACCTCTTTAAATCCGTACATTATTGTTTGTCTTAATTTCAATATTTTCGGA
AAAAGCGAGCGCCCTGGTAAATGTGGTTCAAGCCTGCGAGCCTTTGCTTGGTAACTCAC
CAAATGCAATTCAGTCACGTTCCACACAGTTTGGGTTCAGCCTGGCTTTAGGGAAGAA
TGGGCTCACTAGGCGTTCATAATACGCGGAGGGGAAATACCAAATGCTATTGATTATGG
TTAAAATATGTGTTATTTGACTTTGTATATACAAACAGAGAGAAACCACTAAAG
ACTAGACACATAACTGACCAATGTCTCTGTCCAATCCAAGATCTTATCCCAAGCTCCAA
GTGAGTTGGAATTACAAGTCGCCAAGACCTTCATCGATCTAGAAAGCTCCTCTCCAGAAC
TAAAGGCTGACTTGAGACCATTGCAAATCAAATCTATCAGAGAAGTATGTTAAAGTTAT
ATAATTTGGAAGCAGCAACATTGTGATTTCTTCTAAAGGGGTTCTTTGCAGTAATTTTTT
CAAAAAAGAGTGATTTTGAGCAGTATCTGTATGAAATTTTCATGTGTTTCGAGAAAAATAG
TAATTTCCGAGAGCTGTCAATACCATGAACGTTGCGATGAGCCTTTGAACTATAAAGGCTT
CCTTGGTTCAGTACCAATATCGATGAATAAAATAGAAGCACGCGAAAAAGACCTTACCCCA
AGGAGAAGAATCACAAACCTTTTTTTGTTATGAATGAACCAATTCAGTTACTAATTTAT
TTCAACGCTGCTTGATTCTTATTGTTTAGATTGATGTCACCGGTGGTAAGAAAGCACTAG
TCCTTTTTGTCCAGTTCAGCTTTGTCTGCATACCATAAGGTCCAAACCAATTGACCC
GTGAATTGGAAGAAGAAATCCCTGACCGTCATGTTATTTCTTGGCTGAAAGAAGAACTCT
TGCCAAAACCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAATTTGA
CTGCTGTTACGACAAGGTTTTGGAAGACATGGTTTTTCCCAACTGAAATTGTGCGTAAAA
GAGTTAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTTGTTAGACTCCAAGGATG
TTCAACAAATCGACTACAAGTTGGAATCTTTCCAAGCTGTCTACAACAAGTTGACTGGCA
AACAAATTGTTTTTGAATTTCCAAGCCAGACCAACTAA

YNL096C, 190 aa (SEQ ID NO 234)

MSSVQSKILSQAPSELELQVAKTFIDLESSPELKADLRPLQIKSIREIDVTGGKKALVL
FVPVPALSAYHKVQTKLTRELEKKFPDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKVLEDMVFPTEIVGKRVRYLVGGNKIQKVLDDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSQTN

YNL162W, 1333 bp, exon1: 501-504, intron1: 505-986, exon2:
987-1333 (SEQ ID NO 235)

TTCATCACCATATAGACTAATGCGTTTTTGAACGCCAAACCGCAGTGACAAATAGCAAA
TATGTAGCTGTCTATATCGGCATATAATAACAGTTTTCTACCAAATGCTGTCTTACATTCA
GAGATCTTACATCCTTACATCTAAAGTAAACCTAGACATTTACTTCGAGTTATACTTTT
TTTTTATATCTATTTTTTCTCTTGGCGACATTTAACACCTGAATTCGCCTAACGCCA
GGACTGATCCTGCCAGGGAAGGGAGCTTTGTCTAGTGCCAATAGGCCGAGCAGTAGGAA
GGTTACAGCAGCTGGCCCGCAGAGTGATTGGGTACAGGAAATAGCGCAACCTTCTCTTT
TGCCCGGGAAGGCGGTTCAATCTACCTTCGAAGGGCTAGTACATGAGCGCGAAGGAGGC
AGATAATAGCACCATTAAGTGGTCCAAATGCATCTTGAAATCTAATCCTTAATAGAGGAA
AACAACAATTATCAGTAAAAATGGGTATGTTATAACCATAATTCCTAATGGTGAATAAAA

TCAGGACCAATAAAGAAAAGCTAATTTGATTTTTATTGTCAATGAAATTTTCATAATCGTC
ATGAATGCATAAACAGACACACCTAGCAACTGTATAATCTGCGCTAAAAAGGGCGTATA
CACAAAACATAACGATGCGCAATAAAAGTTTCAGCAGTCAGCAATGAAACCGAGATATGCA
GCAACAGAGTATCATATGCATGGAGGATCCTTTCTGTTTTCTGATAATATGCTCTGAAA
AAGCTCCAAACAGCAGTAGCCTATTTGTGAAGCTCAAAAAAGGCTTCTATTTCCCTCG
CTATCTTCAGATTGTGAGTGATATTCTTTGAGGAAGGAAACGTAGAGGGGATAAGTTGG
ATAACTGTTATTTCTTTTCAATATGCTAGATTTTGCTTACCACCTTACTGATTTTTTCTA
ATAATAAACTTTTTTACTAACATTAGTAGCATGTCTCATCTATTTCTTCTATTTAGTTAA
CGTTCCAAAGACCAGAAAGACCTACTGTAAGGGTAAGACCTGTCTGTAAGCACACTCAACA
CAAGGTTACTCAATACAAAGCTGGTAAGGCTTCCTTGTTTGCCCAAGGTAAGAGACGTTA
TGACCGTAAACAATCTGGTTTCGGTGGTCAAACCAAGCCTGTTTTCCACAAGAAAGCTAA
GACTACCAAGAAGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACCAGAGCCCAATT
GACCTTGAAGAGATGCAAGCACTTCAATTGGGTGGTGAAAAGAAGCAAAAGGGTCAAGC
TTTGAATTCTGA

YNL162W, 116 aa (SEQ ID NO 236)

MVRCLIIYFFYLVNVPKTRKTYCKGKTCRKHTQHKTQYKAGKASLFAQGKRRYDRKQSGF
GGQTKPVFHKAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YNL178W, 1223 bp, CDS: 501-1223 (SEQ ID NO 237)

GGTCCACGTCAGTTCCACACAATAACATTTACGTAGTGTTACGCGAAGCAGTTACATCT
CAACTAACATAATTGCTGGTGAGCCTACAACACTGCATGCGTAAACGTCAACGGGATTAC
GTTAGTATTTTTGGCCGCCGGTAAATTCCTTGTTTTTTTTTCTTGATTTCACTTCTTTT
CATGTTCCATTTGGAATAATCTAATTCCTCATGATTAAATGAGACTGTTTTTTTGGTTCCGT
AACATCCATACCTTTCTGTATAATATTCTTGCTGTAAAGTTTGTTTTTTTTATGAAAAA
AACATTTTCTTTTCTTGAGATGAGGCGCCGCGAGCCTTTCTCCCATGGGCAGTGGTAAAT
TTTCCAAATCAATGCAGCTCTTTGAAATACAACAGCATTTCATACATTTTAAGCAATT
TCTAGTTTGTAGATATTGTTAGATTAGTTTTTGAACATTGTTTTGATAACTGAAAAATAA
ACAGCAAACAACTACAAAAATGGTCGCTTTAATCTCTAAGAAAAGAAAGCTAGTCGCTG
ACGGTGTCTTCTACGCTGAATTGAACGAATTTCTCACCAGAGAATTAGCTGAAGAAGGTT
ACTCCGGTGTGAAGTCCGTGTCACTCCAACCAAGACCGAAGTTATCATCAGAGCTACCA
GAACCTCAAGATGTTTTGGGTGAAAACGGTAGAAGAATCAACGAATTAACTTTGTGGTTC
AAAAGAGATTCAAGTACGCTCCAGGTACTATTGTCTTATATGCTGAAAGAGTTCAAGACC
GTGGTTTGTCCGCTGTTCGCTCAAGCTGAATCTATGAAATTCAAATTGTTGAACGGTTTGG
CTATCAGAAGAGCTGCTTACGGTGTCTGTCAGATACGTTATGGAATCTGGTGTCAAGGGTT
GTGAAGTTGTTGTTTCCGGTAAACTAAGAGCTGCCAGAGCTAAGGCTATGAAATTTGCTG
ACGGTTTCTTGATTCACTCTGGTCAACCAGTCAACGACTTCATTGACACTGCTACTAGAC
ACGCTTTGATGAGACAAGGTGTTTTGGGTATCAAGGTTAAGATTATGAGAGACCCAGCTA
AGAGCAGAACTGGTCCAAAGGCTTTGCCAGATGCTGTCAACCATCATTTGAACCAAAAGAAG
AAGAACCAATTTCTGCTCCATCTGTCAAGGACTACAGACCAGCTGAAGAACTGAAGCTC
AAGCTGAACCAGTTGAAGCTTAG

YNL178W, 240 aa (SEQ ID NO 238)

MVALISKRRKLVADGVFYAELNEFFTRELAEEGYSVGEVRVTPKTEVIIIRATRTQDVLG
ENGRINELTLVQKRFKYAPGTIVLYAERVQDRGLSAVAQAESMKFKLLNGLAIRRAAY
GVVRYVMESGAKGCEVVVSGKLRAARAKAMKFADGFLIHSGQPVNDFIDTATRHVLMRQG
VLGIKVKIMRDPKSRTPKALPDAVTIIIEPKEEPI LAPSVKDYRPAETEAEQAEFVEA

YNL182C, 2168 bp, CDS: 501-2168 (SEQ ID NO 239)

CTTTGATAAAATTAATACGGTAAGATACCGTGTGAACATTATAATAACTGCCACGCTTAT
AGCATGTACGCTATACATTTACGTGCTGAGCTCCTAGGAAAGCTCATGAGCAGCCACTGT
ATCGTGAGCATAACTACAACAAAGAATACACAGCGTCACATAGAGGGTTTTTGTAGAGGA
GAAGTTGAAATAGGACTTGATCTTGGGGGAGAGGGGATTTGAAAGCACCATTTCAGGAGT
ATGTGCTGTAAATTGAAGTGTTAGCGCGCGATTACCTGTAAATAAGAGTGATGATTTGAT
AGCGCCATTCTACATCATATGGCAAATGTTGAAAACTGTACGCGCGAACTAAAATTTTT
TTTTACATCCCCTAAATGAAAATTTTAAATCGATGCCCATTCCAAATATGCTTATTTCGA
AGGACGGCTCTGACAAGGGCATATGCGTTAAGATTGATTGTTCAATATTCATAAAACAGG
ATCTTTCAAGGGACGATAAAATGGATGAGCAAGTTATTTTTACAACAAATACCTCAGGAA
CAATAGCTTCTGTACACTCATTTGAACAGATAAAATTTGAGGCAATGCTCCACTCAATCAA
GAAATAGCTGTGTTCAAGTAGGAAATAAATACCTTTTTATTGCTCAAGCACAAAAAGCAT

TAATCAATGTCTACAATCTGTCAGGTTCTTTCAAAGAGAATCTGTTGAACAGCGCTTAC
CATTACCTGAAATCCTAAATGTCTGGAAGTAGTTGAAAATGATGGTGTGAGTATGATA
GAATTCAAGGTGTCAATCATAATTTACCAGACTTCAATCTTCCGTACCTTTTACTTGGCT
CCACCGAATCGGGTAAATTGTACATATGGGAGTTAAATTCAGGGATTTTATTGAACGTGA
AGCCTATGGCTCATTACCAAAGTATCACCAAGATTAAGTCCATTTTAAACGGCAAGTATA
TTATTACTTCTGGTAACGATTTCGAGAGTTATTATATGGCAAACTGTTGACTTGGTATCAG
CGTCCAATGATGATCCTAAGCCTTTATGTATCCTTCACGATCATACTCTACCCGTGACAG
ATTTCCAAAGTTTCTTCTAGTCAAGGAAAAATTTTATCATGTACTGATACGAACTCTTCA
CAGTATCTCAAGATGCTACCATTAGATGCTATGATTTGAGTTTAATAGGCAGCAAAAAGA
AGCAGAAGGCAAAACGAAAATGACGTTAGTATTGGTAAGACCCCAGTATTGCTTGGCAGAT
TTACAACCTCTTATTCTATCAAATCCATTGTACTGGATCCTGCTGACAGAGCATGCTATA
TTGGTACTGCGGAAGGTTGTTTTTCATTGAATTTATTTTATAAACTAAAGGGTAATGCTA
TCGTTAATCTGCTACAGTCCGCCGGAGTAAACACAGTTCAAAAAGGTAGGGTTTTTTCCC
TAGTGCAACGTAACTCACTAACTGGCGCGGAAAAATGAAGATTTGGATGCACTATATGCCAA
TGGGCCAACTTGTCTGTGAGAATGTCTAAATTCAAATGTGTTCATGCCTAGAAATATCAA
TGGATGGTACATTATTATTGATCGGTGATACGGAGGGGAAAGTTTCTATTGCGGAAATTT
ACTCAAAACAAATCATTAGAACTATCCAACTTTAACTACATCACAGGATTCAGTTGGAG
AAGTGACCAATCTCTTAACCAACCTTACAGACTCGAACGTGGAAATTTACTTTTTGAAG
GAGAATCCAAAGGCAAAACCACTAGTAATAATGGTCACAATTTTATGAAGATACCAA
ACTTACAAAGAGTTATCTTTGATGGTAAAAACAAAGGCCATTTACAGGATATTGGTATC
AGATAGGAGAACCAGAAGCAGAGACAGATCCTAACCTCGCATTACCACTTAACGACTTTA
ATGCCTATTTGGAGCAGGTCAAACGCAAGAATCGATATTTTACATATCGGTAAGGTGT
CAAGCAATGTAAAAGTGATTGACAATAAAATCGACGCCACTTCATCTTTAGACAGCAATG
CCGCTAAAGATGAGGAAATTACAGAACTTAAGACCAACATAGAAGCATTAACCTCATGCCT
ACAAGGAGTTACGTGACATGCACGAAAAGCTGTACGAGGAACACCAACAGATGCTTGACA
AGCAATAA

YNL182C, 555 aa (SEQ ID NO 240)

MDEQVIFTTNTSGTIASVHSFEQINLRQCSTQSRNSCVQVGNKYLFIAQAQKALINVYNL
SGSFKRESVEQRLPLPEILKCLEVVENDEGVQYDRIQGVNHNLPDFNLPYLLLGSTESGKL
YIWFELNSGILLNVKPMHYQSITIKISILNGKYIITSGNDSRVIIWQTVDLVSASNDPK
PLCILHDHTLPVTDQVSSSQGKFLSCTDTKLFTVSDATIRCYDLSLIGSKKKQKANEN
DVSIGKTPVLLATFTTPYSIKSIVLDPADRACYIGTAEGCFSLNLFYKLGNAIVNLLQS
AGVNTVQKGRVFSLVQRNSLTGGENEDLDALYAMQQLVCENVLNSNVSCLEISMDGTL
IGDTEGKVSIAEIIYSKQIIRTIQTLLTSQDSVGEVTNLLTNPYRLERGNLLFEGESKQKQ
PSNNNGHNFMKIPNLQRVIFDGKNKGHLHDIWYQIGEPEAETDPNLALPLNDFNAYLEQV
KTQESIFSHIGKVSSNVKVIDNKIDATSSLDSNAAKDEEITELKTNIEALTHAYKELRDM
HEKLYEEHQQMLDKQ

YNL190W, 1115 bp, CDS: 501-1115 (SEQ ID NO 241)

AATGCGCTCCCGTACGTGAGTGGCTGTTGCTGAAACGAGACAATTTCTCAATTCGTTTGT
TTGTGTACTGTATTTGTTATCTTTACTATATATATGTTGTTAAGTTTCTTTTACCAATTA
GTGCTCACTTCTCTCGTCTTTTATTAGGTGTGTGTGTTGCGTAATTTTCGTTTCGCTG
ATTACTTTATATAGTGTAGTTTGTCTTGAATGTAATAAAGACTTCTGTTTATTTTGT
TTGTTATTTAGAAACAGTCTATCTGGTTTAACTTAAACGAGTGAGCTTAAGATAATCTGA
CTACAAGAAAACCAAGCTTCTATTACTTTGTTTCTTTCTCTTTTTTCTTTTTTGAATAAA
GAATTTTCTTTAAGGAGTAACTTAAGCATTTAGCTGCACATTAAACACTTTTTTTTTTA
CTTCTAACTCACACACTTTTGAAGAACATTTATTTTTTTCGACCTTCTTTCCCAAATACC
CAGCGCTTTATAATTGAAATATGAAGTTCTCTTCTGTTACTGCTATTACTCTAGCCACCG
TTGCCACCGTTGCCACTGCTAAGAAGGGTGAACATGATTTCACTACCACTTAACTTTGT
CATCGGACGGTAGTTTAACTACTACCACCTCTACTCATACCACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACCCCAACCACACTGGTACTCACAAGTACGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAACCATAACCGGTACTCACAAGTATGGTAAGT
TCAACAAGACCTCCAAGTCCAAGACTCCAAACCACACTGGTACTCACAAGTACGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAACCATAACCGGTACTCACAAGTATGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAACCATAACCGGTACTCACAAGTATGGTAAGT
ATGCCGCCCTGGTCCATCTAATTTCAACTCCATAAAATTTGTTTGGTGTACCGCTGGTA
GTGCTGCCGTAGCCGGTGCCTTATTACTATTATAA

YNL190W, 204 aa (SEQ ID NO 242)

MKFSSVTAITLATVATVATAKKGEHDFTTTLTSSDGLTTTTSTHTTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTKHDTTTYGPGEKARKNNAAPGPS
NFNSIKLFGVTAGSAAVAGALLL

YNL208W, 1115 bp, CDS: 501-1115 (SEQ ID NO 243)

GGTTATACACATATATATATATTTTTCATTTTAAATGTCTTAGCTTTTGTATCTTAGATGAA
GTTTTAGTTCTGTATATACGATCAAGATATCATACAATCATAAATTCAATTATTTCTTCT
GTTTCCCCCTTTGAGGCATCAAACGAGTGTGTTGACTGATACACACCAACATACTAAGGCA
ACTTTTCTGGCTGCCCAAAGCTGTGGCAGTATGAAACTGCTTTTCGGCTGCATAAAACA
ACCATGTGGAGTTTTTACTGTATTTCGCTTTTCGCCCCGCTAGCATTCTTCGTTTCATGCTA
AAAAATGAGGCGTGGGCTAATATTCAGTATTAATAATTCCGGCACCCGCACAGCCCATACC
GGAAAAGGGGCTGGCTGTGGGCTTTGGCAAAAACTCAATCTGAGCAGTCATTTATAAAG
AAAGACTTTAATTTGTCTTTGCTAAACACTTTGTAAGCCTTCCAAATATAGATCACTTAAGA
CAATCTAACCAAGTGTCCAAATGTCTGCAAAACGAATTCTACTCAAGTGGCCAAACAGGTC
AATATAACCAGCAAAACAACCAAGAAAGAACTGGTGCTCCAAACAACGGTCAATATGGTG
CCGACAATGGTAACCCCAACGGTGAACGTGGTTTATTTTCCACTATTGTAGGTGGCAGTG
CCGGTGCGTACGCTGGATCTAAGGTGTGCAACACCATTCCTAAGTTGAGTGGTGTGCTGG
GCGCCATAGGTGGTGCTTCCTTTGCCAACAAGATATCTGATGAGCGTAAAGAGCATAAGC
AACAAGAGCAATACGGCAACTCAAACCTCGGAGGTGCTCCTCAAGGTGGACACAACAACC
ATCACCGTCAGACAATAACAACAATAACGGTGGATTTGGCGGTCCAGGCGGGCTGGCGG
TCAAGGTTTCGGAAGACAAGGCCCAAGGATTTGGAGGTCTGGTCCACAAGAGTTTGG
TGGTCCAGGTGGCCAAGGATTCGGTGGTCCAAATCTCAAGAATTCGGCGGCCAGGTGGC
CAAGGATTCGGTGGTCCAAACCCTCAGGAATTCGGGGGCCAAGGTCTGTCAGGATTCAAT
GGCGGTTACGTTGGTGAATGGCTCAACAGAGTGA

YNL208W, 204 aa (SEQ ID NO 244)

MSANEFYSSGQQGQYNQNNQERTGAPNNGQYGADNGNPNGERGLFSTIVGGSAGAYAGS
KVSNNHSLKSLGVLGAIGGAFLANKISDERKEHKQQEQYGNNSNFGGAPQGGHNNHHRQTIT
TITVDLAVQAALAVKVSSEDKAHKDLEVLVHKSILVVQVAKDSVVQILKNSAARWPRIIRWSK
PSGIRGPRSSRIQWRFTLVNGSTE

YNL210W, 1313 bp, CDS: 501-1313 (SEQ ID NO 245)

TCATAACGGGTTCTTTTCAAAAAACCGTAAAAATTTGAGGTACACCAACTAAATACAAA
TTGTTTCATCACGGTGACTATATCAAGAACTTCGTAAGGAAACATTTAGAAAACCTCAATA
TAGTAAAGTTTCATCAGCAATCTTATCTGAGTAATATATCTACGATCTAAATATAGGAT
GATCTGCCAGTTTAGGAATCGTACTGTAGATTGCTCTTTGGCGACAGATATAGTGAAATAC
CTTTTACAAAGTTGGATACAGGTTGCCATCACTACCGCCATTTCACTAGCAGAGTATG
TTGAGAAAACCGTAAACTTTGAAAGTTGCAGATGCAGAAATATATATCTGGTTTTGTAGTT
CTATCCGCTAAACGGGACGATCGCATTTTAGCCGCCGACAGTGTTAATATAAGTAATGAA
CTTGGGTTAATTTGATTACGCGTCACAGCTACTAATAAAATAAGACCGAGAGTTTTAATC
AGCTAGTGATACCAAACAATGAGTAACCAACACAGCCCTCAGCCATTTTGTGTTGGACA
CCAAATTTGGTGAAACTATTAGAAGAGCTCCAGGAGGGAAAGCAATTCACAAATAAAAAACA
TATTTCCCGGAAAAAGCATTATATTTGAAGCTCGCTCTTGATTATTCTTTCTTCAGAAAGA
ATTTACTAGAGTTTGTGCGTCCACCCTTGACAAGATAAAAAGGAGTCATTAGACCAAACATG
ACACTATATATATTTTGTGCTGTGGAGGTGGATCTCCTCAATCTGGTATTTACCGACA
ATATATTTGAAATATGTTTGGCCAGGTTTGTTCAGGGAGGACTTGAGGGTTTTTAATA
ATACTTTTACACATATCACGATAACCGCTACGTATTCTCCAAGAAGACTTTTCTCAAT
TGTTCAAAAAAATCAAACTAAGGCTTCTGTACTATGTTTTACAGTTGAGGAAATTTTTC
TGACAAACCAAGAAATTTTACCTCAAACTCAACAGTGGCAGAACTGCAAAAGAGCACTA
ATAAAGTACAGACAAATGGGCGGCAACGGCACGATTTTCATAGTCACTCTAGAAATAAAG
TGAACAAAACACAAATCACTTTTCTCATTGGAGCTAAAGGAACGAGAATTGAAAGCTTGA
GGGAAAAATCAGGCGCCAGCATAAAAATAATACCTATTAGTGATAAAATGACTGCACATG
AAAGGAACCAACCTGAATCTGTTCAACAAACAATACTAATTTCCGGGTGACTTATACTCAA
TTGCATTAGCCGTCACCAGTATAGAGTCTGCATTAATTACTTTGGATTTATAG

YNL210W, 270 aa (SEQ ID NO 246)

MSNQHSPPQFCLDTKLVLLEELQEGKQFNKNIFPEKALYLKLALDYSFRRKNLLEFCV
HLDKIKGVIRPNYDTIYILCLLEVDLNLVFTDNILEICLPRFVSREDLRVFNNTFYTYH

DNRLRLQEDFSQLFKKIKTKASVLCFTVEEIFLTNQEILPQNSTVAELQKSTNKVQTNG
PQRHDFIVTLEIKLNKTQITFLIGAKGTRIESLREKSGASIKIIPISDKMTAHERNHPS
VQQTILISGDLYSIALAVTSIESALITLDL

YOL031C, 1766 bp, CDS: 501-1766 (SEQ ID NO 247)

AGTTTTTTTTCTCGAGAAATTGTGAACAAAAGAAAGCAAAGACACAGAAGATGATAAGAG
AGAGAAACAACGAAGAAAGAAACAACAAATGTTGGGGTTCACCCGAGAGATATTGACATACT
GACCTTAGAAAAGGCATTACTGAGGCTACTGACTAAAGCGCGTTACATAAATGCATAGTA
TATTTCTTGTGTATACGCAGCGGCCAACTAGATCAAAACGTAAATAGCGGGTGAAGTGTTCTGGA
TCTGCAGGTTTGGAGGCCGCAACTAGATCAAAACGTAAATAGCGGGTGAAGTGTTCTGGA
CGTTAGAAGTAACGTCCGCAGATCGAAGCTAAACACGAGATTAGATTTCGGGTAACGGAA
TTGTGATAAATTAAGAAAGACCAGACTATGTGAAAAGGCCACGTAAATGATAGAGCACACA
TTAGCAACTATAATAGACTAGTTTTTCGCATCGCTGGAAGTTCTCGATATTGAATATCACT
TCCAAGAACGCAAACCTAGAATGGTCCGGATTCTTCCCATAAATTTGAGCGCCCTATCTT
CGAAATTAGTGGCGAGTACAATATTGCATTCCATACACTCAGTGCCATCTGGAGGCG
AAATCATATCTGCAGAAGATCTTAAAGAACCTTGAAATTTTCAGGGAATTCGATCTGCGTTG
ATAATCGTTGCTATCCTAAGATATTTGAACCAAGACACGATTGGCAGCCCATACTGCCAG
GTCAAGAACTCCCGGTGGTTTGGACATTAGAATAAACATGGACACAGGTTTAAAAGAGG
CAAACCTAAATGATGAGAAGAATGTCGGTGATAATGGTAGCCATGAGTTAATTGTATCTT
CAGAAGACATGAAAGCATCGCCTGGTGACTATGAATTTTCCAGTGATTTCAAAGAAATGA
GAAACATCATAGATTCTAACCCGACTTTATCTTACAGGACATTGCCAGATTGGAGGATA
GTTTTGATAGAATAATGGAATTTGCGCATGATTACAAGCACGGCTACAAAATTTATTACCC
ATGAATTCGCCCTCTTGGCCAACCTTAGTCTCAATGAAAATTTGCCGTTAACATTGAGAG
AGCTCAGTACTAGAGTCATTACCAGCTGCTTGAGAAACAATCCTCCTGTAGTCGAGTTCA
TTAATGAAAAGTTTCCAAATTTTAAAAGCAAATCATGGCCGCTCTGTCAAATTTGAATG
ATCTTAACCACAGATCCTCTAATATCCTAATAAAAAAGATACTTGTCATTTTAAACGAAT
TACCTGTACATCCGAAGATCTTCCCTATATCTACTCTACGGTTGTTTACAAAATGTATATG
AAAGAAACAACAAGGACAAACAGTTACAAATAAAAGTCTCGAGTTGATCAGCAAAATTT
TGAAGGCCGACATGTACGAAAATGACGATACAAATCTAATTTTGTCAAAGAAATGCTG
AGAATTTGGTCTCAAATCTGCAAGAGTGGGCAAACGAGTTCCAAGAGATGGTCCAGAACA
AAAGTATAGATGAACTACATACAAGAACGTTTTTTTGACACCCCTTTACAACCTGAAGAAAA
TTTTCAAAGTGACATCACGATCAACAAAGGGTTTTTGAATTGGTTAGCGCAACAATGTA
AAGCCAGGCAATCTAAGTTGGACAAATGGGCTCCAAGAGAGATACGAACAGACTCAT
TTGATAAGAAACTTATCGACAGCAGACACTTGATCTTTGGCAACCCCATGGCTCATAGAA
TAAAAAATTTAGAGATGAACTCTGA

YOL031C, 421 aa (SEQ ID NO 248)

MVRILPIILSALSSKLVASTITLHSSIHVSVPSSGGEIISAEDLKELEISGNSICVDNRCPK
IFEPRHWDQPIILPGQELPGGLDIRINMDTGLKEAKLNDEKNVGDNGSHELIVSSEDMKAS
PGDYEFSSDFKEMRNIIDSNP TLSSQDIARLEDSFDRIMEFAHDYKHGYKIITHEFALLA
NLSLNENLPLTLRELSTRVITSCLRNNPPVVEFINESFPNFKSKIMAALSNLNSNHRSS
NILIKRYLSILNELPVTSEDLPYSTVVLQNVYERNNKDKQLQIKVLELISKILKADMYE
NDDTNLILFKRNAENWSSNLQEWANEFQEMVQNKSIDELHTRTFFDTLYNLKKIFKSDIT
INKGFLNWLAAQQCKARQSNLDNGLQERDTEQDSFDKKLIDSRHLIFGNPMAHRIKNFRDE
L

YOL048C, 821 bp, CDS: 501-821 (SEQ ID NO 249)

TAAGTACATGATTTTTGTGTTCATGATATGACTTGTTTTATGACTAACATATTTAATTT
TTATTTGTAAACCGTAGGGGTTTTATGAAGTGCTGACGAATCCTGTTTATTGGAAGCATA
TTTTACTGTTTGC GGTTTGCTATGCCCTGATTTTTGTCACTATTGCTGGTCTCTTTTATG
TCACACTGTGACCGCTTTTAGTGACATGGGCCATACTGTTATTAGGGCCCTCTGGTGGA
TACTGGTTTCAATTTCAATGGATTTTACAAACGAATGTCTTGACTGCCCTTTGTTGTAGAA
CACTGGTCTGACCCATATTACGAATCAGATATTTGATATATCTTTGGTGTGCAAGACC
AAGATGAATTTCTAAACGAGGTGAAGGTATTCCTAAACCACAAAAGCCACATAGAAAAA
TCGATGAACCTGATGCGGTGAGAAATTTCAACACAATAAAGGGAAGTCGGATTTTTAAGA
TTCCCACTACTATTTCAGAAATGTTTTTAAAGTCTCCAATTTTACTTCACTAACATTAC
TGTCGCTAATTCCTATTGTAGGACCAATCTGGCAAATCAACTAATGGCCCCCAAAAAGAA
CCTTTACCTATTTGCAGAGGTACTTTTTTACTAAAGGGATTTCAGTAAGAAACAGGCCAAAG
ATTTTCAGTACGAGCATTACGCAAGTTTCATATGTTTCGGTATGTCTGCCGGTCTACTAG
AGTTAATACCCCTCTTCACAATAGTACCATATCTAGCAACACTGTTGGTGCAGCTAAAT

GGTGTACTTCGCTACTAAAGGGTGAAAGAAAGAAGGAATGA

YOL048C, 106 aa (SEQ ID NO 250)

MFFKVSNFTSLTLLSLIPVGPILANQLMAPKRTFTYLQRYFLLKGFSSKKQAKDFQYEHY
ASFICFGMSAGLLELIPFFTIVTISSNTVGAAKWCTSLKGERKKE

YOR010C, 1256 bp, CDS: 501-1256 (SEQ ID NO 251)

ACATTTCCCAAAAAAGACATTTCTGTCCAAAAGTAGAAGGCAAGAAAACCCTGGAGGAAT
CATAGGCAAAGAAAAGAAAAGAAGATTTCATCTTTAAACTACCTTTCAAGCCTTTATTC
GTTCCCTCGTAAAGGACACACGAAAAAATAAACAGTACCTTGCAGAAGGAGTGCAGAGTT
AGGTGCGAGGGAATCCTTGAAAGCCAAGAGTTTTTTTTCCGTAATGATCTCCCAAAGCAA
CCATCAACATTGTGGTGAAAGTTTAGTGTAAGATGTTCTACTGAACTATCTTAATAGCT
GAGCATCATGTGAGTAAACGAGTAAGCAAGAAAACAACAAAGTAATGTTCAACTTTTCGTA
ACTACGGAAAATAATATATAAGTAGTTAACGAAATTCGAACAATGAGAGCTCTCACATAT
CATCTTCTTTTCCAGTTTAGCCATTATCAGCACAAATAACAAAACACACTCGTACACTC
GCTTCAACTATAACAAAAAATGGCTTACATCAAGATCGCTTTATTAGCTGCTATCGCTG
CTTTGGCTTCTGCCCAAACCTCAGGAAGAAATTGACGAATTGAACGTTATTTTGAATGACG
TTAAGTCCAACCTTGCAAGAATATATTAGTTTGGCTGAAGATTCTTCATCTGGATTTTCCT
TAAGCAGTCTGCCATCTGGTGTGTTTAGACATCGGTTTAGCTTTGGCTTCCGCCACTGATG
ACTCCTACACTACTTTGTACTCTGAGGTTGACTTTGCTGCTGTTAGCAAGATGTTGACCA
TGGTTCATGGTATTCTTCCAGGCTTCTACCAGAATTGGAATCCTTGTTAGGAACCTCTA
CCACCGCTGCCCTCTTCTACTGAAGCTTCTTCTGCTGCTACTTCTTCCGCTGTTGCTTCCCT
CCAGTGAAACTACTTCTTCTGCGCTCGCTTCCCTCCAGTGAAGCTACTTCTTCTGCGCTCG
CTTCTTCCAGTGAAGCTTCTTCTTCTGCTGCTACTTCTTCTGCTGCTGCTTCTTCCAGTG
AGGCTACCTCTTCCACCGTCTGCTTCCCTCTACCAAGGCTGCCTCTTCCACTAAGGCTTCTT
CCTCTGCTGTTTCTTCAAGCTGTTGCTTCTTCCACCAAGCCTCCGCCATTTCTCAAATCA
GTGATGGTCAAGTTCAAGCCACTAGCACTGTTTCCGAACAACTGAAAACGGTGCTGCCA
AGGCTGTCATCGGTATGGGTGCTGGTGTCTATGGCCGCTGCCGCCATGTTATTATAA

YOR010C, 251 aa (SEQ ID NO 252)

MAYIKIALLAIAALASATQEEIDELNVILNDVKSNIQEIYISLAEDSSSGFSLSSLPSG
VLDIGLALASATDDSYTTLYSEVDFAAVSKMLTMVPWYSSRLLPELESLLGTSTTAASST
EASSAATSSAVASSSETTSSAVASSSEATSSAVASSSEASSAATSSAVASSSEATSSSTV
ASSTKAASSTKASSAVSSAVASSTKASISQISDGQVQATSTVSEQTENGAACKAVIGMG
AGVMAAAAML

YOR019W, 2693 bp, CDS: 501-2693 (SEQ ID NO 253)

CATTGATCTCGAGCACAGCTGCTCTTTCTCTCAATGAATTACGTTATATGTTAATCACA
CAAGCATCAGTTTTTTCATCGCAAAGAAAATATTAGAGTTCTTGCAATTCAGATGTACC
TCAATTAATAACTCAATCACCTCCTATGTTCTTGTCTGGTAGTACTGCTTTTGTCTTAATT
ACTGCTGAATCAGCCTTCTAGAAGACCGTTCTGTTTCAGCCGCTCGCCCCTTTTCAAAGC
TTGCGCGGCTGAGTTTTATGAGGGGCGGCTTTTTTGTGAATGGCAATCTACCATTATTAG
TAGCAATATGATTTGCAGATAGATACATATATATCCTTCTGGGTTTCATGTCTCGTTACCA
TCCACACTAATGCATAGGACCAGAAAGAAAGGACATCGAATCCAACACGTATTAATAA
GGACTCCTCATTAATAAGGCTTTTAATATTCAACTTGCTATAGATCACGCACCCTTTTGG
CAAGTCAACCTTAATATTATGATTTCTGTTTGCCACAAAATGACTTGCAAAAATGCT
ACAGAAGCCTCACATTGATGTTCCAGGACAACAATTCGAAGAGAGAAATGAACAAAACC
TTAAAAAACGGGCCAAAAGAAAGGCAGTTTCCAACCATCTGTTGCCTTTGACACAGTGC
CTTCCACCGCTGGTTATTCTTCTATAGACGACAGCAGGGAAGGATTCAAAGGTGTACCTG
TTCCCAACTATTACACGATGGAAGAGTGCTATGACGATGAAACAGACTCTTTTTCGCCAA
ATTTGCAATATTATTGAGAGATACATCCAAATCATCACCTTTTCTGAATACATAGAAAAG
AGAACAAATCTGAATCCAGTAGTTTTTCCAATGAGATCCTCAAAGTTGTTGGAAAAGAAAT
CTGACATCAAAAAATATTCTTGGTATCCAAGAATGGAAAAATAGTGAGGAGAGACTATC
CAAGCACGCCAGTAATTGTCAACGAAACGTTGATGATAAACAGGTTTGAAAAGAACTGGA
TAAAGTTATGGCGCCAAAGAAAACACAAATAAATGAAAGGCTGAATGACAAAAAAAAT
GGTTTACTTACCCAGAACTTATCTTCTCTGAAGAGCGTATTAAACCGTTATATAGAGGAG
ATGATAGTGACCATGTACAAAAGAACAAAAGAAAGCATAAAATACTTCAACAAAAGG
TCGGATATCCCAATAACCTAAGACAATAGTTTGTACATTAAACGAAAAAACATACGT
GGGTTGCCCTAGACTGGACAGTCTACAAGTTTGACGAAATCTTGATCACATTGTTGTCA
TAACTACACTGCCAAAATGATTTCTAACAGGAAAAAACTGCAAAAGATGATACAGAAT

GGGCACCGGGATATCAAAAAGAAGTAATAGATCAAAAATTAAACGACATTTTTGATTATA
TTTTACAGCTAGTAAAAAGTGGTCAAAATATCCGTCAAAATTACTTTAGAAATAATTGTAG
GCAAAATTAAAAAAGTCTGGTAGATGTCATTAATGTCCATACTCCAGATTTCTTAGTTC
TTGCTACTTTAAAGCAGCAGCGAAATGAGAATCTTATTACATATAAATCCAAAAAGCTGA
CAGATGTCTTTCTGTAGTTATCCGATTCCACATTTGTTGTTCCCTCGAAACGAATGT
ATTCGTTCGAACTGAATCTACAAAGAGAAGTAAATGAACATTATGTCTCAAAAAATCATA
TGAAGCACGAACACACTGACGTTGAGAGCATGAGCAGTTCAATGTTCAAAAAAATACAA
TATCAGATATTTCTTCACATATTTCCGTAGATTCGTACGCCGAAGATTTCAAAGGCAAG
GCTACATCAAAAAGCAGTTCAACACCTCTAATGATTCCATTCCAAGAAAATTGACCGGTC
TCGCCCAGCATTCAAGAAGGAAGATCACGGGTGATATAGAAAAATTACAAGACGATGAGA
AAGATAGAGAATGTACTAAGGAAAACTTTTGTGTAAGAAAAATTGATATCATAATTAGAG
AGTCATTGAAGTCTTCTTTAGCGATAGAGACGTTGCCTGGTAAAAATGTATCGCAGTCCA
GTCACGGTGACCAATTTCCAGCTTTAAGAATGCTTTGATAGGCAATGGGTGCAAAAAACA
CAAAGTTTAGAAAACTTTAATACCATATTTCTTCTCAGAGGAACAAAATACCACAACAA
CTATTAACTCAGTAGCTCGCCTACGTCCCAATCAAGTTTGCAACCTCTGTAAAAACACA
AAGATGGAAGAGCCGCCCTTGGCAAAGCCAGAAATCTGCCTGATATAAGGCACAGTATTT
CCTTCGACAAAGAAAAATTCCTTTGATCCATCTGATAAAAGCAGTAGTGTGATAATAGCA
TTCCTTTGAGGAAAGTTAAAAGTGCCGGTGCCTTAAGAAAAAGTCAAACTAATGACTCCT
CAAGTAGTGACGGTCAAAGAAAAGCTCGTCTAGTTTTAGTACTGTGAACACCTTCACTG
GGGGTGGAGTTGGGATTTTTAAGGTGTTTAAAAGTGGAAGTTCTCTGGAAATAAATCAT
CCAGTAGAAGGAATAGTAGCAGTGGCGATGTTTTTGAAAGTGATGATCGTAACGACAAGA
AAAAGAAGAAGAAAAAAGAAGAAATCATTGTTCTTATTTCGGCAAAATATGA

YOR019W, 730 aa (SEQ ID NO 254)

MISVCPQNDLQKCYRSLTFDVPQQFEERNEQNLKKRAKKKGSFQPSVAFDTPVSTAGYS
SIDDSREGFKGVFPVNYTMEECYDDETSFSPNLQYYLRDTFQSSPFLNTRKENKSESS
SFPMRSSKLEKNSDIKKYFLVSKNGKIVRRDYPSTPVIVNETLMINRFEKNWIKLWRQR
KLQINERLNDKKKWFTYPELIFSEERIKPLYRGDDAPCTKEQKRKHKILQOKVGYPNPN
KTIVCHINGKKHTWVALDWTVYKFARNLDHIVVITTLPKMISNRKKTAKDDTEWAPGYQK
EVIDQKLNDIFDYILQLVKVVKISVKITLEIIVGKIKKSLVDVINVHTPDFLVLATLKHE
RNLNLITYKSKKLTDFVPVSYPIPTFVVP SKRMYSFELNLQREVNEHYVSKNHMKHEHTD
VESMSSSMFKKNTISDISSHSVDSYAEDFKRQGYIKKQFNTSNDISI PRKLTGLAQHSRR
KITGDIEKLQDDEKRECTKEKLLKKIDIIRESLKSLLAIETLPGKNVSQSSHGQDIS
SFKNALIGNSKNTKFRKSLIPYSSSEQNTTTIKLSSSPTSQIKFATSVKHKDGRAAL
GKARNLPDIRHSISFDKENSFDPSDKSSSDNSIPLRKVKSAGALRKVKNTNDSSSAGSK
KSSSFSTVNTFTGGGVGIFKVKSGSSSGNKSSSRNSSSGDVFESDDRNDKKKKKKKK
KKSFLFLFGKI

YOR027W, 2270 bp, CDS: 501-2270 (SEQ ID NO 255)

AATTTTCCCCCGTCATAAGTTCTTATACACGGCTGGCTCTGATGGCATAATTTTCATGCT
GGAACCTACAAACCGCAAGAAAAATAAAAAATTTTCGCCAAATTTAACGAAGACAGCGTGG
TTAAATTTGCTTGTTCGGACAATATTCTATGTCTGGCAACTTCTGATGATACTTTCAAGA
CAAACGCCGCAATTGACCAAACTATTGAACTAAACGCAAGTTCAATATACATAATATTTG
ACTATGAGAACTGATATCTTCGTGAAGATTTCGTGTAGTATGATAGAACATTCCAGAAAAA
AAATTCAGATTTCATCGCTCTCTCTTCGCTTCTCCTCCTTTAAGGAATAAAGAAAAAATCA
CATACATAGATTAAAGTAAATAGGATCTGCTAGAAAAATTATATATAGATCAATCATCTTA
TTAAGGTATCTTGTTTAAGCCCAAAAGTCTGCTCCCAATTCCTCACTGTAGCTACTAAA
ACAACCTATACGCAAGAAAGATGTCATTGACAGCCGATGAATACAAACAACAAGGTAACG
CTGCATTTACCGCTAAGGATTACGATAAAGCGATAGAGCTCTTCACTAAAGCTATTGAAG
TTTCTGAAACTCCAAACCATGTTTTATATTCTAACAGGTCCGCCTGTTATACTTTCTTTAA
AGAAATTTAGTGACGCATTGAATGATGCTAATGAATGTGTCAAAATCAATCCATCTTGGT
CTAAGGGTTATAATAGACTCGGTGCCGCCACTTAGGTCTTGGCGATCTCGACGAAGCTG
AAAGCAACTACAAAAAGCCTTGGAGTTGGATGCCAGTAACAAGGCCGCCAAAGAAGGAT
TGGATCAGGTTTCATCGTACCCAACAGGCAAGACAGGCACAGCCTGATTTAGGGTTGACAC
AGTTGTTTGTGCTGACCCAAATTTAATTGAAAATTTAAAGAAGAACCACAAAACCTAGCGAAA
TGATGAAGGACCCTCAATTAGTGGCTAAACTGATTGGGTACAAACAAAATCCGCAAGCTA
TTGGCCAAGATCTGTTTACTGATCCAAGATTAATGACCATCATGGCTACATTGATGGGGG
TTGATTTAAACATGGATGATATAAACCAATCAAACCTCCATGCCAAAGGAACCGGAAACCA
GTAAAAGCACTGAACAAAAGAAAGATGCTGAACCACAAAGCGATTCCACTACGAGCAAGG
AAAATTCCTCTAAAGCACCAAGAAAGAAGAAAGTAAGGAATCCGAGCCAATGGAAGTTG

ATGAAGATGACTCTAAAATTGAGGCCGACAAGGAAAAGGCCGAAGGTAACAAGTTTTTACA
AGGCACGTCAATTTCGATGAAGCTATAGAGCTACAACAAGGCGTGGGAACGCATAAAG
ATATTACCTATTTAAACAACCGTGCTGCTGAATACGAAAAAGGCGAATACGAGACAG
CTATTTCTACCTTGAATGATGCTGTTGAGCAAGGTAGAGAAATGAGAGCGGATTACAAGG
TCATTTCCAAATCATTTGCGCGTATTGGTAATGCCTATCACAAATTGGGTGACTTGAAGA
AAACTATAGAATACTACCAAAAATCATTGACCGAACATCGTACTGCTGACATTTTGACCA
AGTTAAGGAATGCTGAAAAAGAATTGAAGAAAAGCTGAGGCGGAGGCGTATGTTAACCCCTG
AAAAGGCGGAGGAAGCCCGTCTTGAAGGTAAGGAATATTTTACCAAGAGTGATTGGCCGA
ATGCTGTTAAGGCTTACACTGAAATGATCAAAAAGGGCACCTGAAGATGCTAGAGGATATT
CTAATAGAGCTGCTGCACTAGCGAAGTTAATGTCTTTCCCTGAAGCTATCGCAGATTGTA
ACAAAGCCATTGAAAAAGATCCAAATTTTCGTGAGAGCTTATATCAGAAAGGCCACCGCAC
AAATTGCTGTTAAAGAATATGCTTCCGCTTTGGAAACACTAGATGCGGCCAGAACCAAG
ATGCTGAAGTGAATAATGGTCTAGTGCAAGGGAAATTGATCAACTGTACTACAAGGCCAA
GCCAACAAAGATTCCAACCTGGTACCAGTAACGAAACCCAGAGAAACCTATCAAAAGG
CCTAGAAAGATCCTGAAGTGGCTGCGATCATGCAAGATCCTGTTATGCAAAAGTATTTGC
AGCAGGCCCAACAGAATCCCGCTGCTTTACAAGAACACATGAAAAATCCAGAAGTATTCA
AAAAGATTGAGACGTTGATCGCTGCTGGTATCATCCGGACTGGCCGCTAA

YOR027W, 589 aa (SEQ ID NO 256)

MSLTADEYKQQGNAFTAKDYDKAIELFTKAIIEVSETPNHVLYSNRSACYTSLKKFSDAL
NDANECVKINPSWSKGYNRLGAAHLGLDLDDEAESNYKKALELDA SNKAAKEGLDQVHRT
QQARQAQPDGLTLQFADPNLIENLKNPKTSEMMKDPQLVAKLIGYKQNPQAIGQDLFT
DPRLMTIMATLMGVDLNMDINQSNMPKEPETSKESTEQKKDAEPQSDSTTSKENS SKAP
QKEESKESEPMEDDEDSKIEADKEKAEGNKFYKARQFDEAIEHYNKAWELHKDITYLNN
RAAAEYKEGEYETAISTLNDAVEQGREMRADYKVISKSFARIGNAYHKLGLDKKTI EYYQ
KSLTEHRTADILTKLRNAEKELKKAEEAYVNPKEAEEARLEGKEYFTKSDWPNAVKA YT
EMIKRAPEDARGYSNRAAALAKLMSFPEAIAIDCNKAIEKDPNFVRAYIRKATAQIAVKEY
ASALETLDAARTKDAEVNNGSSAREIDQLYKASQQRFPQPGTSNETPEETYQ RAMKDPEV
AAIMQDPVMQSILQQAQONPAALQEHMKNPEVFKKIQTILIAAGIIRTGR

YOR031W, 710 bp, CDS: 501-710 (SEQ ID NO 257)

CTGCAGAAGTACAGCTGCCTTTATTTCTTGTTGGTCATTTATTGCTTTTATTTTCAAGTCA
GATATACAAGAAAATCAAATCCCATCGTCAACGTCACGTATAAACGATTAATTTACAGTA
ATACCATACTCTACCAACATTATTTTAGTCCGACGTTCCAGTCTGTAGGTGTTCCAAATC
CTTCTGGCATTGACTTCTGTGCAGAAACCCCTTCAAATGAGTTCACCTTTACGTCAGATC
GCATAACAACCGGTCAATATATTTTTTTCTTTTGCTAAACCCCTACTGCAAGCACTTTTFA
AGAAAAAGAACAATAAATGCGTCTTTATTGCTGTGTGGAAGTGATTTTGTCTTTTCGGAC
AAAAAAAGGATAGGGATGCGAGAGGGCTGTGAAGTAGTGATCAAGCGGGGCTATATAAG
AAGGGCGCACATCGTCCCCCTAAGAATAGCGAAGCGATATTACACTGAACACTACAATG
TCAATAGTACTCAATAAATATGACTGTAAAAATATGTGACTGTGAAGGCGAATGTTGTA
AGGACTCTTGTCATTGTGGGAGCACCTGCCTTCCAAGCTGTTCTGGCGGTGAAAAGTGCA
AATGTGATCACAGCACCGGAAGCCCTCAATGTAAGAGTTGTGGTGAAAAATGCAAAATGCG
AAACCACGTGCACTTGTGAAAAGAGTAAATGCAATTGTGAAAAATGTTAG

YOR031W, 69 aa (SEQ ID NO 258)

MTVKICDCEGECKDSCHCGSTCLPSCSGGEKCKCDHSTGSPQCKSCGEKCKCETTCTCE
KSKCNCEKC

YOR096W, 1474 bp, exon1: 501-644, intron1: 645-1045, exon2:
1046-1474 (SEQ ID NO 259)

AAACCCATACACAATGAACCTTATCACACCCAAACATATGATATGGTATTAAAAAATGAA
AAAAATTCATTATTCTTTAGCGTAATTATTGAAGAAAAAACAGTGCGCGCGGTAATTTTT
TGTCACCTCAGTAAGTACGAGAGAGCCGAATGTACTCCCCCGGCTAGCTGGAGACCATGGC
TCTGCCTAGGATTTCTCTTATGCTTTTCTTTTCCCAATCACTTTGTTCCGGCGAGGCCCG
CGAAGCTCGCTTTCTTTACGCTAGCAATCATGTTCTTGCCAGCGTCGTAGACTACTGTA
TGGCAGTTGCTGCACTTGCCATGAATATCCTAGTGAAGCCTCTATGCAATAATCCAGTTA
CTGCGTTAGAATCCTGGTAAAATGTCTAATCTTATTACATTACAGCAACGTATTAGATTT
TGATTGAAAATTAGTCTTGGCACTTGGTATATATCTTATTTTAAAGAAAGCTGAAAGGAA
GAAAGATCATCAGAACACATGTCTGCTCCACAAGCCAAGATTTTGTCTCAAGCTCCAA
CTGAATTGGAATTACAAGTTGCTCAAGCTTTTCGTTGAATTGGAAAATTTCTTCTCCAGAAAT

TGAAAGCTGAGTTGAGACCTTTGCAATTCAAAGTCCATCAGAGAAGTATGTTATTAATTTG
AATCTAAACTTAAGAATAATGGAGAGTAACAAAGGAAAAAAGTGTGAACGGGACGATACC
AGAATGTTTCAATCTAGAAAAGTATAAAAGATAAGGACTAGGACTCAAATGTATTTGGCT
GACTATCGCCTGAACCTTGATGCTAAGCAAATACCATATCTTCAAGAAAAAGCCTACTCC
AGTGTTTAAGAAGAAGGGAACGATTTACTAGATCATGCTATACGCAGTAAGGTTCTGATA
GTTAATTACAATCGGTCCAAGTCTAAGCGGTGTCGTCCATGCATATATCATTTACAAGT
TACTGGCGTCAACTCTTCAAATATTCAAAATATCACCTAATCAAACCTTACTAACATTTTC
CTTTTTTGTTCCTTCTTTTATAGATCGACGTTGCTGGTGGTAAGAAGGCTTTGGCCAT
TTTTGTTCAGTCCCCTCTTTGGCTGGTTTCCACAAGGTTCAAACCTAAGTTGACCCGTGA
ATTGGAAAAGAAATTCCAAGACCGTCATGTCATCTTCTTGGCTGAAAGAAGAATCTTGCC
AAAGCCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACCTTGACTGC
TGTTTCATGACAAGATCTTGGAAGACTTAGTCTTCCCAACTGAAATCGTTGGTAAGAGAGT
TAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTGTGTAGACTCAAAGGATGTCCA
ACAAATCGACTACAAATTGGAATCTTTCCAAGCTGTTTACAACAAATTGACTGGTAAGCA
AATTGTTTTCGAAATTCCAAGTGAACTCATTAG

YOR096W, 190 aa (SEQ ID NO 260)

MSAPQAKILSQAPTELELQVAQAFVELENSSPELKAE LRPLQFKSIREIDVAGGKKALAI
FVPVPSLAGFHKVQTKLTRELEKKFQDRHVIPLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKILEDLVFPTEIVGKRVRYLVGGNKIQKVLDDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSETH

YOR248W, 803 bp, CDS: 501-803 (SEQ ID NO 261)

ACCCATTTTACAAATTTTTTTTGCTATTTGAGCCATAGTACCCATTAATAGGTCTCGTCC
ATTCCTTTGTTTTTTTTTATTGTTTCAATTACACTACATAATTAAAAATCACATCACTT
TCACTCTCACCTTAGTCGTTCTTTATCAACCAAAAAATAAAAAATGCTTCAATCCGTTGT
CTTTTTCGCTCTTTTAACCTTCGCAAGTCTGTGTGTCAGCGATTATTCAAACAATACTGT
TTCTACAACCTACCCTTTAGCGCCAGCTACTCCTTGGTGCCCCAAGAGACTACCATATC
GTACGCCGACGACACCCTACCTTTTTTGTACCTCAACGGTCTACTCCACGAGCTGGTT
CACCTCAACTTCAGCCACCATTACCAATGCGGCCTCCTCCTCTTGTCCACCTCTTCGGC
CTCTGGATCTGTAACCCCAAGATCCACCCATGAAATTACCTCCACCTCGACTATCACGTC
CACTTTGCTGCTAACCTTCATGACTCCACTACTTTGTCTCCATCATCTACTGCAGCAAG
TGTCAGTGACGAAGATTCAAACAACAAAGATGCAAAGGTCAAGTCTTTGAACAGGCTTC
AACTTCCAATGGTTGCGTCCCAATCACAAAGTTTGTCACTGTCAACCAATGAGCCGTTAC
CCAGTACGTTACAGTCAACCCAAATACGACTACACAATACGTTACTGTCAACGGTGCACC
TTCTGTTACCACTACCTCTCCAGGTAACGTACAATGGTACAACACCCTTCGATTACTAA
TTCGACCAGTTGGTGAATTATGA

YOR248W, 100 aa (SEQ ID NO 262)

MTPLLCLHLLQQVSVTKIQTTKMQRSSPLNRLQLPMVASQSLSLSPMSPLPSTLQSP
QIRLHNTLLSPVHLLPLPLQVTYNGTTPLRLLRPVGEL

YOR293W, 1255 bp, exon1: 501-552, intron1: 553-989, exon2:
990-1255 (SEQ ID NO 263)

AACTTTCGAAATATATACTCTGAGTTCTTGCTCCCCGTTTTGTACGATGTTCCCTAATGCA
AACACACGTCCTTTAAAGATCCCCGTGATAGGTTTCATTAAAGGCAACTTCCATACACGTT
GAAGTGCCAATTTTTTCCCTACATCCAAGCATTCTGGGTTTGTATGGGTGTTACACCGGT
TTTTCTTTTTTTATTTCCAGAGAAGTACAATTTTAGGCGGGTTTCAAATTTCCCCTGTGTG
CGAGAAACGCTCCGGTACGCCTAGGCTCACTCCGGTCTTCTCCCCATTTCTATCAGCGC
GATAGGCATACCTGTGGGAGAGCGGCACTAGGGAGACCGGTGGGAAGCACCGTATCTAGTA
ACGACGCTCTTTTGCAAAAATATCCATTAATTGCATGTAACCTTAGATTAACACTGGTAT
TAAGATTTTCGCAATTTTGGGCTGGATTATTAAGGTCGAGTAGCAAAGTTTAGCAAGAACA
GTACGAACTAAGTAGCCAAGATGTTGATGCCAAAGGAAGACAGAAACAAGATCCACCAAT
ACTTATTCCAAGGTATGTTTTAGAATAACTTTCAGAAAGCATGAAGATACACGGAAAGTC
AAGCGAGGGAAGTTATGCGTATACACAGTAGCGGTAGTGTGCATTACATACACGATGTT
TCAAACACACAGATGGATACCATGCATATGAGGTTAAAGGATTTCTTATGAATATATTAG
TGGATTACATAGAAGAAATTACAAGGAACCGTGTGACGACATTTTCGAAAGGACAGCACA
AGGCCATCGACCCTGGAGACGTATGAAATATGGTATACGTCTTATTTGGGCAAGAAAA

CGGTAAACTGTTTTACGCGGAGATCCAACCTTTTGATCCTTACCGAGTACCACGAATCAT
CTATATGATCTTTTACTAACTTATCTTCAATTTCAACGGAGAGATGTAAACATCATTCT
CTCCTATGATAATTTCTTTTATACAGAAGGTGTTGTTGTCGCCAAGAAGGATTTCAA
CCAAGCCAAGCACGAAGAAATTGACACCAAGAACTTGATGTCAATTAAGGCTTTACAATC
CTTGACTTCTAAGGGTTACGTCAAGACTCAATCTCATGGCAATACTACTACTACCTT
GACTGAAGAAGGTGTTGAATACTTGAGAGAATACTTGAACCTTGCCAGAACACATTGTTCC
AGGTACCTACATTCAAGAAAGAAACCAACTCAAAGACCACAAAGAAGATATTAA

YOR293W, 105 aa (SEQ ID NO 264)

MLMPKEDRNKIHQYLFQEGVVVAKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLRREYLNLPFHIVPGTYIQERNPTQRPQRRY

YOR312C, 1432 bp, exon1: 501-507, intron1: 508-914, exon2:
915-1432 (SEQ ID NO 265)

TATTTACAAGCTAGATAAAAAAAAAAATCAAATAGCAAGCTATTCTGTCAATATCTTAAGGT
GCTGATTGTTTGTAGGCACGAAGTAAACAAGCTCTTCCCAAACAATAAATACGGTTTTT
CGGGACTGTTTACCCGTACATTTACGTTTCCGACGGCGCGATGCTATCTTTGAATTTTT
ATCTCTTTTACGGTAACCCCATGACCAGTAGGGCGGCTTACTACCGAAGAGAAAAATGTCC
GCGGCCTAGACAGTTACTTCCAGGCCAGGGCCAGGCCACACGGACAGAGGCAGATTCCA
AGTTGTTCCGCATAGTCTGTCTAGCTCTTTCTCAATTTTCCGCCAGATTCTGTCTAATTT
CTTTCCGCTCGAGTTGGCAACAGTACGAAGAAGTAACTCTAATAGATAGATATAACCGTT
TTTGAGGGCATTATTTTGCAGAAGATAATAGAAGAGAACCCTAACAAGGAATCAAGCA
AAGAAAAAGTATGTAATAGAATGTATTGTATGCTTGTGGAATGAATGTCAATGTAGCTAT
TTTATATGGTGAGCTCAAATTGAATGAACATATCGTGGAAATTTAAAAATACTGAAGAATA
CCCAATAAGTCAATGCAACCTGTGAATGTTTTCTGAAATACGCCGAATACTGAATACG
ATTATTACCATAAATTGCTTCTAGAAGGAAGGCGGTGTACCATTTAATACTGATGATATG
GTTAATATCATTGTGAGAAGTCTTACATGAGGACTATAGAATACTACCATCCAGGAATTATA
GAGGAAATTAAGTGAATCAGAGATCTATTTTGAACATTCATTTACATGTAATGTCTGTC
AATAAAGCAATATTTTTTGAATATGCAAGTTTACTAACAAGAATAAATTTCTTTTTTGATT
TTTATCTTTAACAGTGGCTCATTTCAAAGAATAACCAAGTCATTGGTCTGTTTACCAAC
TGAATCCGTTCCAGAACCAAAGTTGTTTGAATGAGAATTTTGTCTTCAAATGAAGTCAT
CGCCAAGTCTCGTTACTGGTATTTCTTGCAAAAATTGCACAAGGTTAAGAAGGCTTCTGG
TGAAATTGTTTCCATCAACCAAATCAACGAAGCTCACCAACCAAGGTCAAGAACTTCGG
TGTTTGGGTTAGATACGATTCAGATCTGGTACTCACAACATGTACAAGGAAATCAGAGC
CGTATCCAGAGTTGCTGCCGTGCAAACTTATACCAAGCATGGCTGCTAGACACAGAGC
TAGATTTAGATCTATTACATCTTGAAGGTTGCTGAAATTGAAAAGACTGCTGATGTCAA
GAGACAATACGTCAAGCAATTCTTGACCAAGGATTTAAAATTCCCATTACCTCACAGAGT
CCAAAAATCTACCAAGACTTTCTCTTACAAGAGACCATCAACCTTCTACTAA

YOR312C, 174 aa (SEQ ID NO 266)

MYLAHFKEYQVIGRRLPTESVPEPKLFRMRIFASNEVIAKSRYWYFLQKLHKVKKASGEI
VSINQINEAHPTKVKNFVWVRYDSRSGTHNMYKEIRDVSRVAAVETLYQDMAARHRARF
RSIHILKVAEIEKTADVQRQYVKQFLTKDLKFLPHRVQKSTKTFYKRPSTFY

YOR369C, 932 bp, CDS: 501-932 (SEQ ID NO 267)

CTTCTTACAAGTTAATGAATAGTATATATGTAAAAAATCTGCTTCATGTATATA
CGCACCTCGTTATTGAGGTATTGCGAATGTAGCAGTTGAATAAGCAAAGACGAGGTTTGT
ACATCTTGGCATATTAAATGGTTATTTCCGGGTTTGTTCGGCTCAACGGTGATATAAAA
AGAAATCCAGTACTGTTTACCATTGTGCATCCGTACATTTGATTTGTTTACAACATCTTC
ACATTTCCATTGTGGAATCATTTTATTTTTTTCAGAATACCTTACCCGCAAGCAAACCTT
CAAGCAAACCTTACAATTTGCAAAATTTTCATCGAATCTCCGCAGGACATATTATAAAGT
TATGTCTATCTCTTATCACAACAGGTCTATAAGTGTTCCTTGTTCATTTGTTTTCCCAAT
TCAAACTCTTCACGGAGCAGTTTAATTATCTTACTGTGCAAGAAGTCAAAAACCTAGACT
ATATATTATTGAGAAGAAAAATGTCTGACGTTGAAGAAGTCGTTGAAGTTCAAGAAGAAA
CTGTTGTTGAACAACTGCCGAAGTTACTATCGAAGATGCTTTGAAGGTTGTTTTGAGAA
CCGCTTTGGTTTACGATGGTCTAGCTAGAGGTTTGAGAGAATCTACCAAGGCTTTAACCA
GAGGTGAAGCTTTATTGGTTGTTTTGGTCAGCTCTGTTACTGAAGCTAACATTATCAAGT
TGGTTGAAGGTTTGGCTAACGACCCAGAAAACAAGGTTCCATTGATCAAGGTTGCTGATG
CTAAGCAATTAGGTGAATGGGCTGGTTTGGGTAAGATCGACCGTGAAGGTAACGCCAGAA
AGGTTGTCCGTTGCCCTCCGTTGTTGTTGTCAAGAAGTGGGGTGTGAACTGATGAATTGT

CCATGATCATGGAACACTTCTCCCAACAATAA

YOR369C, 143 aa (SEQ ID NO 268)

MSDVVEEVVEQETVVEQTAEVTIEDALKVVLRTALVHDGLARGLRESTKALTRGEALLV
VLVSSVTEANIIKLVEGLANDPENKVPLIKVADAKQLGEWAGLGKIDREGNARKVVGASV
VVVKNWGAETDELSMIMEHFSQQ

YPL047W, 800 bp, CDS: 501-800 (SEQ ID NO 269)

GGTTAGGGGCCAAGATTACGTTCCAGCTTTCGATGTCCGACCAGATTGGGAATCTTACGA
CTATGCAAAGTTGGATCCAATAACGACGACGACAAAGAATTCATCAATAACATGTGGGC
CTGGGATAAGCCAGTTTCCGTCATGGCGAACCAAGGAAATGTTGACGGTAAGGTCTT
AAAATAATCTCTTCGTACTATCCTTCATGTGCGCTTTTATTATAAAGTATGCTAGGTAGT
TTTATCTATATCTTATTTATGACGCAATATAGGGTAACAGAGTTTTTCTGCTCTGAAACT
TCCGCAGAAAAAAATCAAGTTTTCTTTTCGTATCTTGGATTATTGTTATATAATAGAT
GCATGTATTATATGTATAGCAGTGATTGTCTTATTTTCTTGATTCTGAGGAATCGAAGAA
GTAACCTTAGCGTTTCTTCCGTTGAGCAGAGCAGTATAATAATCCTTCAAATTCCTTAGGT
TACGGGGTTTTCTGTGCGATGACCGAAGAACTATTACTATAGATTCTATTTCAAATG
GGATACTGAATAACCTGTAAACCACATTGATCCAGGACATTGTAGCTCGGGAAACCACTC
AACAACAATTGCTGAAGACAAGATATCCGGATCTTCGCAGTTATTATTTGACCCGAACG
GATCTCTCGATATTAATGGACTACAGAAGCAACAAGAGTCCTCTCAGTATATTCACTGTG
AGAATTGTGGCAGGGATGTGTCCGCAAACAGACTAGCAGCTCATTTACAGAGATGTTTGA
GTAGGGGTGCTAGACGTTGA

YPL047W, 99 aa (SEQ ID NO 270)

MTEETITIDSISNGILNNLLTTLIQDIVARETTQQQLLKTRYPDLSYFDPNGSLDING
LQKQQESSQYIHCENCGRDVSANRLAAHLQRCLSRGARR

YPL090C, 1605 bp, exon1: 501-506, intron1: 507-900, exon2:
901-1605 (SEQ ID NO 271)

GTAAGCAGAAGCCGGAAGAAGACAAGAGGTTCAATTCAGAGAAAACATCCGTACATTCCGAG
TTCTCATTGAACCCATACATTTCAACTATTTTACATAGTTCGTTTTTTCATGTGTAAAT
TGTCATCGACGCGCCGGAGCATCGGAAAGTTGGAACGTGCGCGATTGCACCAATCCCCT
GGGGCCGTGCATTCTGTAGGCAGGAAGCCACTGGACACTCTGCCCGTTCCCCTTGGAAAG
ATTGGCGTAATTCACGCTCCTCTATCGATTCTAGCGGGAAGTTATCTCTCTGGTAAG
CGTTGGAGGAATGCCGCTACCTAGGTAAGTCTACTGGGTGGGAATTCAGTACCGACGTC
TAGGAACATCATGATGCTGCGAGTTTCTTTGAAATTTTCATATACAGTGTTACCAAGGATAA
AGTGGTTAATGCTTATTCGTCATTGAATTTTATATTTGCTTAAGAGAAGTGACAAAAGA
GTGAAGACAGACTATACATCATGAAGGTATGATTTATGATACTATTATTGAGGGGCAACA
GAGAACCTTTATATGTGGAAGAAATGGCATGAAAGTTTGAAGTGAGAAAGAACTAAACAGA
ACCAGACGTCGTAAAGATTTTAGAATTTTATGGAAGAAAGCAGGAAGACTACCATAT
ACTAATTGATGCGTTTGTGGCGTTATTTTAAACAAACAGAGCGGGTTTACATATACTGT
TACTACAAACCGTGAAATTGAAGCAGTTCATATACTTGGAGTATAGTCAATAAAGACAA
GCTTTTTTCATCTTCCACTTAATAATTTCTCTAGAGTAATAAACTTCACCCTATTCAAACA
TTAATTTTGCAATAGTATACTAACAATTTTCTTAATAACCTGTTGAAAATTTAAATAG
TTGAACATTTCTTACCCAGTTAACGGGTCTCAAAGACCTTCGAAATTGATGATGAACAC
CGTATTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTCGATGGTGAAGCCGTTGGT
GACGAATTCAAGGGTTACGTCTTCAAGATCTCTGGTGGTAACGACAAACAAGGTTTCCCA
ATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTGTTGACCAAGAACGTTTCT
TGTTACAGACCAAGACGTGATGGTGAAGAAAGAGAAAGTCCGTCAGAGGTGCCATTGTT
GGTCCAGATTTGGCTGTCTTGGCTTTGGTCATTGTCAAGAAGGGTGAGCAAGAATTGGAA
GGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAGAGAGCTAACAACTCAGA
AAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTTCGTGATTTCGTATCAGAAAGAGAAGTC
ACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAAAGATTGGTTACTCCTCAA
AGATTGCAAAGAAAGAGACACCAAGAGCTTTGAAGGTGAGAAACGCTCAAGCTCAAAGA
GAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTGTCTGAAAGAAAGGCTGAG
AAGGCTGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCTTAA

YPL090C, 236 aa (SEQ ID NO 272)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVDGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPDLAVLALVIVKKGEQE

LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKEKTYTKAPKIQRLVT
PQRLQKRHRQALKVRNAQAQREAAEYAQLLAKRLSERKAKEAEIRKRRASSLKA

YPL137C, 4331 bp, CDS: 501-4331 (SEQ ID NO 273)

GTCTCAGTGATGCAATCATCATGGCACGGGCATTAATTAAGGTTAAGGAACCACTTCTCT
ACGCCATACTCCAAACAATAACAATATTAGACCTAGCCAATTGATACCCATGAGCGTGCA
GTCATTGCCATGGATTATTCATCTCTTTTCGCTGTTCTCTTTCTTTTCAAGTTTGTCTATC
ATCATGCCTTCACTTTTGCCTTTCCATCTTTCTTTTGTCTGCAAAATAAAGGGAAGAGGG
GTAAAAACGCAAGGAAGAACAAGAAGAAGAGGGTAGTGCAAGAAAAAGAAAAAGAAAA
AAAAAAAAGTAATCTTGATACCGTGAGCAAATAAGCTAACGGAAAGCGTAAGAAAGAA
GAGCGTGTGTTTGGGAAATAACACCACAGCATAAAGCTAAAATTTCAGTTTATATACTAT
AGTAGTCCTATAGAAATTGCGAATAACGGAAACAATAGTCCACCAAGCAAGCATAGGGA
GTGGAGATAGCATCTAGGTTATGATAACTAACACCGAGTTTCGATGTGCCCGTAGATTGGT
TGTATAAAGGTAAGAGTAGACGGAAGACAAATACGAAGCCATCGAGGCCTTCTACGTCGC
CAGCCTCCTCTTCATCTACGTCCTCTTCGAAAAACGGAGACAATAGCACGAGTGGTAACA
GGTCTAGCAATGATAAGCCTCGTGCGAGGTCTGTCATCTGTATCCAATGCAGCACTTTGTA
ATACTGAGAAACAGATTTTGAAGAGGAACGATGGTAATACCTCTGCATCAGACACTGATA
ACATACCGCTACTTACTCCTATTAATAGCGGTAACCGGAGCGATTCCGCTGACATTGATA
ATCCGGCTACCGTAGACGCCATAGACCTTATAGATAATGATGACAACGGCTCAAGTACTC
AATTTGTAAAGGAAAAACGTTCCACTTCTATATCCAATGCTGTGGTCTCGTCCAAACCAA
GACTGGCCAGTTCTGCCATAAACGCCACCGCATCTTCTTCTGTTGGCAAGGGAAAGCACC
CGCCAAATTTCTCACCATCTAATGCTACTCTCAAGAGAAGCAACTCGACTAGTGGAGAAA
AGACTAAAAGGTTCGATTTTGGATCTTTGTTTAGCAAACGGTCTACCTTCTTTCAGCTT
CCACTGCCAAGAAACCATTAACCTGTTGTTAATACTAGCACGACTGAGAATGAGTCTGGTG
GCATTAAAGCAGTTGCGACTCCTGATCCACGGGTGAAGGAGATATCATACCAATGAGAG
GAGTGGCACCAACAGCTAGCAAGCCACAGACACCTATACTCCCTCCCTGCACTTGCAG
TAAAAGACCTATCTACAGTTTCATTGAAAAGGGTCTCGTTTGGCGTCGATAAATTCGAAT
CCGATCCTCCCCAACAACTTCTTCAAGAACCCAAAAAGGGAACATCCTTATCCCTG
ATGACATGATAAGCGAGGTTCCCTTCTATTTCCGTTGGGTATTTCCAGTAGCAACCAATCGG
CCAAGTCAACCAATTCCAACATTAAGGGACCGTTGTACACTAAGAAGTCTAAAGAATATA
TACTCGCCCTGGAAAATCAAAGTTGGCTTTAAGGGAGGCTGCTAAGCATCAGCAAGAAG
CTCATTTTGTCTGCTAATAGAATAGCCTTTGAAGTAGCCAATTTTAAGACTGCTTCGGATG
CAGGCGGTAAAGCTTACTGAAAAGTCATCAGAAGGCACCATTAACGAAGCAAAGAGAAGAGG
TGTCACTCCAAATGTTGAAGCTGATCGGGAGCTTGAGAATAATAAACTTGCAGAAAACCC
TCTCAAAGCCGGCATTTGATAAGCCCATTCATATGCATGAGCACTATTTCAAGGAACCTG
ATCAAGATAAGTACCAAGACGGTCATTTCTATTGAAAATAACGAAGTTACGCTGGATGTTA
TTTACACAAGATGCTGCCATTTAAGGGAAATTTTACCCATTCCGTCTACCCTAAGACAAG
TAAAGGACAAGACAGCTCCCTTGCAAATATTGAAGTTTTTGAACCCCTAAGCCTACCTTGA
TCGATATTCTTTCTTTTGTGATTTTCATCACCATTGCTCCCATTCACACGATTGTTTTCG
ACAATGTAGCTTTAAACCAGGATATGTTTCAAGATAATTATTTCTGCTTTTGGTAAACTCCA
CAGTTTGGACAAATTGAGTTTAAAGAAATGTACGAATCGACCAAGATGGATGGAAATTAC
TATGTAAGTTCTTTTGTCTAAACAAATCACTGAACAAGCTCGACATTTCCCAAACGAAAA
TCAAATCTGACCTTGCTGAATCACTATATCGCCATAACATGGATTGGAACCTGTTTACTG
ACGCTTTGTCTCAGAGATCTCACAAACCTATAGAAGAATTGTTATTCAATGGTATTCAAT
TTAGCAAATTCCTTACTCATGCTTTTGCACGTTTACTGACATCCTTTGCTACCCAAAAAA
ACTTTCCAGAATCGGGCATCAGGCTTGGTTTAGCAGGTGCCACTACTTCCAATATCTCTC
AGGATTGTCTGAAATTTATCTTCAATTGGATGTCTCAATATAACGTCCAGGGTGTGGATC
TAGCGTTTAAATGATCTGTCCACTATGATTAAGCCAATGGTTGGTAAACTATCTGCTCTAT
CATATGATAACTTAAGATATTTTCAATTTTGAACAGCACTAATATTTTCGACTTCTTATGATT
TAGCTTTGCTCTTGAAATATCTTTCTAAGTTGCCTAACCTGATTTTTTTGGATTGTAGTA
ATTTGTGCGCAATGCTTTCTTGACATTTTACCCTACATGTACAAGTATTTACCAAGATTTT
CGAACCTGAAGAGGATACATTTGGATAGCAATAATTTGACATTAAAGGAACCTAGCTGTG
TTTGTAAATATTTGATTAAAGTGCAAATCGCTCTCGCATGTGTCAATGACTAATCAAACG
TTGAAAACCTCTATCTAATGAACGGCACAGATTCTCCCGTTCAACAACTAACACAGACG
GCGACTTGGATAGTTGAGCACATTTGGACGTTAAGGGCCAATTTGCTAAAAATAGTTTTT
CATCCACACTTTACGCATTTGCTAGAGACTCTCAAACCTGATTGGTTTAGATTTTGACT
ATGATTTGATATCAGAAGAGATTCAATCAAGAATAGCACTGTGCTTGATGAGAAATATGA
AACGGACCATGGATTTCGACTTTCCAGTTAGATGAATTGGATTTCGCAAGATGATTTGCTAT
TCGATGGCTCTTTAGTAACATGACCGCTGAAAGTGTGTTTAGAAAACTGAACTTGTAA
CGGATAAGAGTACAAAGGTCAAAAAAGACACCACGAAGAGATATTTGCTGAAAAAATATA

TTGAAAAGTTCCATATCTTGCACCATAATGTTTCAGCATACAATAGATACTATGTTTCGAAA
AAAGGAAATCAGGTGAATTGCCATTGCAAGAAAAAGAAAACCTTGTAAGATTACTCCTTT
TGGAACAAAAC'TTATGCAATATACTAGAATTGTTTTCGCATAATCCGAATCTGAATGATG
TCCTTGGATCCAGCAGGGATGATTGCAAGGAAAGTGTGACTCCAGCGAAGATTCAAAT
TACCAGCATTGAAGCACGTTGAATCCGGATACCATGTTCCCGAAGAAAAATACAACCTG
AGAATGATGTAATTACAGCAAGACCACATTTAATGGCCACCGATTCTGGTAAACTATTG
ACGTTTTTCACAGGCAAACCATTTGGTGTTCAGCATACATCATCTAGTACTTCTGTAGGTT
GTAAAAAGCAGGAAGAAGAAGAAGGTGAAC'TACATAAATGGGGTTTCTTCTGTTTCAGCAGC
AGAGGTC'TTTATACCCTGAAAATGAATCAACAAGGCAGACACCTTTTGCATCAGGTGATA
CGCCTATCAACACAGAAACAGCTGGTAAGTCAACTTCATCTCCTTCAGTTTCAACTTCTA
CAAATGAAACTGCTTACCAC'TAGTTTATTATTAGCCAGCTAATCCTAAGATTTTACCAAAAA
TTCCATCCGGTGC'TGCTTAAAGATCCGGCAATCATGAAGGCTAAAGGTATTGATTCTATCG
ATGATTTGATTTCAGAACGTTAACTCCAACAACATAGAATTGGAGAACATTTATGGTGAAT
CCATTCAGAAATAGCGCTTCGACATTTACACCAGGCGTGGATTCTGATGTATCTGCGCCCA
ATACCGATAAAGGATCCGTAGAAACATTGCCTGCAGTCTCAACTGACGACCCAAATTGTG
AAGTCAAAGTCACTGCTACCTATGACAAACTATTAAATAATTTGTCGATGGAGAGGTCAA
TCAGACTTTGA

YPL137C, 1276 aa (SEQ ID NO 274)

MITNTEFDPVDWLYKGKSRRTNTKPSRPSTSPASSSTSSSKNGDNSTSGNRSSNDKP
RARSSSVSNAALCNTEKPD LKRNDGNTSASD TDNI PLLTPINSGNRSDSADIDNPATVDA
IDLIDNDNGSSSTQFVRKRSTSI SNAVSSSKPRLASSAINATASSSVGKGKHPPISSPS
NATLKRSNSTSGEKT KRSIFGSLFSKRSTSSSASTAKKPLPVVNTSTTENESGGIKAVAT
PDRVKEISSPMRGVAPTASKPQTPI LPSPALAVKDLSTVSLKRVSFVDFKESDPPQQQL
PSRTPKKGNILIPDDMISEVPSISVGISSNQSAKSTNSNIKPLYTKKSKEYILALENQ
KLALREAAKHQOEAFHFAANRIAFEVANFKTASDAGGKLTEKSSEGTTITKQREEVSPPNVE
ADRELENNKLAENLSKAGIDKPIHMEHYFKEPDQDKYQDGH SIENNEVTLDVIYTRCCH
LREILPIPTLRQVKDKTAPLQILKFLNPKPTLIDILSFCDFITIAPIHTIVFDNVALNQ
DMFRILISALVNSTVLDKLSLRNVRIDQDGWKLCKFLLLNKSLNKLDISQTKIKSDLAE
SLYRHNMDWNLF TDVLSQRSHKPIEELLFNGIQFSKIPYSCFARLLTSFATQKNFPESGI
RLGLAGATTSNISQDCLKFIFNWMSQYNVQGVDLAFNDLSTMIKPMVGKLSALS YDNLR
FILNSTNISTSYDLALLKYLSKLPNLIFLDLSNLSQCFDILPYMYKYLPRFPNLKRIH
LDSNNLT LKELAVVCNLIKCKSLSHVSMTNQNVENFYLMNGTDSFVQQTNTDGDLDSSS
TLDVKGQFAKNSFSSTLYAFARDSPNLIGLDFDYDLISEEIQSRIALCLMRNMKRTMDST
FQLDELDSQDDLLFDGSLVTMTAESVLEKLNLLSDKSTKVKKD'TTKRYLLKKYIEKFHIL
HHNVQHTIDTMFEKRKSGELPLQEKENLVRLLLLEQNLCNILELFSHNPNLNDVLGSSRD
DSKESVDSSSESKLPALKHVESGYHVP EEKIQPENDVITARPHLMATDSGKTIDVFTGKP
LVFKHTSSSTSVGCKKQEEEEGELHKWGFVQOQORSLYPENESTROT'PFASGDTPI NTET
AGKSTSSPSVSTSNNETATTSLSFSPANPKILPKIPSGAVLRS AIMKAKGIDSIDDLIQNV
NSNNIELENIYGESIQNSASTFTPGVSDVSAPNTDKGSVETLPAVSTDDPNCEVKVTAT
YDKLLNNLSMERSIRL

YPL159C, 1262 bp, CDS: 501-1262 (SEQ ID NO 275)

AAACAAAGCGATTGAGTATTACGTTAAGATCTCCATTTGCTATGCTAAATCCTGCCTAC
TCAACAGCATTATATCGCTACCAACAGGTGTGGTCAAGAGGTCATTGACTCTTCTCTGTC
GGTATGAAAAATTTAAAAATATATAATAACATAAGTTTGCATTATTAATATTAATATAAA
TCAACGTATCAACCATAAAGAACCATATAATCATATAATTTGTTTACCTTAATGGCGATATCG
CCTTTTATCACCATCGACGATAACAAACGCCTATTCTGTCTACCGTTTCTTTTTTTCGCT
CGCAATATCAGAATCGTTTATCCCAAAGGGTAGTTATAGCAACTATTTAAATAACTTAGA
TGTTTCTTTAACTTATTCGGTCATACGTACACAAACACCCGCTAGATATAGCACTCCTTG
CTGTGCAACATTATAAAGGTGCTTTTAAAACTACTAATCGTATATTTCAGCAGGTCAGAAC
GCAAAGTCGGACGATAAACTATGTTGAAGCTAGCTCGTCCATTTATTCGGCTTTTATCAA
GGAACATGCCATTTCTTCAGGAATAGTTCTCACTTCTAGAAAGATTTCAGTCTTCTCTTA
CGTTCTTAAGTAACCAGTCTTTACTATCTAAAAATCAAATGAAATCCAAAAGAAAAAAGG
GCAGTAAAAAGGCAGCGTACCATCGTCAACCCCGGAACACGAACATACTGCACCAC'TTA
TAAAGCAAAACAAGACAATCACAAAGAAAGAACATAGCGATGTGAGAGGTTCTCATTTTAA
AAAAGAAAGAAAGCGATTTTTCGTGGCTACCAAGAGTACCATCCACCTCACATTTAAAGC
AGAGTACATGACCACAAATGTACTCTATTCTGGATATAGACCTTATTCATCAATCCCA
ATGACCCGAAGCTAAAGGAAGACACCGGAAGTACGTTATACGAATTTGCGATGAAGCTTG
AAGATTTAAATGAACCTCTATCACCATGGATTTCTCTGCCACTGGACTTGAATTC'TTTT

CAGAGTGGGAGAATATACCTAGTGAAC TACTGAAAAATTTGAAGCCTTTTCATCCACCTA
AGGAAAAATCAATGAACACAAATGAGCTTATTCATGTAAGTGCTAAGAGAAATACATTAG
TTGACAATAAAACAAGTGAGACGCTTCAGCGGAAAAATGGATGAATTTTCAAAGAGAAGAG
GAAAGGGGAGAAAAAAGTCAGTAGTGACGTTGCTCCAAATGAAGAAAAAACTTGAGGGAT
GA

YPL159C, 253 aa (SEQ ID NO 276)

MLKLARPFIPPLSRNNAISSGIVLTSRRFQSSFTFLSNQSLLSKNQMKSKRKKGSKKAAY
HRQPPEHEHTAPLIKQNKITIKKEHSDVRGSHLKKRSDFSWLPRVPSTSHLKQSDMTTN
VLYSGYRPLFINPNDPKLKEDTGSTLYEFAMKLEDLNEPLSPWISSATGLEFFSEWENIP
SELLKNLKPFFHPPKEKSMNTNELIHVSAKRNTLVDNKTSETLQRKMDEFKRRGKGRKKS
VVTLLQMKKKLEG

YPL175W, 1940 bp, exon1: 501-514, intron1: 515-568, exon2:
569-1940 (SEQ ID NO 277)

ACGTTATTTTCAAACACATACGAAATCGCTGGACTTTCTCACTAAAGGCTTCCGGAGCC
TGCGGTTCTTCCATCCCCATCTCTTCCACATATACCGGGGGTTCGATGGCATTCCCTATA
GCTTGCTCAAAGTCCGCGAGTTTAGCTCATCTTGTGAGTTATTTGCTGGTTCTTCAACA
TTCGGAAGAGTAGTGTAGCCCCTAGTATTCACCATATCCTTTGTATACTCATATGCGAAC
TTGTCTAATACAAATGTATACCAAAAAATAACAGCTTGAAAAAAATCTCAGGGTCTTTTCAT
TGAATAATCTCATTCTGCTATTTTAAAGTTTTCGTTTGCAACCCGAGACTGTGCGAGCTAG
AAAAATTTCAATTGATACGATTTAAAAATAATCGATGCCAGTAATAGCCTCAAAAACTTAT
GCAAAAAATACGAGATAC TATAAACTACAGCTTAGCTAACTCTAACATTATTATATAAAAC
AATGGGCTTCAATATAGCGTATGTCTAGCTCACAGCATGTGTTCCAAATACATTAAAGAA
GATCTCTTTTGTGTTGTGATACTAACCAGTAAAGTTGAGAGTTATAACAATGAAATAGGA
TGCTGTGCGACTTTTTTTATCCACAGTTAGGTGGAGTCGAAITCCATATATATCATTTAT
CGCAGAACTAATCGATTTGGGCCATTCTGTCGTCATTATAACTCACGCTTACAAAGATC
GAGTCGCGGTACGACATCTTACCAACGGTCTAAAGGTCTATCACGTACCATTTTTTGTGA
TTTTTCAGAGAAACCACTTTCCCCCACTGTTTTTTTCAACATTTCCAATAATAAGGAATATTC
TTCTCAGAGAGCAGATCCAAATGTTCATTCTCATGGTAGCGCTTCCACGTTTCGCTCACG
AGGGAATTCCTCATGCTAATACTATGGGATTGAGAACTGTGTTACGGACCATTCACTCT
ACGGTTTTAATAACTTAACGTCGATTTGGGTGAATAAGTTGCTAACATTTACCTTGACAA
ACATAGATCGGGTTATATGTGTTTTCTAATACATGCAAAGAAAAATATGATTGTTAGAACAG
AATTAAGTCCTGATATAATCTCAGTAATTCCCAACGCGAGTGGTGAGCGAAGATTCAAC
CAAGGGATCCTACTGCTGCGACCAAGAGAAAAACAAAGTAGGGATAAGATAGTGCCTGG
TCATCGGAAGGCTCTTTCCAAACAAAGGGTCCGATTTACTTACTCGCATAATTCGGAAG
TTTGTTCCTCACATGAAGATGTCGAATTTATAGTAGCGGGCGATGGTCCAAAGTTCATAG
ATTTTCAACAAATGATTGAAAGTCATAGACTACAAAAACGTGTGCAACTCTTAGGCTCTG
TTCCACATGAGAAAGTCAGGGATGTATTATGTCAAGGTGACATATATTTACACGCTAGTT
TAACAGAAGCATTTGGTACAATTTCTAGTTGAGGCCGCATCTTGTAATTTGCTAATTTGTA
CGACACAAGTCGGAGGAATTTCCCGAAGTGTTTACCAAAATGAGATGACTGTTTTATGCAGA
AGACATCCGTTTCTGACCTTGTTCAGCAACAAATAAAGCTATCAATATCATAAGAAGTA
AAGCTTTGGACACTTCCPTCTTTTCATGATAGCGTGTCTAAAATGTACGACTGGATGGACG
TAGCCAAAAGGACAGTAGAGATATATACTAATATATCTTCTACTTCTTCCGCTGATGATA
AAGATTGGATGAAAAATGGTAGCAAACTTTTACAAAAGAGATGGAATCTGGGCTAAACATC
TTTATCTGTTATGTGGAATGTAGAGTACATGCTTTTTTTTCTCTTAGAGTGGCTATACC
CCAGGGATGAAATCGATCTAGCTCCAAAAATGCCCCAAGAAAACAGTGTCTAACGAGACGA
AGGAAGCAAGAGAACTTAA

YPL175W, 461 aa (SEQ ID NO 278)

MSSSHKVESYNNENRMLCDFYPQLGGVEFHIIYHLSQKLIDLGHSVVITTHAYKDRVGV
HLTNGLKVYHVPFFVIFRETFPTVFPSTFPIIRNILLREQIQIVHSHGSASTFAHEGILH
ANTMGLRVTFTDHSLYGFNNLTISIWNKLLTFTLTNIDRVICVSNCKENMIVRTCLSPD
IISVIPNAVVSSEDFKPRDPTGGTKRKQSRDKIVIVVIGRLFPNKGSDLLTRIIPKVCSSH
EDVEFIVAGDGPKFIDFQQMIESHRLQKRVLGSGVPHEKVRDVLCCQDIYLHASLTEAF
GTILVEAASCNLLIVTTQVGGIPEVLPNEMTVYAEQTSVSDLVQATNKAINIIRSKALDT
SSFHDSVSKMYDWM DVAKRTVEIYTNISSTSSADDKDWMMKVANLYKRDGIWAKHLYLLC
GIVEYMLFFLLEWLYPRDEIDLAPKWPKKTVSNETKEARET

YPL180W, 2900 bp, CDS: 501-2900 (SEQ ID NO 279)

CTCAATGGGAATTGAGTGAAGATCAGTCTGATCGAGAGGAATTTGTACGATTCGTGGAAA
ACCAGCATTTTCGTAGAAAAAGTTGATACGATTTACAACGGTTATAATGAAAGTCTATCAA
TGATGGACGACCTGACTAGAGAGTTACTACTATGGGAGAAAAAATATTCAAATAACACTA
ATGCCATTCAATAAACGCAAAACACTGCAATATTATTCTCAACCAAAGTATAACTGTAAT
GAGGCGAACAACACATCTATACATATATATACATCTATATGGATATAAAAACGACTAAT
TCAACGTTGTTTTATCAACCGAGCTTACTCTTGTACGGGTAACCGCAAGGATAGCTAGT
TGCGGATGGTATAGCGATTTGGCTGGCAGCATGATTAAGGAATCCAAACATCTAATGGAC
TAGCACATTCTATCGATTTACGGGTCAAGTAAACATAGATATTGGGATATATCATATATC
CTTACTGAGTAACCTATAATTATGGTTCATCGAGGAAGGACTTTGAAGTCAGACACTGATG
TAACATCTCTTAATGCGTCAACAGTATCACACCAGTCAAAGCCATTTAGACAGTTTTCGA
CTAGGTGAGAGCAAAGAGTAACGCAAGCTTCAAAGGTTTTCGTAGAGTTTTAACACATG
ATGGCACCCTGGATAATGATTATTTAATAAGCACACGTTTCTCAGAAATGCAAGAGTT
CTGATGCACTTTTCAGAAAGCGAAGCATTAGTGGGTGAATATGACAGCTTTAACAAGAG
TAAAGTCCAATCAAGGAAAAAGATCAGCATCTTTTATAGTCCGGTGCATAATACGCTGC
TCAGTCCAAAGAACAGCAGTCATTCTAATACTGGAAGTCTGGTTTTCGGCTGAAACCAC
GAAGAAGTAAAAGTACCCAATCTGTTCTGAGTCTTCGAGATGCGCAAGAATCTAAAAAGA
GTGAATCTACTACTGACGAGGAGGTGGAATGTTTTTCGGAAGACAACATTGAAGATGGAA
AGGTGAATAATGATAAAGTAATAGCCGAGCATGTTATGCCTGAAGAAAAAAGAATGTGC
AGCAATTAAATCAGAATGAATTACAATCCCCGGATTCAATAGATGAACAAGAAGAAGATA
AATCAGGTACTGATGGAAAGGAAAAATCATAGAGCTGTATCCTTACCATTACCTCATTAT
CTTCCAATAACTATTTTCGGAGAATCAAGCCATTCTATAGAACATCAGAAAGATGGAGAAA
CATCTCCAAGCTCAATTGAAAACAAAAGTGAATGCAACAAGTGAATCAATGAAGAGGGGC
AATCAAAGGTGACGAAGGAAGCTGATATTGATGACTTGTCCAGCCATTCTCAAAATTTGA
GGGCCTCATTGGTTAAAGCGGGCGATAATATATCAGAAGCACCATATGATAAAGAAAAAA
AAATCTTGATGTTGGTAATACCTTAGCTGCACATAAAAGTAATCAAAAACCAAGTCATT
CAGATGAACAGTTTGATCAGGAAGATCACATTGATGCCCTAGGAGTAATTCATCAAGAA
AAAGCGACTCGAGCTTTATGTCTCTTAGGAGACAAAGTTCTAAACAACACAAATTATTA
ACGAAGAAGAAGATCTAATCAAGCCTGATGATATTTCTTCCGCTGGTACCAAGGATATTG
AAGGGCATAGCTTACTGGAAAATTATGCGCCTAATATGATTCTCTCCAGTCGACTGGAG
TTGAACGTAGATTTGAAAATTCATCATCCATCCAAAATTCGCTTGGGAATGAAATTCATG
ACTCGGGTGAGCATATGGCTTCAGGTGATACTTTTAATGAACTGGATGATGGCAAATTCG
GCAAGAGCAAGAAAAATGGTGGAAGATCTCAACTTGGCCAAAATATACCGAATCTCAGT
CTACTTTCCCCACCATTGCTAACATCGGTAGTAAAGATAATAATGTACCACAGCACAACT
TTTCGACCTCCATATCGAGTTTAACCAATAATTTGAGGAGAGCTGCTCCTGAAAGCTTCC
ATGGTTCAAGAATGAATAATATTTTTACAAGAAAGGTAATCAGAATCTACTTCTGAGAT
CCAACGATCTCAACAAAAATTCTGCAGCCCCGGCTCTCCATTGTCCAACGAACATATTA
CATCTAGTAGCAACTCCGGTAGCGATGCAACAGACAATCCAATCAGGTGCCAAATTTA
ATAGCTTCGCCCAGTTCCTTAAATCAGATGGGATTGATGCAGAATCAAGAACACAAAGAA
AATTATGGTTGCAGAGGGAGAATTCTATTATGGACTTAAGTTACAAAAATGACGGTAGTG
ACTCTATCTTTATGGCAGGAAACATTGATGCGAAAAGGGAGTTTGAGAGAATATCCCATG
AATACTCTAATGTAAAAAGATTTTACAACCCATTAGATGAAGCATTGTTGAGAGTACAAC
CTATAATAACGGGAAATGCAATAATATCAGGAAAAAAGCCATAACGATGCTCAGTCAA
TCGCACATTCTAGCAGTGATACAGATCATAAGGATGAGGACGATTTGCTCTTTACTAACT
ATGACAAAAAATTTGATGATCTTTATCCACATCTTGCAAGTGCAAAGATTACGGCAGTGT
TGTCGGGTATATGGAAAAGCGAAAGTTACTTATTTAACAAGGATGTTAATCCAATCAACA
AGAATAGGACAACGAGTACAAACCACAGCGTTGGCCACACTGCTTCACAGAATGCACGTA
ACTTGCTGAGGGGCCCCGATGGGTTCCAGCAGCACTTTGCACCACCAACGCGTCATTAAT
CTCTGCAGCCGACTACGAGGGCAGTGAATCGCAGGATGGAAAATGTGGGCTACATGCATA
CACAGCCACAACAAAGGTGA

YPL180W, 799 aa (SEQ ID NO 280)

MVHRGRTLKSDTDVTSLNASTVSHQSKPFRQFSTRSRAKSNASFKGLRRVLTHDGLDND
YFNKHNVSQKCKSSDALFRKRTISGLNMTALTRVKSNOGKRSASFHSPVHNTLLSPKNSS
HSNTGTAGFGLKPRRSKSTQSVLSLRDAQESKSESTTDEEVECFSEDNIEDGKVNNDKV
IAEHVMPPEKKNVQQLNQNELQSPDSIDEQEEDKSGTDGKENHRAVSLPLPHLSSNNYFG
ESSHIEHQDKGETSPSSIIETKLNATSVINEEGQSKVTKEADIDDLSSHSONLRASLVKA
GDNI SEAPYDKKKILDVGNTLAHKSNQKPSHSDEQFDQEDHIDAPRSNNSRSDSSFM
SLRRQSSKQHKLLNEEEDLIKPD DISSAGTKDIEGHSLENYAPNMILSQSTGVERRFEN
SSSIQNSLNEIHDSGEHMASGDTFNELDGKLRKSKNGGRSOLGQNI PNSQSTFPTIA
NIGSKDNNVPQHNFSTSISSLTNNLRRAAPESFHGSRMNNIFHKKGNQNL LRSNDLNKN

SAAPASPLSNEHITSSTNSGSDANRQSNAGKFNFAQFLKSDGIDAESRTQRLWLQRE
NSIMDLSSQNDGSDSIFMAGNIDAKREFERISHEYSNVKRFYNPLDEALLRVQPIITGNA
NNIRKKSHNDAQSIAHSSSDTDHKDEDDLLFTNYDKKFDDLYPHLASAKIQAVLSGIWKS
ESYLFNKDVNPINKNRTTSTNHSVGHTASQARNLLRGPMGSSTLHHQRVINSLOPTTR
AVNRRMENVGVMHTQPQQR

YPL218W, 1212 bp, exon1: 501-528, intron1: 529-667, exon2:
668-1212 (SEQ ID NO 281)

TGATACAAGACAGGCATTAGGAAACACATGAGTTTTGCATATGTATTATGCAGGTTTCATT
TGTTCCCTTCCCTTATTTCTTTTCATAGTATTTATTTTATTTATTTATTTATTTT
GGATTTTATTTTATTTCTTTTAAATGCTAAGAAAGTAATTCGCATAAATAACGTTGTG
CTGGCCTCGATAGGTACCTATAGTATACAGAAGCTTACGAAAAGCTCCTGCAGGATGGCA
CTTCTAAAATTTCGCGCTCAACATGGCCGTATTGTACATTATATCGTTCATCATTATATC
GTATACGCCCCGATTACCCGACAACCTCCGTCTGCAACGCGTTGACCAGAAAACCTCGAACA
AGAGATCGCATAAAAAACCAAAAGGAAACGAATTACTTGTCAAATAGTTATTGTAATGGA
TCCTCTAGAAAAGGCAACAGTAGATTTATTTCTTCTTTCTAGAAAACATCATTATAACT
AACAAATATATAATTGGAATAATGGCTGGTTGGGATATTTTGGTTGGTGTATGTTATCAC
CCTGTTACAGTTTTTTCGGATACCTAGTTTTTATTCAATGTGGTAAACATTGAATGTTTTCA
GCTTAAGATCTATTTTTTTTTTCTAGAAGAAATTGCGTCCCTTACTAATTTATTTTAC
TGTACAGTCAGAGATGTGTTGGCTTCCCTTGGTCTGTGGAACAAACATGGTAAACTACTT
TCTTGGGTTTGGATAATGCCGGTAAGACCACATTGCTACATATGTTAAAGAACGATAGA
TTGGCAACCTTACAACCAACATGGCATCCAACCTCTGAAGAACTGGCTATTGGTAACATT
AAGTTTACAACCTTTCGATTGTTGGGTGGTCAATATTCAAGCTCGTCGTTTATGGAAGGATTAT
TTCCCAGAAGTTAATGGTATCGTCTTTTTAGTCGATGCTGCTGACCCCTGAAAGATTGAT
GAAGCACGTGTCGAATTAGATGCTTTATTCAACATTGCCGAATTGAAGGACGTTCCTTTT
GTAATTCTTGGTAACAAGATCGATGCTCCAAACGCCGTTTCTGAAGCGGAGCTACGTTCT
GCTTTAGGATTATTGAATACCACTGGCTCTCAAAGAAATTGAAGGTCAAAGACCAGTTGAA
GTTTTCATGTGTCCGTTGTTATGAGAAATGGTTATTTAGAGGCGTTCCAATGGTTATCT
CAATATATTTAA

YPL218W, 190 aa (SEQ ID NO 282)

MAGWDIFGWFRDVLASLGLWNKHGKLLFLGLDNAGKTTLLHMLKNDRLATLQPTWHPTSE
ELAIGNIKFTTFDLGGHIQARRLWKDYFPEVNGIVFLVDAADPERFDEARVELDALFNIA
ELKDVPFVILGNKIDAPNAVSEAEELRSALGLLNTGTSQRIEGQRPVEVFMCSVVMRNGYL
EAFQWLSQYI

YPR102C, 1025 bp, CDS: 501-1025 (SEQ ID NO 283)

TTCTTTACAAATTCACCTTGCAATTATTGAAGGAGTGCTATTCTTCTGTTTTGCCACCCTTTT
GCTGTTTTCCCTCATATCACATAATACCCGGAGAGGCTCTTTCTCGGACAGCGCAACAT
CCAACCATCTAAAGGTATGGGTGTAAGTACGATGCGATTATTTCAATTAAGTTCTGTCTT
TTTTGTATATAAGTAAAAAGAACGGTGAATATCCATAGAAATACAGAGAGCGACGCAACA
GCGCGCAGACTCTACGGGTAATAGACTCACATCCACGTGACCAGTTTCCAATCGAACTTT
TTCACCTTGCAGGGAATTATTGTTTCACTAGCAAAGGTAGCCCACTTACCACTCAGCTAT
GCGAAAGTTTCATTGTTTGATACATCTTGATAGTAACCGCAGGCTTCTTTCTTAGTTCAT
ATTTTATTGTATTTCAACTAATATTATTTTTTTTTTTCAGTGGAAAGGGAAGGTGAACCAAGA
ACATACAAACATAGCCAAAGATGTCTGCCAAAGCTCAAAACCCCTATGCGTGATTTGAAGA
TCGAAAAGTTGGTCTTTAAACATTTCTGTTGGTGAATCTGGTGACAGATTGACCAGAGCCT
CCAAGGTTTTAGAGCAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAAACTTCTCTGCTACCGGTAACCTTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACCGTTGGTAACTCCCAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGATGCTGATGTTTTGGACA
AATAA

YPR102C, 174 aa (SEQ ID NO 284)

MSAKAQNPMRDLEKIEKLVLNLSVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR
RNEKIAVHVTVRGPKEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKRCCKGTGNSHKTTKEDTVSWFKQKYDADVLDK

YBL003C, 899 bp, CDS: 501-899 (SEQ ID NO 457)

TATATGACGGCAAGTGTCTCACTGTTGCATTACGCGATGTTTCTTTTCTTTGTTCTTGTAAAG
CGCGATTTTACCAGAACTAGATGGCGCTCGTGATCCTGAAAACGGGGAGAAATTTTGAGAAC
ACCGCTTTATTAGGCGAAGCGGTGGGCACAGCTCACGCGTAAGGTGTTCCCATTTATTTCTCA
AAGTGATGCGAATTTTCAGAGAACACATTAACCTGGGGGCCATAAACGCGACGTGCTACCATT
TTCGTTACGTATACTTAGGCCAGAGATTACAACATGACTACTAATATCAAACATAACTCTAT
ATATAAGGGATGAAGATGTATGCTTTCTTAGAATTTCAAACATGTTCCGTTAAAGTTTACT
TTTCGATTTCAATTTGACTGCGATGATGCTTTTCTTAGGTAGTTTTTTGTTATTAAATAGTA
TCATAAATCTTGTCTTTTACATAAGAATTAGGAAAGTACAGAACAAAGAGCAAATTTAATA
TATAATGTCCGGTGTTAAAGGTGGTAAAGCTGGTTTCAGCTGCTAAAGCTTCTCAATCTAGAT
CTGCTAAAGCTGGTTTAAACATTCCCAGTTGGTAGAGTGACAGATTGCTAAGAAGAGGTAAC
TACGCCAGAGAAATGGTTCTGGTGCTCCAGTCTATCTAACTGCTGTCTTAGAATATTTGGC
TGCTGAAATTTTAGAATTTGGCTGGTAATGCTGCTAGAGATAACAAAAAACAGAATTATTC
CAAGACATTTACAATTTGCCATCAGAAATGATGATGAATTGAACAAGCTATTGGGTAAATGTT
ACCATCGCCCAAGGTGGTGTGTTTGCCAAACATTACCAAAACTTGTGTCCAAAGAAGTCTGC
CAAGACTGCCAAAGCTTCTCAAGAACTGTAA

YBL003C, 132 aa (SEQ ID NO 458)

MSGGKGGKAGSAAKASQSRSAKAGLTFFVGRVHRLRRGNYAQRIGSGAPVYLTAVLEYLAA
EILELAGNAARDNKKTRIIPRHLQLAIRNDELNKLGNVTIAQGGVLPNIHQNLLPKKSAK
TAKASQEL

YDR442W, 893 bp, CDS: 501-893 (SEQ ID NO 459)

TGAACGGGTGCAAAATTTACTTTAACACCCAAAAAGTATATGCGTATATATATATATTTATC
CTTGTTATTTTTGTAAATTTAGACTATGCAACATAAGATTCCTGCGATGTAAGAACTACTTGC
TAATCAAGAGAACTTCAACAATTTCCATCGCAGAGACGAAAAAACTGGAAAAAATAAAAA
GAAAAAATTGAAAAAGAATCGCGACTTCCGATTACATAACCTTATACGGAGTATGATACCAT
TCTTGACATCATCAACACACCATCGCAGACCCACGTGGCCGCTTCGTGTGCCTTGAAAAATAC
AGCCTTAAACGCAATCTCATTCGCGTTCTGTGGAAATGTCTCGGACTACACGCTGGGCGTG
CATCACCAAGTGAAATGCCGTACCGCCCCGCTTCCGGTTTTGTTTTTATAAATCCGACTGGA
GAAATAGACTTCTGGGTTTACACCCCGGAATAATACTAAAACCAAACTGGTAAATAGGGCT
ACAGATGAGCAGGAAAAACGTTGCCGGAAGTTTATTTATCCGAGAGAAATAATTGATGAAG
AAGTAGCGGTATGCACAGTAGCGGCGGAAGTATTAGCAATTTTTACTCTGGTGTGCACAAGA
GTGTTTCATCATTTTTTTCACGGCTAGGATATGCCATGGAATATGGCCATCTTCGCCATCAGA
GAGACCGTACCACACGTTTAGAGCAGCCAGGTTGCGAACTCTTCTAAGATGGTTTCCAGCA
ATTGTGTACTATCAGAATGTGGACAGTTTAAAGGTTGACTGCGAATTTGTCCAAACCGTA
TCACCGTCGCATTTTTTGAATTTGATCAAAGCACCCTCCTAATAGCACAGCGATGCTGTGA
GTGTGCCAGTGGGAACGGGTGCTGA

YDR442W, 130 aa (SEQ ID NO 460)

MSRKTLPKVVLSERIIDEVAVCTVAAEVLAIFTLVCTRVFIIFFTARICHGIWPSSPSE
PYHTFRAARLRNSSKMVSSNCVLSECGQFKRLTANLSQTVSPSHFLNLKAPLLIAQRCEC
ASGNGC

YDR529C, 884 bp, CDS: 501-884 (SEQ ID NO 461)

GAGTCTCCGGAGTTGACCAAGTCATACAATGTGCTACTGACCAAGAAATGGATCTGTGTAGT
TCCAAGATCGCATGCCAAGAGTGGACCGCCATTGATGTTAAACATTAACCTCCACGGGGTACT
GTGGTATGATCCTCGTTAAAGACAGAGAAAACTAGAGAACCTCACTGAAGATCCTCATCTT
GTGGACAAGTCGTTACTGCAATGCGGTTTCCCCAACACAGCAGGCCAAAAACCAACAGAGTA
TCACTATTAAAGGTCTATTAGCCATATGTACATTGTCTATAGATGTGTAACCTGCGCTGTGATC
TTGTTTTGACCAATCAGGAGCGACGCGCTTTTATCGGGTCACCCCGCGGGGGGCGCTGACA
ATTTACTTTTCATAGAGCAGTAATAAAGGGAAGAGATGTAAAGCTTGGAAAAATAGCAGTA
AAGGTTGTTGTTGGACAATTTATCAGAATATTAGTAACTGTAATTAACGTTCCAGAAAGAA
CAAAATGCCACAGTCTTTTACGTCTATTGCGAGAATTGGTGACTATATTTTGAAGTACCCG
TCCTCTCCAAGTTATGTGTTCCAGTTGCCAATCAGTTCATTAACCTCGCAGGTTACAAGAAG
TTAGGGCTCAAATTTGACGACTTAATTGCAGAGGAAAAATCCCATCATGCAGACCGCTTAAAG
AAGACTCCCTGAAGATGAATCTTATGCCAGAGCATATAGAATAATCAGGGCTCATCAAACCG
AGTTGACTCATCATTTACTGCCAAGAAACGAATGGATCAAAGCCCAAGAGGATGTTTCCTTAC

CTGTTGCCATACATATTAGAAGCTGAAGCTGCAGCTAAGGAGAAGGACGAGTTAGACAACAT
AGAGGTCTCCAAATGA

YDR529C, 127 aa (SEQ ID NO 462)

MPQSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRR
LPEDESARAYRIIRAHQTELTHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELDNIE
VSK

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 463)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCTAAATATGTACTCTTTTATTTTT
TTTAAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCCGTGTG
AGCCTAATGTTTAAATGCCTAATTTTTTCTAAAAATGCAGCAACATACATATGTTGAGTCGTA
TAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTCAGGACATTTTAAAC
ATCCGTACAACGAGAACCCATACATTACTTTTTTAATATTTCTTTTTGTTCACCGCCTTC
TTTTTATTTTTATCCGAAGATCTTTTGGAAACCGCTCTGCGAATAGCGAAGCTAGGATACCA
AATTGAAACTTGGACATAACTCATCATTAAGAAGTATACTGTTAAGAGAGGCATTCTATTTTC
GTGTATTATAACGTTTAGCATCAGTTACCCCTTGAAAGCCCAACATATACAAAAATACGCGTC
CAAGATGTCCTACTAAAGCCCAAAACCCCTATGCGTGATTTGAAGATCGAGAAATTTGGTCTTGA
ACATCTCCGTTGGTGAATCTGGTGACAGATTAAACCAGAGCCTCCAAGGTTTGAACAATTA
TCTGGTCAAACCTCAGTTCAATCCAAGGCCAGATACACTGTCAGAACTTTTCGGTATCAGAAG
AAACGAAAAAATGCTGTTACGTTACCGTCAGAGGTCCAAGGCTGAAGAAATTTTGAAA
GAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACAGAACTTCTCTGCTACCGTAACTTC
GGTTTCGGTATTGACGAACACATTGACTTGGGTATCAAGTATGACCCATCCATCGGTATTTT
CGGTATGGATTTCTATGTCGTATGAACAGACAGGTGCTAGAGTCACTAGAAGAAAGAGAT
GTAAGGGTACTGTTGGTAACTCCACAAGACAATAAGGAAGACACCGTCTCTTGGTTCAAG
CAAAAGTACGACGCTGATGTGCTCGATAAATAA

YGR085C, 174 aa (SEQ ID NO 464)

MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTFVQSKARYTVRTFGIRRN
EKIAVHVTVRGPKAEIILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSIGIFG
MDFYVVMNRPGARVTRRKRCGTGNSHKTTKEDTVSWFKQKYDADVLDK

YGR106C, 1298 bp, CDS: 501-1298 (SEQ ID NO 465)

GCAACATTACCACTTTGTACGGAGCGTCAGAAAGAACGCACCTCATCATTATTATGAGAACA
GTACGATACCTTCTGTCTGAGATACGCTTCGTTGTTATAATACAAGTGAAACCGCCACGGAT
AATTAGCACAATTGAACACAAGGGATATCATTTGTGTGACCTTTGTTCTCTCATATTGTC
TGTGAACCCCTTAGTAACCTATTAATGTTTATTTTCATGAGACTAGTCAAAACATTCAATAACA
GTTTTTCTATATGAGAAAAAATGAAAAAATGAAAAAGCAACAGTACGATTATT
ACACTGACTATGCTGCAGTTTCCGCAATAGCAAAATTTGTGTACATTACACGAAAGAAAGAA
AGAACGCTATTTCTTATAAGAGCAAACCTGTTGATAAGTTTATAGCAAGAATAAAAAAGGGTAA
AAAGTCATTGATAATAACCACTGCTGTGACTATATATAATAAGAATCGAACTGTAAAGTTAA
AGCAATGGTGTTCGGTCAGCTGTATGCCCTTTTCATCTTCACGTTATCATGTTGTATTTCCA
AACTGTGCAAGCAGATTTCATCCAAGGAAAGCTCTTCCTTTATTTTCGTTTCGACAAAGAGAGT
AACTGGGATACCATCAGCACTATATCTTCAACGGCAGATGTTATATCATCCGTTGACAGTGC
TATCGCTGTTTTTGAATTTGACAATTTCTCATTTATGGACAACCTTGATGATTGACGAAGAAT
ACCCATTTCTCAATAGATTCTTTGCCAATGATGTCAGTTTAACTGTTTCATGACGATTCGCCCT
TTGAACATCTCTCAATCATTTATCTCCATTATGGAACAATTTACTGTGGATGAATTACCTGA
AAGTGCCTCTGACTTACTATATGAATACTCCTTAGATGATAAAAGCATCGTTTTGTTCAAGT
TTACCTCGGATGCCTACGATTTGAAAAAATAGATGAATTTATTGATTCTTGCTTATCGTTT
TTGGAAGATAAATCTGGCGACAATTTGACTGTGGTTATTAACCTCTCTTGGTTGGGCTTTTGA
AGATGAAGATGGTGACGATGAATATGCAACAGAAGAGACTTTGAGCCATCATGATAACAACA
AGGGTAAAGAAGGCGACGATGATTTTTAAGCTCCATCTGGACTGAAGGACTACTAATGTGT
TTAATAGTTTCTGCGTTGCTATTGTTCAATTTGATTGTTGCACCTTTCTTGGATATCTAATTT
GGATATCACATATGGTGCCTTGGAAAAATCAACAAACCAATAAAAAAACAATTA

YGR106C, 265 aa (SEQ ID NO 466)

MVFQGQLYALFIFTLSCCISKTVQADSSKESSSFISFDKESNWDITISTISSTADVISSVDSAI
AVFEFDNFSLLDNLMIDEYPPFNRFANDVSLTVHDDSPNLISQSLSPIMEQFTVDELPE
ASDLLLEYSLDDKSIVLKFPTSDAYDLKKLDEFIDSCLSFLEDKSGDNLTVVINSLGWAFED

EDGDDEYATEETLSHHDNNKGKEGDDDDILSSIWTEGLLMCLIVSALLLFILIVALSWISNLD
ITYGALEKSTNPIKKN

YGR182C, 854 bp, CDS: 501-854 (SEQ ID NO 467)

CCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAACGACTTAGCGAAGCT
TATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCATTACAGGTTACTAAC
AATGCATAAATTATGAGTAGTCTTTTTCATCACTATATAAAACCTTTTCAAACGAAACGCT
GTTTTGTGGTACTATCTTTGCAGGTGCCTTTGTTTTCCAACTGTATTTGATACTGCTAT
TACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGTCAAGGCTCGAATAG
CTGCAGGCGATGGAGACGACGATGATGAGTAAACGCTGATTATGTCACACATATACGTGCAA
ACGCTCTCTCTCTCTCTCAAGCTATATAAGTGGCACTCGTCTTATTTATTATTTTATTT
TGGCTGGTTGTTTCATGTTCAACCCAACCTCATAAAGGCACTCAACTTCATATTTTGACACAA
ATCTATGTCTCGCCAAAGCGCATTCAAATTTTCAAGATGGAAATAGACACGAACGAGCCTGTC
TGTCAGATGTTCAAAAATCCTTATTATAATTTTATATTCTACTAAAGGAAAAAGAGAATTA
GGAAAAAGAATAACTCATTTTATGTATATACATATATTTTGTACATATCTATACCAAGCAAG
TATAGTCAATACTGTTCTTCGACGTTATTTAAACGTAATAGCATTTTCTTGGTATCCTTTGA
ATCTTATATACAAGTACGAGTACATACTGCGCAGTAAATTGATCCTGATGGTGTTTAGAT
TTCCGACAGAAGCGGAGGCGTTCTGGATTCTGGAGATGTAAGCCTTTGA

YGR182C, 117 aa (SEQ ID NO 468)

MSRQSAFKFQNGNRHERACLSDVHKILIIILYSTKGKRELGKRITHFMYIHIFCTYLYQASI
VQYCSSTLLNVIAFSWYPLNLIYKYEYILRSKLILMVCLDFARSGGVLDSDGDVSL

YGR183C, 914 bp, exon1: 501-503, intron1: 504-716, exon2: 717-
914 (SEQ ID NO 469)

AAATACAAATCCAAGAAACCTCGATGAGGATGACTCTGATGATAATGATGACTCTGATGAGC
GAGAGATTGGTAGATTCAAGCCCTCTACTATGTTTTATAGTTGACATATTTGTATATAAAA
ACTTATACATTATTAAACATTTGCGCGTCGATTGACTTTTATTATTATTAAACAAAGAAGTA
ATACCAACCTAATTACAAATACTTCGAAGTGACTATCATAAGTTTCTTATCTAGCGAAGGC
AACTTTTGAACCTCCCAAGTTGTTAATATGTATCATTATACACGACCCAATCAAACGCGGGGA
AGTCAATGCCGAAAGAATTCTAGGACCTAAAAGCTGCTCAATCCTTGGGCCTTTCCCTAATG
ACATCCCCTCTCAAACCTTAGCTTAGCAGTTGTATTTAATGTCTGTACCGGATAGTCAATA
ATCGTTGAAGGTTGATTTTCATATCCTTCGCAATTTTCGTAAAGCAACAATAGCAATACGGAC
TAAATGGTATGTTGGTGTGTGTGTGTGCTTTCACATTTTCAGGCTAAAAATGTTATCCGT
GGAATCTTCTTAGCCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAAC
GACTTAGCGAAGCTTATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCA
TTCAGGTTACTAACAATGCATAAATTATGAGTAGTCTTTTTTCATCACTATATAAAACCTTTT
TCAAACGAAACGCTGTTTTTGTGGTACTATCTTTGCAGGTGCCTTTGTTTTCCAACTGTA
TTTGATACTGCTATTACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGT
CAAGGCTCGAATAGCTGCAGGCGATGGAGACGACGATGATGAGTAA

YGR183C, 66 aa (SEQ ID NO 470)

MSFSSLYKTFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAAGDGD
DDDE

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 471)

GGGCTTTTCCAGTGCCGCGGCCTCGAGATCCAGGCACCAGGAAGTAGGCACGCTGTGTATTC
TAACACATTGAAGGGCTTAGGCCCCGCTGACGTGGGGTCTAGTTCCACTTTTTTCATTACCTTT
TCTCGGTCTTTTCTTGCTCCCAAGGCCGTTAATGGCCTGAAACAGTTTTGTGACTTTGGAC
TTATGATAACGATGTTTGTCCGGGTGCCACCGGATTCTATCGCGGCGAATCAAGTCTAGTCT
GTTTGCATCCATCAAGGCACTGCTCATTGTGTAAATTTGTTCTACGCTTTTGTGCATCAATCA
TATCTAAACTCACAGCCGCTAGGGTAGGTGTGCCTGGCAGTGGTAAGGTAGCCCGCTCGTCT
TTGGTCATGCGCCAATACTGTGCAACGGCCCGCGCGTAGCGTTCTTTCGGCTTCAACCTTAGA
GCTGATACCTTTTGCCTGGTCAAAGGCGAAAACGCTCTACCTCGCTTTCAGTCTGCTTTTCGC
TTTCATGACTTCGTTTCAAGCGGTCTCTTTTCGCTCTCGGTTGTAACACACTTGTAGCCTGCT
ATGCTTTTCAACGTAAGCGTAGCCTCATGACTAGTTGTACCAACGCCCTTTCTTTT
CTTTTCTTCTTTCGACTTTCGGCGTATTCATCGCCACTGGTACAAGCCGTATGGTGCTTT
TTTGCTCATTTTTCGTTTTGACGTTGCGATGGTTTTTCGCGGACCAATCGCATGGGTGGTGG
ATGTTGTCTTTGCTAGTTGCAACGTAGTCTTCTTCTCTCCTGCGCTTTCTGACGAAAATTGG
CCTTACGTATCTTTTTTTCGGCGTCTGTTGTCTCATCGCTGTTTCATATAATCGTCTGCTACTCA

TATCGGCGCTTTTACTGCATGCTGTCTTTTGAAGAGAGTTTCATTGAAAAGTAGTGAAGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAGGAAAAAGCTTACATACGGAAAGAGAAAAAAAAAAAA
AAGAAATTTTAA

YKR040C, 167 aa (SEQ ID NO 472)

MTSFQAVSFALGCNTLVACYAFTVLEKRSIMTSCTNALSFLFFLLTLRRIHRHWKPYGAFL
LIFVLTLRWFRGPIAWVVVDVVFASCNVVFSPALSDENWPYVSFFGVVVVIAVHIIVVTHI
GAFTACCLLKRVSLKSSEEKKKKKKKKESLHTEREKKKKKF

YOL127W, 1343 bp, exon1: 501-513, intron1: 514-927, exon2:
928-1343 (SEQ ID NO 473)

TCTTATCTTGTATGCCCGATATAGCAACCTTGTGGTACCAATCTAACGGTTTCCGTACTTT
GCAATGAAGAGATGAGGAGGCATGGGTCACTTATTTAATATGTACGGGTGTTTACATGGAGT
TGCTTTCTTTTTTGTCTCAGCAGTCATTGTGCGCCAAAAAAGAGAAAACCGTGAGCCGAA
GTCCACGCTCTGGAGTTAGGCTCTCCCATTTACGGAGAGAAGCATTTCTCAGCCTGGGAGCC
CCGTTGGAACAGTCAGGCTAAACTGGGCCTTCTACCCACTGCTTGCTGTTTCTCACTGGAC
GCACAAGGGGATTTTCTTTCTACCTTCGGCTTGCCTCACTGCGTTGGGGCTTCCCAATGCA
CTTCGTTGCTATGCATACAATCTTTTAGATATTATCTTTTAAAATTATTTTAAAACAATTTT
AAATGTATCTCATATGCTTTTCTTCTGCTGTTGAAAAGGCTAAACAAAGAAGATCAATAAGA
TAAATGGCTCCATCTGGTATGTGAAGTGAATATTAATAGCACGAGAAAATTGAGAGGAAG
ATAGATGGGAAGTAGTAGAGTTGATATTGATGAGATACGAAAACACACGTAAATAAACTAT
CCGACGACAAGAATAGTGCATTAAGGACTTGATTAAAGATATGGTGAGCAACGTAATTATCGG
GCTCAACAGTTTATTAGCAATCGTTTGTAGAGAAGCGTTGATGCTGTGGAAGTTGTTCTTTT
TACTACCAACAGCCATTAACAAATCCATTAGAGTGTTGTTGTTCTGCTCAGATTCAA
GAAAATTATTCCATCCTCATTATACTTTTTTCTTCTATTTCTGCTCCACGTCGAGGTATCA
AGGAACATAGTTTACTAACATTAACGAATTCATCTCTATGAATTTACTTTTGTATAGCTA
AGGCTACTGCCGCTAAGAAAGCTGTGCTTAAGGGTACTAATGGTAAGAAGGCTTTGAAGGTC
AGAAGTTCTGCTACCTTCAGACTACCAAAGACCTTGAAGTTGGCTAGAGCTCCAAAATATGC
TTCCAAGGCTGTTCCACATTACAACAGATTGGACTCATAAAGGTCATTGAGCAACCAATCA
CTTCTGAAACCGCTATGAAGAAGGTTGAAGATGGTAACATTTTGGTTTCCAAAGTTTCCATG
AAAGCTAACAAATACCAAATCAAGAAGGCCGTCAAGGAATTATACGAAGTTGACGTATTGAA
GGTTAACACTTTGGTTAGACCAAACGGTACCAAGAAGGCTTACGTTAGATTGACTGCTGACT
ACGATGCTTTGGACATTGCTAACAGAATCGGTTACATTTAA

YOL127W, 142 aa (SEQ ID NO 474)

MAPSAKATAAKKAVVKGTTNGKKALKVRSATFRLPKTLKLARAPKYASKAVPHYNRLDSYKV
IEQPITSETAMKKVEDGNI L VFQVSMKANKYQIKKAVKELYEVDVLKVNTLVRPNGTKKAYV
RLTADYDALDIANRIGYI

FIG. 2:

YBL051C_homolog_1 1229bp PathoSeq: 1..1229; CDS: <1..>1229 (SEQ ID NO 285)

AGAGAACGTTATTGAAGAGGAGAGAAAAGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTGCA
TCAAATGCTTCTATGGCTTCTTTATTGTCTAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGAGT
GTGGCTGGCACAATCCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAAACAATTC
CTGTTCAATGCCCCACCAGTAGAAAATTAATTTTAAATGATCTTGAAGTTTTTGGAAATTGTACACTCAA
TTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCAAATTTG
AATATTTCTCAACGGAATATCATATCAATTTTATGTAATTTATTGAATTTATTAGAATTGTTTGAT
AATGGGTTGATAATAATTAGAAGAAAACCAGGATACATTGCTCAGTGATAAATCAACAATCTATT
ATTCTTAATTTCTCAACAGGTGTCTGGGCCAACTCACCAGCAACAACATCAACAGAATCAACTTCAA
CAACAGCAACAGCAACAACATCAACATCAACATCCCTTCACTTCATCATCGATGATGAACCTTCAT
CAATTTGGGTGGTACATTAGCTGTTCAGCGCACCCCTGAATTTATTAAGATCCCAATCGCAATCAGCA
TTACCGTTGCCAAGATTGAGACAGCAAACTCTACACCAATTCAACAAAAATCAACAAGTTTCAGCAC
CAAAATCAACCACCACAACAACAACAGCAACAGCATGTTCAACCACAATATAATTATTACAATCAG
CAATCTATTTCAAAGCCAAACCACATTTCTGCGAGACCTTATTCTCAATCATATAATTTTATCAACAA
CAACAGCAACAGCAGCAACAACAAGCTCAACAACAAGCTCAACAACAACAACAACAACAATTAACA
TATCAACAGGGACACCAGTCACAAGTTTCAACACCTACATTGAATTTCTTAGTGCTGCTGCATTA
CTTAGATCAAGTAGCAGTAGATCATTTGTTGATGTGAGATCCACACCTCCCACAAGTAGTTTGTGCT
CAACAGCAACAACAACAACAACAACAGCAACAGCCGCCACTAACTTCATCAATCCATGATTCT
CCAACACCACATCATCTTTACCACCTTCAACAGCAGCCACCACAACCAATCATTTACCTATCCAAT
TACCATCAGGGGTTGGATCTCAACCAAAAACCTCCATTGGC

YBL051C_homolog_1 409aa (SEQ ID NO 286)

RERIEEEKREKRGQLEEQHRSASNASMASLLSAASTTAATKNLSVAGTNPSHTTERMFLNLPFNNS
SFNAPPVEINFNDLEVLVLYTQLVLYRDDITKSTFELAISPANLNISQRKIIISILCNYLNLLLELFD
NGLIIIRKPGYIAQCITQQSIIPNSQQVSGPTHPPQHQQNQLQQQQQQQHQQHPSHSSSMNLH
QLGGTLAVPAHPELLRSQSALPLPRLRQQTSTPIQQNQVQHONQPPQQQQQQQHVPQYNYNQ
QSIQSQPHSARPYQSYNIYQQQQQQQQQQQAQQQAQQQQQQQLQYQQGHQSQVSTPTLNSSSAAL
LRSSSSRSFVDVRSTPPTSSFAQQQQQQQQQQQPPLTSSIHDSPTPHHHLPLQQQPPQPNHYLSN
YHQGVGSQPKTPL

YBL051C_homolog_2 2153bp public: 1..2153; CDS: 501..2150 (SEQ ID NO 287)

ATAAACAAAAAAGAAGCACGAACGTGGGGCAACAACAACAACAACAACAACAACAACAATTT
CTGGAATCAAAATTGAACCTCAACCAGCAGCGCGCGGACAGAAAAATATATTAACAGAAT
ACTTTTTTGTATTCAACTCTCTAACTCTTTCTATTTTTTTTTTTTTTCTATATACACTGTAAATC
AATCAACAATAGCAGGATATCCATTATATACAAATAGATAAACTGTTTAATTAATTAATTAACCTG
ATTTGATTTGGGAAAAACAATTTTATATTTGGAGAAATTGAATTTCAATCATTTTAAACAATTC
AAGCTTTAATTCCCACTATCAAAATTTCAATTTTATTTTGTTTTTCATTATTTTTTTTTTCCCTTTC
TTTCTTTCTTTCTTTCTTTTGGGAACAAAGTAATAGCCGATAAAATAAATAATTCACATAGCCCA
ATTCATATTACATTGACTTTTTGACAAGAGGTATATATAATGGATTTTAGAAATTTATCAACTACAC
CGAATCAAAATGGGCACTGTAATGCAACGTCGTCCTCTCTATCATCATTTATCGTCAGCCTCGGGCT
ATTCCTTCTTCAATTTATGGTGGAAATCCTACACCAATCCCAACAATCCAATACCAATAACAATA
GTAGTGGCAATAGTAATAACAACACTCATGGCAATAACACTCCCAATTTATCAACTCAAAGATTGA
CAATAATAGGAATTTACAATCCCTTGTGGATAAACCAACCATCTATTGCTCCTTCTAATGTTGTTT
CTTGGGTGGAACAGCAACAACAACAACCCCTTGATCTGTTGGAAAAATAATACTAAACAGACTCCA
GTAATGATGCTTCTGCTACTAATAATAATAATGTTAATGTTAATGTTAATGCCAATGCCAATGTTA
ATGCCAATGCCAATATCCATGCCCCAAACCATGTCAACACAATGTTAATGCAAAACACAACAGCAA
CTAGTATTAAATGCTTCCACGATTTTAAATACTACACCAAGTATTAAATGACACTAATGATAATGCCA
AAAAATTAATGTTTCCATGATTAGTAATAACAATAACAATAACAGTAACAATAATAACAACAACA
CTAACAATAGTAGTACAGGAAGTTCTAACAATTGCAACATGCTTCTCTGTTTCTAATGCAACGA
CAATGAATAACAGTAATAGTATCAATAGCACCACAACAATACTACAATTAACGAAGCTGATGATG
ACGAGTTAATTCCTACTGCGATTGTGATTAAAAATATTCATTTGCCATTTAAAAGGAACAATTTGT
TAGATGTGATGACAAAAATTAAACTTTGCCATTACCATATGCCTTTAATTATCATTTTGATAATGGTG

TGTTTCGTGGATTAGCATTTGCCAATTTACATCTACAGATGAGACATCAGCAGTAGTAAACCAAT
TGAATGGAAGAGAAATAGGTGGAAGAAATTTACGTGTTGAATACAAAAAATGCTTCCGGGCACAAG
AAAGAGAACGTATTGAAAGAGAGAAAAAGGGAGAAAAAGAGGTCAATTGGAAGAACAAATCGTTCTG
CATCAAATGCTTCTTTGGCTTCTTTATTGTCAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGA
GTGTGGCTGGCACAAATCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAAACAAAT
CCCTGTTCAATGCCCCACCAGTAGAAATTAATTTTAAATGATCTTGAAGTTTTTGAATTTGTACACTC
AATTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCATAT
TTGAATATTTCTCAACGGAAAAATCATATCAATTTATGTAATTATTTGAATTTATTAGAATTTGTTTG
ATAATGGGTTGCTACTAATTAGAAAAAAACCAGGATCCATTGCTCAGTGATAACTCAAAAAATCTA
TTATTCTCTAATTTCTCAACAGGTGCTGCGGCAACTCACCAGCACCACCATCAAAAGAATCAACTTC
ACCAACAGCAACAGCAACACACATCAACATCAACATCCTTAACATTCATCATCGATGATGAACCTT
CATCAATTGGGTGGTACATTAGCTGTTCCAGCGCACCATGA

YBL051C_homolog_2 550aa (SEQ ID NO 288)

MDFRNLSTTPNQMGTVMQRRPSLSLSASGYSSSNYGGNPTPNPNNSNTNNNSSGNSNNNTHGN
TPKLSTQRLTNRRNLQSLWINQPSIAPSNVVPWVEQQQQQLDSENNTKTDSSNDASATNNNNVN
VNVNANANVNIHAQTHVNTNVNANTTATSINASTILNTTPSINDTNDNAKKINVSMISNNNN
NNSNNNNNNNTNNSSTGSSNIANMLPSVSNATTMNNSNSINSTNNNTTINEADDDDELIPAIKNI
PFAIKKEQLLDVMTKLNLPYPYAFNYHFDNGVFRGLAFANFTSTDETSAVVNQLNGREIGGRKLRV
EYKMLPAQERERIEREKREKRGQLEEQRHSASNASLASLLSAASTTAATKNLSVAGTNPSTTER
MFLNLPFNSSSFNAPPVEINFNDLEVLLEYTLVLVYRDDITKSTFELAISSIFEFYSTENHINLC
NYLNLELFDNGLLLIRKKPGSIAQCITQKSIIPNSQQVSGPTHPHHHQKNQLHQQQQHTSTSTS
LTFIIDDEPSSIGWYISCSSAP

YBL066C_homolog 3254bp PathoSeq: 1..94/2146..3254, public:

95..2145; CDS: 501..3251 (SEQ ID NO 289)

ATAAAAAAGAAATACAATTAATAATTTTCTTCTGTGAAAAGGCAATTTCCGGTCTAGTAGTA
AACAAAGCTTAATAATTTCTCCCATTCAAATTTACAACGGACGATGCAGAAAGTAGTTTCAAAT
CAGTTTCTTTTCTTTTATATATTTTCTTACTTTCTCTTCTTCTTCTGACAGTATATTAATA
AATATTCTTTTTAACTTATTTTTCAATCAAGAAGGTACTGAAGATATCAATTAACCTCTCAGTTAAA
TCCATATTACCAGTTGTGGAATAATCAGAAGAAAAAAGAGAGAAAAATCACGGGAATTAC
GTTCTCAACAGAAAAATAACAATAATTTTTTTTATTTCATTCCAAGGTATAACAAGAACGTTAGGAA
TAATATAAAATTATCACCAAAGCTGCCATCAAGTGTGTCGACAACCAATCGACTCCTCCCTTAAC
TAGAACCATGAACCTCAACATTTGTTTCTATAGAAAAATGAAGTTTGAAAAAGGTAAAGTGAGAA
TTTTGCCTAAACCATCCCCTACACCAACCAACCCACAAACCCCATTTGCCATTACTTCCAGCTCAAA
CTAAACCTGTAAACTCAAAAAGAAAAATCAGCAGCCAGTACACCTGGAAATGAATCAAAGAAATCAA
GAAATCAAATTTCTACAGCTTCAACACCCAACAGTGCTACACCAACATCAGTCGGAACACCTCCAC
AGAAAATTTCAAACCAACAGGTCATAGGCCAGTGACTTCATGTACTTTTGTCTGCAACATAAAA
TCAAATGTAATGCTTACAGATAATTATCAAACCCATGTGAAAGATGTAAAAAATGGGTTTGAAAT
GTGAAATTGACCCCGAATTTAGACCTCGCAAAGGGTCACAAATCCAATCATTGAAACTGGATGTTG
ATGAATTGAAGGCCAAGATTGAAATGTTGACTAAAAATGAATCTTTGCTCACACAAGCTTTGAATC
AACACAATTTGAACCAGCTTCGCAACAGCAACAATGTCTGGATCGCAATCTCAACAACAACATC
CTCCAAATCCACAACGTGCATTGTATATACGTCTGCAAATCATCACCACAAGTTGCATTAGCA
ATGCATCGCCAATTCCTTCTGTGACAAGTATTCAACAAAAATGCACCGTTGACTCACGAAAAATCCG
ACAATTCTCCATACGCTTTAAATACACCAGAAAAATGAAGAATTACAACCAATCTCAGAATTTA
TTTTGGGTGACGTTACTTTGCCATTAAACAGGGCCAATGAGTTACACGACAAGTTTATGACCACAC
ATTTACCATTTTTGCCAATAATAATATCTCGATCTGCCACCGAATTGTATCATAAATCTCAATTGC
TTTTCTGGGCCGTGATTCTTACCGCAAGCTTATCAGAACCAGAACCCAACTTTATATGTCGTTGG
CATCCTTAATTAAACAATTAGCAATTGAAACATGTTGGATTAAACACCAAGATCAACTCATGTTA
TCCAAGCCTTGATCATACTTTCAATATGGCCGTTACCTAATGAAAAAGTTTTGGATGATTGCTCTT
ATAGATTGTTGGATTGGCAAAGAACTTGTCTATTACAATTAGGTCTACATCGTGGTGGAGAAATCA
TTCAAGAATTTAGTCGGAATCAAGTAAGTCTAGGACCTGATGCAGAAAGGTGGAGACTCGTTTCA
GGTTAGCAGTTTTCTTTTGTGAACAGTTTTGGTCATCATTGTTGGGGTTGCCACCTTCAATAAACA
CTACTGATTATTTATTAGAGAATGCTCGTGTTGATAAATCGTTGCCTAAAAATTTCCGTTGTTTGA

TTTCGCTATCTATTTTCCAATGCAAATTAGTTAATATTATGGGTATTAGCGTTACTAGACCAGACG
GTTTATTGGAGCCTCTGAATCGTGGTTCACCTTAGTTTATTGGATAGAGAATTGGAAAGATTAA
GATTTAAACTTCAATTTGAAGAAGGGGGGCCAATTGAAGTATATTATTTGTATATTAAATTGATGA
TCTGCTGCTTTGCCTTTTTACCAGGTACACCTATCGAGGATCAAGTCAAGTATGTCAGTTTTCAT
ATTTATCAGCAACAAGAATCGTGACAATCGTTTCTAAAATGGTGAATGACATTTTCATTGATTGAAT
TGCCAATATATATCAGACAAGCAGTGACATATAGTGTTCATGTTGTTCAAATTACATTTGTCAA
GATATTTGATTGACAAGTATGTGGATAGTGCTAGACAGCTGATTGTTACTGTGCATCGTTTATTTA
GAAACACGTTGAGTTCCCTGGAAAGATTGCAAAACGATATTTCTCGAACAGCCAAAGTTCTAGAAA
ATTTGAACATGGTGTGTATAATTATCCTGAAATATTTTAAATGATCTGGAAAAAGAGGATTCAA
GTATTATCACCAGAATGAGGTCACATTTGACAGCATCTTTATTCTATGATTGGTGGTGTGTAC
ATGAGGCAAGAAGACGATCAGTACTTGATAAGGGGAAAAGACAGGCTCAGCCTAACAAAGAAATCT
TGCCCTTGCCATTTTACAACCAATCATAAGGATGATTTCAGACAATTACCACGACATCACCTTA
ATGGAACACTATTACTACATTAGTTCCAACGTATCAAGCTATGAATCAAGCAAACTGAAATCTT
TTGATTCCAGCAAACCACTTGAAATAAATGGTATTCCCTTACCTATGCTTGAAGCTACTGGTTCAA
CAAGAGAAGTTTTAGATTCTTTACCCTCGCAATCTTTACCATCACAAAGCACCACCTCTCAGCAGT
ATCCAATGCAGCAAGATCAACAACAGCAAGAACCATCACAAACAACAACAAAGCACCCTGCAGC
AACTGCAGCAATACCAACAACAGCAGCAATCGAATCAACAGCAACCACATCTTCAACATCAAAGAC
AGTTTCAACAATCACCACCACCGCAATTTTCAATGATTTCTTCAACGCCGCCCTTCAGCAACCAC
CTTTTATTTTGGCAAACCTACCGTTACCACAACTTATTTGCCAAAGATTGATGAAATGAATATGT
CACCAGAAGTAAACAAGAAACTCTGTTGCTCCATTTGCATCTCAAATCACCAACTTTTTTGTATC
AACAAACAAGTGGATGGTTTAATAATGATAACCAAGATGACGACTTTTTTGGGTGGTTTGTATGTTA
ATATGATGCAAGAGAAATAA

YBL066C_homolog 917aa (SEQ ID NO 290)

MKFEKGKVRILPKPSPTPNPQTPLPLPAQTKPVNSKRKSAASTPGNESKKSRSKSNSTASTPNSA
TPTSVGTPPQKTSKPTGHRPVTSCFQRQHKIKCNASDNYPNPCERCKMGLKCEIDPEFRPRKGS
QIQSLKSDVDELKAKIEMLTKNESLLTQALNQHNLNHASQQQQSSGSQSQQQHPPNPQRALSYTSA
NSSPQVAFSNASPIPSVTSIQQNAPLTHENSNDNSPYALNTPENIEELQPISEFILGDVTLPLNAN
ELHDKFMTTHLPFLPIIISRSATELYHKSQLLFWAVILTASLSEPEPKLYMSLASLIKQLAIETCW
IKTPRSTHVIQALILLSIWPLPNEKVLDDCSYRFVGLAKNLSLQLGLHRGGEFIQEFSRNQVSLGP
DAERWRTRSWLAVFFCEQFWSSLLGLPPSINTTDYLLNARVDKSLPKNFRCLISLSIFQCKLVNI
MGISVTRPDGLLEPSNRAGSLSLDRELERLRFKLQFEEGGPIEVYLYIKLMICCFALPGTPIE
DQVKYVSFAYLSATRIVTIVSKMVNDISLIELPIYIRQAVTYSVFMLFKLHLSRYLIDKYVDSARQ
SIVTVHRLFRNTLSSWKDLQNDISRTAKVLENLNMVLYNYPEIFLNDSENESSIIITMRSHLTAS
LFYDLVWCVEARRRSVLDKGRQAQPNKKILPLPFYNQITKDDFKTITTTSPNGTITTLVPTDQ
AMNQAKSKSFDSSKPLEINGIPLPMEATGSTREVLDSLPSQSLPSQAPTLQOYPMQDQQQQEPS
QQQQQKHSQQSQYQQQQQSNQQQPHLQHQRFQSSPPQFSMISSTPPLQOQPFILANSPLPQTY
LPKIDEMNMSPEVKQENSVAPFASQITNFFDQQTSGWFMNDNQDDDFLGWFDVNMMEK

YBL078C_homolog 908bp public: 1..908; exon 1: 417..449, intron 1:
450..533, exon 2: 534..908 (SEQ ID NO 291)

TTATTATTACTATGACACACACTTACTCTCTCTATGTCTCCGCTTACATCACACATCATACGTTT
GAAACACCCACCCCTTTTCTTATCTACAAAAAATAACAACTCACTATACTACTAAAC
CTTTTTTTTTTATTTATTTATTTGTATTTGTATATTAATCAAATATTATCATTCATCTATATA
TACATCCCATCGATTCTGACATAATAGTATGTATGATCATACAGAGGGGAAATCACCCTTTTT
TATTATTACCAAGGTCTCAATGATTAGTGTGGCTAGCGTCTGTTACTACTTACCCCGTGTGTAG
ATAATTGCCACTCAATCTTAAATTGACCATCGACCACAAAAATAATATGGAATAATACTAACAGA
ACTTAGAAACATCACTCATAATGAGATCACAATTCAAAGACGAGCATCCTTTTGGTATGTATTACA
TGATTTTTAGTCTCTGAATCTTCTCCGATCATCATATACTAACATTTTCGTGGGTGTTATCTT
TAATAGAAAAGAGACAAGCCGAGGCAGCCAGAATTGCTCAGAGGTTCAAGGATAGAGTACCAGTCA
TCTGTGAAAAGGTTGAGAATTCGGATATCCCCGAAATTGATAAACGTAAATATTTAGTGCCAGTGG
ATTTGACTGTTGGTCAATTTGTTTACGTTATTAGAAAAAGAAATCAAGTTACCAAGCGAAAAAGCCA
TTTTCATCTTTGTCAATGACATATTACCCCCAACCGCTGCATTAATCAGTACAATCTACGAAGAAC
ACAAGGACGAAGATGGTTTCTTATACGTTTATACTCTGGAGAGAATACTTTTGGCGAGAACTAG
CAATTGACATTTTCATCATTAGATTTTCAGTGATATCCCTGATTATGTTTAA

YBL078C_homolog 135aa (SEQ ID NO 292)

MRSQFKDEHPFEKRQAEAAARIAQRFKDRVPVICKVENSIDIPEIDKRKYLVPVDLTVGQFVYVIRK
RIKLPSEKAIFIFVNDILPPTAALISTIEEHKDEDGFLVLYSGENTFGEKLAIIDISSLDFSDIP
DYV

YBR073W_homolog 2891bp PathoSeq: 1..2891; CDS: 501..2888 (SEQ ID NO 293)

GTGGCACATCCCAGGAAGTAGAGCATGGACAGTTCGTATGGTATTGCTGTGCATACGATACAAAAA
AAACAGAAACGAGAAAAAATCGATCGTCAACCTTTATCAACTCATCTACAGCAGCAGCAAAGTT
CGTCCCTAAATATGAGTCAAGTCCAACAGAAACCCAAATCGTTTGGTAGATTGTATACCATGTACT
ACTTTTCATTTTCCATTTGTTATGCTTACGACAACTGAAACCATGCTACTTCATACGTTTGTATTGA
TGTTTGCCTTATTGTTGCTTATGGGATCTACGCTTATTGCTTCAAGTATCATGTTTGCATCT
CCAGAGCATACTATTATGTTTGGCATGGATATTAGTACCATCAACGGTTATGCAAAGTAGCGCT
GTCTACTTAGTTTATAGTTTAAAAATTTGTTAATATAAACCCAAAGTTTCTAACAGGCTCTGTTT
GCTCGACTAAAAAAGAAATTTTGTCAAACGCGTATCAGAATGTTTACCCTTTTTTTTTTACCACAG
ATCAAATGAATGTTTCGACCTAATGCTCCGTTTCGGCTCCTAGACCAATAAAGGGGGGTGTTGCGG
TGTTGTCAGAAAGTAGTAAACGAAAATTGCCCACTACCACCAATCCTAAACCTGCAAAGATTTTGA
CTACCGATCCCGGCTCAACAAAATACGTGATCCAATGGAGAAAGAAAACCTTCAAAGAAGAACAAAA
CATGGGACGGTGATGGGTATGCCGTGATTAAACAGCTTGAGAATGGGGCATGCGAGATATCTATCA
AGAACTCTGATGGCAAACCTATGGGAAAAGAGTGTTTACTGCGACACCTAACCTTGACGACGTGA
TTAGTGTGGGACCCATGAAATTAGAATTAGACGAAAAAGTAGGGTCTAACTCAACTCCCCAGACAG
TGACACGTGTTACCCACCAGTTCAAAAAGGTTGCTCCTCCACAGCTAGTAGTCGGAAACCGCTTT
ATGACGACTGTCCGATGCCATCGCGTTGCTCCTCCTCCAAAAGCCAAAGATTATGTCAAAGTAA
ATATCGATCCACATTTGGCAAAAGTGCTTCGTCGCCATCAGGTTGAAGGTGTGAAGTTTATGTATG
AGTGTTTAATGGGGTACCGTGGGTTTGGCGGCACGGGTGTTTGTAGCAGATGAAATGGGGTTGG
GGAAAACGTTGATGACAATCACTACAATCTGGACGTTGCTCAACAAAACCCGTTTATGGAAAAG
GTGCAGTGGTAAATAAGGTATTGGTGGTGTGCTGTGCAGCTTATTTCCAATTGGAGACAGGAGT
TTAGGAAATGGTTAGGTGCTAATAAGCTAAACGTGTTGACGCTCAACAACCCAATGTCAAACGAGA
AACAGGATATACTCAATTTTGGAAAGTTGAATGTATGTAACCAAGTGTAGTGGTGAATTATGAAAAAC
TTGTGGCACATTTTGTATGAACTCTCAGCGGTCAAGTTTGTATTGTTAGTGTGTGACGAGGGCCATC
GTTTGAAGAATAGTGCAAATAAAGTATTGAATAATCTTATCAAGCTCAATATTCCGAAGAAAATTG
TTTTGACGGGTACGCCGATTCAAAACGAGTTGGTAGAGTTTACACGTTGATCTCGTTTCTCAACC
CGGGTGTGCTTCCCGAGCTAAAAATGTTTTCAGCGAAACTTTATAACACCTATATCTAGGGCCCGAG
ATATCAACTGTTTGAACCTGAAGTGAAGAAACCGGTGAAGAGATATCGCAGCAGTTGATTGAAT
TGACTCAGAGTTTATTCTTAGACGTACACAACGCGATTGCTAATTAATGACACAGAAACATG
ACATTTTGTGTTTGTTCACCTACATCGTTGCAGCTCAAGTTGTTTCGACTATATAACCAACTTGA
AGAAATTTAATCAGTTTGAAGCATTTACCATGATCAATTTGTTTAAAAAGATTTGCAATTTCCCTT
CGTTGTGGCCGACGACGAGTTATTTAAAAAGATGTTTGAAGAAAAGTTAATTTGGGGATGGCAT
CCGGTAAAAATAACATTTCTGTGCGGTTGCTATTGGAATTTGCTTCGCTTGGGGAAAAGATTGTCT
TAATTTCCAACCTACACCAAGACTTTGGACTTGTGGAACAGGTTTTCGCAAGGTCAGCCTAACAT
TTTCGAGATTAGATGGGTGACCCCCAACAAATGTGCGTAGCAAGTTGGTTAATCAGTTTAAACAGA
ACCCCGACATAAACGATTTTTTATTGTGCTCGTAACTCTGGCGGGATGGGGATCAACTTGGTGGGG
CTTCGAGGTTGATTTTGTGTTGACAATGACTGGAACCCAGCGACCGATTGCAATCGATGTCGCGAA
TTCACAGAGACGGACAATGAAACCGTGTTCATTTATAGGCTATTACACCGGGGTGTATTGACG
AGAAAATCTTTCAGCGACAGCTCGTGAAGAACAAATGAGTTCCAAGTTTTTGGACAATGACGCCA
CGTCCAAATCTGATGTGTTTGAATGATGTTTGAAGAATATTTTGGATAGATACATCGACAA
TATCCAATACTCATGATTTATTAGAGTGTGTGTGTGAGGGCGACGGGTGATGTTGAGTCAGCCAA
CCATAGAGGAAAGCGAACCACCCCCAAAACAAGCATGGGTTACTGCATTAGAGCTTAAGAAGAAGA
TTGACGATGGTGAAGCGCTAAAGAGGACGGCTGTTAAATTTGCCTTGAACGATTATCGACACTACA
ATCCAGAGGTGAACCGTAATTTGGATTTTGAATCTGCGCTACACCGAATTGCTAACAAATCAAGCT
ATGAAAATAAGCAATTGCCAATTACATTTATAATGCTGAGAGTAACCTAATTAA

YBR073W_homolog 796aa (SEQ ID NO 294)

MFTLFFFTTDQMNVRPNAPFRPPRIKGGVAVVQKVVKRLPTTNPKPAKILTDPGSTKYVIQW
RKKTSKKNKTWDGDGYAVIKQLENGACEISIKNSDGKPMGKRVFTATPNLDDVISVGPYELELDEK
VGSNSTPQTVTRVTHQFKKVAPPTASSRKPLYDDCADAIALPPPPKAKDYVKVNIDPHLAKVLRPH

QVEGVKFMYECLMGYRGFGGHGCLLADEMGLGKTLMTITTTIWTLLKQNPFFMEKGAVVNKVLVVCPU
TLISNWRQEFKRWLGANKLVNLTNNPMSNEKQDILNFGKLVVYQVLVVNYEKLVAHFDELSAVKF
DLVLCDEGHRLKNSANKVLNLIKLNIPKKIVLTGTPIQNELVEFHTLISFLNPGVLPKLFQORN
FITPISRARDINCFDPEVKKRGEEISQQLIELTQSFILRRTOAILANYLTQKTDILLFVPPSTSLQL
KLFDYITNLKKFNQFEFTMINLFFKICNSPSSLADDELFFKKIVEEFNLGMSGKINILVPLLE
IASLGEKIVLISNYTKTLDLLEQVLRKVSLEFSLRDLGSTPNVRSKLVNQFNTNPDIVFLLSSKS
GGMGINLVGASRLILFDNDWNPATDLQSMRIHRDQGLKPCFIYRLETTGCIIDEKIFQRQLVKNKL
SSKFLDNDATSKSDVFDNDLKNIFEIDTSTISNTHDLLECVCEGDGSMLSQPTIEESEPPPKQAW
VTALELKKKIDDGEALKRTAVKFAINDYRHYNPEVNRNLDFDSALHRIANNSSYENKQLPITFIMS
RVTN

YBR086C_homolog 2643bp PathoSeq: 1..2643; CDS: 501..>2643 (SEQ ID NO 295)

AAAGAATTTCAAATTTAGTTTGTAGGTGATAATTATCGTTCGTCCTTTCTTAACCTACCAATTTTGA
CTTTGTGTACTCATACGATGGTTGTTATTAGTTAAAGTTGCTTTGCTTTGCTTTTCAATTTCAATT
TCACAATTGAATTTCAAGATAGAAATAGTTTCACTTTTCTTACAATCGGCTAAGATTTTTTTTCA
TTCTTCTAATTTAGTTTACAGAATAGAAAGAATAGTTTGTGTTTGTGCTCATATTTACAATCAATT
GGTTATTGGTGTATTATTATTTTTTTGGTTCTCTTTTTACCCCCCTTCCGTCTAATTGAGTTA
TTGTTTGAATAATTTATTACTTATTCAATATATTTTTTTCTTCTTCCCTTCTTCAACTTCTTC
TTTATACATTTCAATCAACCTTCCAACAATCCTATAATTACTTACTTACCTTCTTCAATTGGATTA
ATTGGATTTGAATTGTTACAATTGAATCTTCAACGAGATGACTTTACCAATTCAGGATTTAGAAC
CTGATTATTATATTTCCGTCAATTTATCCTACCACCGATAATGGATCACCACCCCAAGCTGAAA
AATCATTGAAAACATTAATTGATTTATTATACGATAAAGGGTTTGCCTCCCAATTTAGACCTGGTG
ATTAGACCATTTGTTAGTCTTTGTTAAATGTCTTACACAAGTTTCTGAAGAAGCTGAAAAAG
ATTTAATTAAAAATTATGAATTTGGTGTACGGGTAAAGATGACGTGTAGCTTCTAAACTTAGAA
TTATTTATCAATACTTAATTTATCCACAATCAGTTGGTGGATGTGGTATTACTCTAATTTCTGGGG
ATTGGAATTTGTCAACAGTATGTTTCCAATTACTAATGCCTTTAATGAAACCACTTTAGTTGAAG
ATTTAAAAATTAATGTTACTCAACCAATTTATCAATTGCCACTATCAAAAAGACATATGGAGTTG
AAGTTGCTCTTTATTTTGAATATATAAAACATTACACTTTTTGGTTATTATTGCTTTCTATTATTG
GTCTTGATCTCATTTTAGAAAAGATAAACGATTCCTGTTAACTTTTGCTTTATCAATTTGCTTT
GGGGGGTTTTATTCTTGCATCATGGCATAGAAGAGAACACATTGGTTAATGTATGGGGTGTTC
AAAATAGTCATTTAATTGAAGACATAATTCGAATTGGCTAAAGTCAATGAAAGATATGAAGAAA
AATCAACTTATTTCCATGCAAATAATACCAATGGATTTCAGATTTTTAAACAATTCGCATTTATCC
CCATTGCCTTGGTGTGTTGTTGGTGTGTTGATTAGTTATCAATTGAGTTGTTTCTGTATTGAAATCT
TTTTAACCGATATTTATGATGGCCCCGGGAAATCTTTATTGACTTTATTACCAACGGTTTAAATCA
GTGATTTGTGCCAATTTTGACCATTTGTTATAATGCTGTACGGATATTATTATTAATGGGAAA
ATCATGATAACCAATATAGCAAAAATAATTTCTATTCTTGTAAACCTTTGTGTTGAATTTCTTGA
CTGGTTATGTTCCATTAATCATCACTTCATTCATATATTTACCATTTGCTCATTTGGTGCAACCTC
ATTTAGGTGATATTAAACCACTATTGCCACATATGCTGGTGAAAATAGATTCTACACCAAATACT
TGTTGAAATTAAAGAGTCAAGAAGAATTTAAATCAATCAAGGTAGATTAGATGCTCAATTTCTTTT
ATTTCAATTGTCAAAATCAAGTTATACAATTTGGTATTGAAATATATTCTCCATTGGGTTTAAGAT
TTGTATTTAATTTTATTGAAACGAAAATTCAGAAGAAACCTCAATTACAAACTAAAGATGATAACC
CTGATGAATCTATTTGGTTACATAATGTCAAGATTATCGTTGAAACTTCTGAAATATAATGTTGATG
ATGATTTTAGAGGATTAGTTTACAATTTGGATATTTGATAATGTTTGGTCCAGTTTGGCCATTGG
CACCATTGGTTTGTATTATTTCAATTTAATTTTTTTCAAGTTGGATAATTTTAAATTTATGAATG
GTAAATATTTCAAACCACAGTTCCAAGAAGAGTTGATTCTATTTCATCCATGGAATTTAGCCCTTT
TCTTGTAGCATGGATTGGATCAATTTATTTCCCGTGGTCACGGCATTTTACCGTCATGGTACTG
CTCCACCAAAATCTATGGGTCAATTTGCCCTTGATGATAAGCTAGTGTTCATGTTTCATCTCAGTTT
TCTTGGTTTTTATTAATGTTTGTTCAGAACATGGATTTTTGATTTTGAATTATCTTTTATTTGAAT
TCTCTTCTTTGTTCAAGAGTCAAGTTGAATGGGAAAATGATTTTGTGATAATGATATTAATTTGA
GACATGATTATTATTCTGGGAAAGTAAACCAACTTATAAGTCCACTCGGATGAGTTGTGGGAGA
AGTTTACCCCAATCAACTTTGAATTTCACTGGTCTTAAACCAACCGCAGAACTGATGATAAAG
TTGAAAAAATTGCTTCTACCGAAGATGCTTATCTGACTTCTGCAGAAAAATCTACTACTACTGCTA
CTT

YBR086C_homolog 714aa (SEQ ID NO 296)

MTLP IQDLEPDYIISVNYPTTDNGSPTPQAEKSLKTLIDLLYDKGFAAQIRPGDLHDHLLVFVKLSS
YKFSEEAEDLIKNYEFGVTGKDDVLASKLRRIYQYLTYPQSVGGCGITPNSGDWKFVTSIVPITN
AFNETTLVEDLKINVTQPNLSIATIKKTYGVEVALYFEYIKHYTFWLLLLLSIIGLVSHFRKDKRFS
LTFAFINLLWGVFLASWHRREQHLVNVWGVQNSHLIEEHNSSELAKVNEREYEEKSTYFHANNNTNGF
RFLKQLAFIPIALVFVGVLSIYQLSCFCIEIFLTDIYDGPGLSLTLLPTVLISVFPILTIVYNA
VTDIIKWNHNDNQYSKNNSILVKTFLNFLTGYVPLIITSFIYLPFAHLVQPHLGDIKTTIATYA
GENRFYTKYLLKLKSQEEFKINQGRLEDAQFFYFIVTNQVIQLVLKYILPLGLRFVFNFIETKIQKK
PQLQTKDDNPDESIWLNHVRSLKLEYNVDDDFRGLVLQFGLIMFGPVWPLAPLVCIIFNLIFF
KLDNFKLLNGKYFKPPVPRRVDSIHPWNLALFLLAWIGSII SPVVTAFYRHGTAPPKSMGQFALDK
ASVHVSSSVFLVLLMFVSEHGFLILSYLLFEFSSLFKSQVEWENDFVNDIKLRHDYYSQKVKPTY
KVHSDDELWEKFTPQSTLNTGPKPTAETDDKVEKIASTEDAYSTSAEKSTTTAT

YBR093C_homolog_1.1784bp public: 1..607, PathoSeq: 608..1784; CDS:
399.1781 (SEQ ID NO 297)

CGGTAATTATGTCACAAAAACAAACAATCAACATATTTAAATCGTTATCCCAACTTTGTTCAGTTTTTA
CTAACACCTTTTATTTTGTGTTATACAAATTCACAAATCAATTACTATAACTTTTTTTTGAACCGT
GGGCTCTGTTTAGTTTAACTTCTTGTAGTTTTTATTATTCGATTGGGTAGCTCAATAACTGCATT
TCGTACAATAATGTTAATTCAATTCATAATTCGATGAACCGAACACACAAAAAACATCCAGTTCT
GGAGAGATTTTTCAAAACTTCTATTATAAATAGAACCCCTATAAGTCCATAATAATTCAATTGAAGG
ATTATTTTCTTTTCCCTTTTCTGATTACTTTACCAATTTTCTTCTCTCAAAAAAACACCTTCT
TCATGGTTTCTGTTTCTAAATTAATCAATAACGGGTGTTTATTAACTAGTCAAAAGTGTTTTCCAAG
ATGTTGCTACTCCGCAACAAGCTTCTGTGCAACAATACAAATATACTCAATTTTCTTGGCGGTAGTG
CCCCTTATATTCAAAGAAACGGATATGGGATTTCTACTGATATCCCTGCTGGTGTGAAATTGCTC
AAATTCAATTGTATTCAAGACATGGTGAAAGATACCCAAAGTAAAAGTAATGGTAAAAGTTTAGAAG
CAATTTATGCTAAATTTGAAAACACAAAGGTACTTTTAAAGGTGATTTGTCATTCTTAAATGATT
ACACTTATTTTGTCAAAGACCAGAGTAATCTAGCTAAGGAACTAGCCCAAAAAATCTGAAGGAA
CCTATGCCGGTACAACCAATGCCCTTGCGTCATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTAT
ACAAGGAAAACCTCAACTTTACCAATCTTCACATCCAATTTCTAACAGAGTACATGAAACTTCAAAGT
ATTTGCTAGAGGGTTTTTAGGTGATGATTATGAAGAAGGTAAAACGTCAAGTTTAAACATCATCT
CTGAAGATGCTGATCTTGGTGCCAATAGTTTGAAGTCCCTAGAAAGTGCATGTTCCAAGAACAAAGAAC
TGAGCAGTAGTACTGCCAAAAAATATAACACAACATATTTAAATGCTATTGCTGAAAGATTAGTTA
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CTTATGGTAACGATCTTTCCAAATATTTATTTCAATGGTGCTGGTAATAATTACACCAGAATCATTTG
GTTACATGATTTTGAATTCATCTTGGAACTTTTGAAGGACACTAAGAATCTAATCAAGTATGGT
TATCATTTGCTCATGATACTGATTTGGAAATTTTCCATTCTGCTTTAGGATTATTGGAACACAGCTG
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GTGCCAGAATATACACAGAAAACTTCAATGTGGAAACGATGCTTATGTTAGATACATTATCAACG
ATGCTGTCTGCGTCCAAATTCACAAATGTGCTACTGGTCCAGGGTTCTCTTGTAAACTTGATGATTTTG
AAAATTTCTGTTAAAGAAAGAAATTGGAGATGTTGACTTTGTTAAACAATGTGGTGTCAATAGTACCT
ACCATCTGAGCTTACTTTCTACTGGGATTATAAAAAATGTCATTACAGTGCTCCTTTAGAATTGT
AA

YBR093C_homolog_1.461aa (SEQ ID NO 298)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHERYPSKSNKSLKLEAIYAKFENYKGTFGKDLNFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAFAKYGSLYKENSTLPIFTSNRNHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKESSTAKKYNNTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLLELLKDTKNSNQVWL
SFAHDTDLLEIFHSALGLLEPAEDLPTSYIPFPNPVYHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSLTFYWDYKNVTYSAPLEL

YBR093C_homolog_2.1871bp public: 1..1752, PathoSeq: 1753..1871;
CDS: 501..1868 (SEQ ID NO 299)

GAGTTTTATGGGATTGGGTTTTTCAATTAAAGACTCTTCGTGATAATGCAATACCAAAACCAAAAT
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GAAGAAATTGGTCAAAATTTGACAATGTTTAGTAACTTTATATCTTGGTGTGGGATGGTGCCACA
AATGGAGATTGTTGAGTGTACATGAAAAATACGTAGTTAAATTTTGTTCCTGTGTTTATTATTTA
GCCACTTTTTTATCCGATTCTTCATATTACCTTTGGTAAAGTGATAAGATTAATATCATATTAGTA
AAACACCCCCAATGATGAATGTTTGTATTTATAGCCAGACTATAAAAAATTACGGGGATTTAATTCCG
CGACTCACCCACGTTCTCACACAGTATGTGCTTTTTTCATAAGTATGATTGAACCCCTAAAATATC
AACTTTCATAATAAACATAATTCTTTCCAGACAATAAATGGTTGGTTTATCACGAGTACTTAATG
CTGGGTTTATTCTAAGTGGACAATCTGTTTTCCAGGATGTTGCTGCCCCACATCAAGCATCAATTG
AACAAATATAATATTGTCAAGTACCTTTGGTGGCAGCGGTCCATATATTCAAATTCAGGGTATGGGA
TTTCTACTGATATACCAGAAAAATGCACTATTGAACAAGTTCAAATGATTAGTAGACATGGTGAGC
GATTTCTAGTAAAGGAGATGGGAAATACTTTAATTCAGTGATGGAAGTTTTCAAGAGATATGGTG
AATTTTCATGGAGATTTATCTTTTTTAAATGACTATGAGTATTTTCGTTACTAATCCAGATTATGATG
AAAAGGAGACTACTCCTAAAAACTCAAAAGGTCCATATTTTGGAACTACAAATTTATTACGACATG
GAGCTTATTTTAGAAAAAGATATCAATCACTATTTGACCAAAAGGAGAAGCTTGTGTGTTTACTA
GTAATTCTGGAAGGTGTTATCAAAGTGGTGTCTATTTTCGCTCGAGGATTTTATAGGAGATGATTACT
CAGAAGATACAGTTGAATTTGTTGTTGTTGATGAAGACAAAAAATGGGTGGTAATTCATTGACAC
CAAGATACGCTTGTAACCTTTGAATCAAGATTTACACAAAGATTTGGTGAATCAGTACGATAAGA
CTTATTTGGACGATATTTTATCTAGATGGCTAGTACAACTCCTGGATTAGATTAAAGTGCAGATC
AGGTCTCGTCATTATTTCTTTGGTGTGCTTTGAGATTAACGTTAGGGGGTATTCTCCATTCTGCA
ATCTATTTACAAAAGATGAATTTATCAGAAGTGGGTACCGAAACGATGTTGGTAATTACTATCAAA
CTGGTCCAGGTAATAATATGACAAAGGTAATTGGCTCACCTATGGTGGAAAGCGTCGTTGAAAATGC
TTCAAGAAGATTCAAAAATTTGGTTGACATTTACCCATGATACTGATATTGAGATGTATTTGACAT
CTTTGGGATTGATTGTTCCACCAGGGGATTTGCCCGTTGATCGAGTACCATTTCCCAATCCATAA
ATGCAGCAGAATTTTCCCTCAAGGTGCTAGAACCTTACACTGAAAAATTGAAATGTGGTGAAAAG
AATATGTTAGATTTATTGTGAATGATGCAGTTTATCCATATCCGGATTGTAGTGGAGGTCTGGGT
TTACTTGTGAATTGAATGATTTTATCAAATAGTTAAAGTCGTTTACATGATGTTGACTATAAGC
TTCAATGTGAAGTGGACGGACCGGAATTGACATTTTATTGGGATTATAAAGACAGAAAGTATA
ATGCGCCGTTAATAGATCAGTAA

YBR093C_homolog_2 456aa (SEQ ID NO 300)

MVGLSRVLNAGFILSGQSVFQDVAAPHQASIEQYNIVKYLGGSGPYIQNSGYGISTDIPEKCTIEQ
VQMISRHERFSPKGDGKYFNSVMEVFVKRYGEFHGDLNFLNDYEFVTPNDYIEKETTPKNSKGPY
FGTTNLLRHGAYFRKRYQSLFDQKEKLVVFTSNNGRCYQSGVYFARGFLGDDYSEDVFEVVDDED
KKMGNSLTPRYACKTLNQDLHKDLVNQYDKTYLDDILSRWLVDNPGDLDSADQVSSLFLWCAFEI
NVRGYSFPFNLFTKDEFIRSGYRNDVGNYYQTGPGNNMTKVIGSPMVEASLKMQLQEDSKIWLFTFH
DTDIEMYLTSGLIVPPGDLVDRVFPFNPYNAAEFFPQGARTYTEKLKCEKQYVRFINVDVYP
YPDCSGGPGFTCELNDFIKLVKSRLHDVDYKLQCEVDGPAELTFYWDYKDRKNAPLIDQ

YBR093C_homolog_3 1888bp PathoSeq: 1..1656, public: 1657..1888;
CDS: 500..1885 (SEQ ID NO 301)

TGTAGTATAAATAAGGGTATGAAATACCAACATCCAGAATATCAACGAGATAGAAGAGAGGAGTT
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TCAATCTCAGGTAAAGAAAGTTTATATTCCATCACTATATAACAACAATCAGGCTTTGCAAAAAA
CATTAAAACTAATACTGGTAATATGGAATATAACGCCTCGTAGTTCTACGCACGTGGCATCCTT
TATCTATTTATTCAATTTACCCCTAATTTATGAATTAGCTTAATAAGAGCAGTCAAATTAACACGG
CTCAATTAATAGTACTTAATAATATGAAGCCGATCAATTAACCGATCCTTTGAATAATTTGAAAAT
AAAAATAAGTAATATAAATAGGTATGCATTTCCCTACATTTATTTCCCTCTTTCTATTTTAATTTG
TTTCCTAAACAGCAACAACAACAATTGAAATTCAAAAATGGTTTCTGTTTCTAAATTATTGAACAA
TGGATTGTTATTAGCTGGTCAAAGTGTCTTCCAAGATGTTGCTACTCCACAGCAAGCTTCTGTGCA
ACAATATAACATCGTCAATTCTCTTGGCGGTAGTGCCCTTATATTCAAAGAAACGGATATGGGAT
TTCTACTGATATCCCTGCTGGTTGTGAAATTGCTCAAATTCAATTGTATTCAAGACATGGTGAAAG
ATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAGCAATTTATGCTAAATTTGAAAACCTACAAAGG
TACTTTTAAAGGTGATTTGGCTTTCTTAAATGATTATACTTATTTTGTACTGATAAAAAACAATTA
CGAAAAGGAACTAGCCCAAAAAATCTGAAGAACTATGCCGGTACAACCAATTCGCTTGCGTCA
CGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAATTCACATTACCAGTTTCTC
TTCCAATTCAGGTAGATGTTACCAAACTTCAAGATATTTTGCTAGAGGATTTTATAGGTGATGACTT
TAAAGAAGGTAAAATGTCAAGTTTAAACATCATTTCTGAAGATGCTGATGTTGGTGCCAATAGTTT

GACTCCAAGAAGTGCATGTTCCAAGAACAAGAACGGAGCAGTAGTACTGCCAAAAAATATAACAC
AACATATTTAAATGCTATCACTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAAG
TGATGTCAACAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTCTG
TGATTTATTCACCAATGAAGAGTTTATCAAATATTCTTATGGTAATGACCTTTCCAACATATTATTC
TAATGGTGTCTGGTAACAATTACACCAGAATCATTTGGTTCAGTGATTTTAAATCTTCTTTAGAACT
TTTAAAGACACTAAAAACTCTAATCAAGTATGGTTATCATTTGCTCATGATACCTGATTTAGAAAT
TTTCCATTCTGCTTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTCCC
TAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAATG
TGGAAACGATGCTTATGTAGATACATTATCAACGATGCTGTCGTGCCAATTCCTAAAATGTGCTAC
TGGTCCAGGGTTCTCTTGTAACCTTGATGATTTTGAAAATTTTCGTTAAAGAAAGAATTGGAGATGT
TGACTTTGTTAAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATTA
TAAAAATGTCATTACAATGCTCCTTTAGGTGATTTTAA

YBR093C_homolog_3 462aa (SEQ ID NO 302)

MVSVSKLLNNGLLLAGQSVFQDVATPQQASVQQYNIVNSLGGSSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERYPSPKSNKSLKSLYKFNKGTGKDLAFLNDYTYFVTDKNNYKETSPPKNSGKT
YAGTTNALRHGAAPRAKYGSLYKENSTLPVFSSNSGRYQTSRYFARGFLGDDFKGKTVKFNII
EDADVANSITPRASCKNKERSSTAKKYNITYLNAITERLVKPNPGLNLTTSDVMNLFVWCAYE
INVRGSSPFCDLFTNEEFIKYSYGNLDSNYNSGAGNNYTRIIGSVILNSSLLELLKDTKNSNQVWL
SFAHDTDLFIHLSALGLLEPAEDLPTSYIPFPNPVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVFVKQCGVNSTYPSLFTFYWDYKNVTYNAPLGDF

YBR093C_homolog_4 1886bp PathoSeq: 1..102/1038..1062/1078..1886,
public: 103..1037/1063..1077; CDS: 501..1883 (SEQ ID NO 303)

ACTACTTAAATTGGCATATCCAAACAACTTGAAGTAGGAGTTTCCTTATTTTTATTTTGTATTTA
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TGCACAATCAATTACTATAACTTTTTTTGAAACGTGGGCTCTGTTTAGTTTAACTTCTTGTAGTT
TTATTATTCGGATTGGGTTAGCTCAATAACTGCATTTCGTACAATAATGTTAATCAATCTAAAT
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TAGAACCTTATAAGTCCATAATAATTCAATTGAAGGATTATTTCTTTTCCCTTTTCTGATTACTT
TCACCAATTTTCTTCTCTCCAAAAAACACCTTCTTCATGGTTTCTGTTTCTAAATTAATCAATA
ACGGGTGTTTATTAACTAGTCAAAGTGTTTTCCAAGATGTTGCTACTCCGCAACAAGCTTCTGTGC
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GATTCCCAACAGCAAGTAGTGGGAAAGATTATGAGAAAATTTATGCTAAATTTAAAAACTACAATG
GTACATTCAAAGGTGATTGTGTCATTCTTAAATGATTACACTTATTTTGTCAAAGACCAGAGTAACT
ATGCTAAGGAACTAGCCCAAAAAATCTGAAGGAACCTATGCCGGTACAACCAATGCCCTTGGCGTC
ATGGTGTCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAACTCAACTTTACCAATCTTCA
CATCCAATTCTAACAGAGTACATGAACTTCAAAGTATTTGCTAGAGGGTTTTTAGGTGATGATT
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TGACTCCTAGAAGTGCATGTTCCAAGAACAAGAAGTGAAGCAGTAGTACTGCCAAAAAATATAACA
CAACATATTTAAATGCTATTGCTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAA
GTGATGTCAACAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTCT
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TTTTCCATTCTGCTTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTCC
CTAACCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAAT
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CTGGTCCAGGGTTCTCTTGTAACCTTGATGATTTTGAAAATTTTCGTTAAAGAAAGAATTGGAGATG
TTGACTTTTATTAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATT
ATAAAAATGTCACTTACAATGCTCCTTTAGAATTGTAA

YBR093C_homolog_4 461aa (SEQ ID NO 304)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERFPTASSGKDYEKIYAKFKNYNGTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENSTLPIFTSNRNVHETSKYFARGFLGDDYEEGKTVKFNIIIS
EDADLGANSLTPRSACSKNKESSTAKKYNTTYLNAIAERLVKPNPGLNLTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLELLKDTENSNOVWL
SFAHDTDL EIFHSALG LLEPAEDLPTSYPFPNPVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFIKQCGVNSTYPSELTFYWDYKQVNTYNAPLEL

YBR181C_YPL090C_homolog 1635bp public: 1..938, PathoSeq:
939..1635; exon 1: 500..505, intron 1: 506..930, exon 2: 931..1632
(SEQ ID NO 305)

ATATATATATATTTATGTATTTTTTTTATTGTTGTTTCAGGAATTTTAAACATGTTTCATGAATAATGA
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TAGCCCTACTTTTACTTGTACGATACTGCATATTTTGTGTTGTGCGAATAGTTAGCGTAATAATC
TTTTTTTTTGTGTGTGTGCGGTTTACTTACTCTTCTCTTCGCACATATTTTATTAGAGCTTAC
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AGAGTAGGAGTTTAAACAGGATAATTGGATTCAATAAGAGGAAAAATTTTATCGTCGTGATTA
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GACATTTTGTAGACTACGTAAAAGTACTTTTCGATTCAAGGAAACCAAATTTTAGTATCTATCAACA
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TTCAAAGGTTACATCTTCAAAATCACTGGTGGTAACGATAAAACAAGGTGTCCCAATGAAACAAGGT
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GATTTTCGTTGTTAGAAGAGAAGTTACTAAAGGTGACAAAACCTTACACCAAGCTCCAAAGATTCAA
AGATTAGTTACTCCACAACTTTACAAAGAAAGAGAGCTTTGAAAGCTAAAAAAGTCAAGAATGCT
CAACAACAAAGAGATGCTGCTGCTGAATACGCTCAATTGTTGGCTAAGAGATTGCATGAAAGAAA
GAAGAAAGAGCTGAAATTTAAAAAGAAGAGAGCTGAATCTTTAAAGAACTAA

YBR181C_YPL090C_homolog 236aa (SEQ ID NO 306)
MKLNI SYPANGTQKSMIDDDTKLRVSTEKRMGQVEGDSVGDEFKGYIFKITGGNDKQGVPMKQG
VMHPTRVRLLSKGHSCYRPRRTGERKRKSVRGCI VAQDLSVLALSIVKQGDNEIEGLTDTTVPKR
LGPKRANHIRKFFGLTKEDDVRDFVVRREVTKGDKTYTKAPKIQRLVTPQTLQRKRALKAKKVNA
QQORDAAA EYAQLLAKRLHERKEERA EIKKKRAESLKN

YCL016C_homolog 1520bp public: 1..1079/1081..1520, PathoSeq: 1080;
CDS 501..1517 (SEQ ID NO 307)

GTGACGAGAACTTCTGTCTCTCGAGTCTGCCAACTGCCTCTAACAGCAACAACAATAAGAACAAT
GATAACGGAGGAGGATTATCCCATACAAACAGAATAGTTGTTGGTGATGTTGTTGGGGTTGGTGGT
TCTATATTAATTTGTTGTTGGCCGTTTATTTTACTTGAGAAAGAGAAACAACCGTGATTATGAA
GGTGGATGGACTTTCTGGAGAAAGAATGAGAAATTTGGGAAGTGATGAGTTCTTCAATGGTGAATTG
GGTGTGAGAGACAGAAATATTAATCAAGGATCAAAATTTTAAACAAGGCTTATTTGGATGAGGGT
GGTTTCTTGTAGTATTTGTAGTTGAATTTTAAATTTTGTACCTTAAAGCTTTTAAATTTAAT
TTTAATAAAAAAGTGGTGATTGTCGCAAACTTCAAGAGTATATTTGGTGAAAAAATTTTG
GAAGTGAACGCGTCTAACATCTTATACCTCTAAGCAAAATGTCAGAGTACTCTGTGTATCAACAGT
TGAATGAAGATACAAACGCAACTAAATATACCTTATAAATTAATACAGCTACCATCAAAGATACTAA
ATCAACTTGAATCCAAGTCAACTAACTTGATATATAAATCTGATATCAATTCCTTAGCATTATGCA
CTGATTACAGAACTTTCAAGTTACGACAAATGAACCATTCCAATACAGTCTTGCTATTGAACAAAG

AACCTGACAACAAGTTAATTGGGTTTCAGAAAACCAGTTATGAATATGAGTTGACAGAAATCAAAG
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TAATACCAAATTGATGAGTTTACAAGTGCACGAGTTTCTCCGGAAGATGTTTCATCCATCATCA
CGCCCCCTTATAATGACTCAATGGTAACATCAATCATACACAAATTTGCACTATAGAAAGTGAGA
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CTCCATTGGACATCAGTCAATTGGCAGGCTATTACTGCTCCCAATCGAAAACAAAATATTGTATG
TCGACCCAGAATCTTTATCAGAAAATTTGAGTCAACGATTCAAAGAATTGTTTGAATTGGATAAAA
GTTGGAATATGATGAGTTTATTCCATTCAATAAAAAGTTTGTCTGCGGTAAGGTCGACT
CAATTATTTTAAAGTATGGCAAGAAGAAGAAAGTTGGTAGAGATAGATTATAGTCTGTCTAGAT
AA

YCL016C_homolog 339aa (SEQ ID NO 308)

MSEYSVYQQLNEDTNATKYTYKLLQLPSKILNQLESKSTNLYIKSDINSLALCTDSETFKLQRMNH
SNTVLLLKNKEPDNKLIGFQKTSYEYELTEIKSIDTSDIPIFNGQTAQQPIDLIALEDNSICSHQE
FLSNWYELGGCEIDNGAYIMSADIITELLYLLITKLMSLQVHEFSPEDVSSIITPPYNDMSVTSII
HKFCTIESEKYQLNDLKITQWFGIVEMSKINHMTDISEFLINWKTSLPSFYNPPLDLSQLAGYYC
SPIENKILYVDPESLSENLSQRFKELFELDKSWNYDEFIPFIKKFVPAGKKVDSIILKYGKKKKVG
RDRFIVCPR

YCR073WA_homolog 710bp PathoSeq: 1..710; CDS: 315..707 (SEQ ID NO 309)

GGTGGGGTTCCCATTTTAATTTAAAAAAATTTTTTACCATCCAAAGGATTTTATTTACCCAAAGAC
CAAAAAATTATTATTGAAATGGGGATTAAATGGGGATAATTTTATTTTGCTGATGAAAAGATT
AGTACCCGTTTGAAAGTCCGTGATTCAAATTATGGTCAAGCTAAAAGAGAAATATTTGATTTAATTA
CTGGTGATAAAAAACCAAGATTTTCCATGTTGATGAATCATTAATTGATGATTCTCAAGAAGCTG
CTGATGAATATGAAAAACAATTGATTAATAATTTTGCTAAAAAAGATTCCGGTGAAATTACCTTTAT
TTGATTTATTTTATTAGGTTGTGCACCGGATGGTCATATTGCTTCATTATTTCCCTAATCATGGTG
AACAATTGAGAGAAAAATTAGCTTGGGTTTTACCAGTATCAAATGCTCCTCTGGGACCAGAAAAATA
GAATAACTTTATCTATCCCAGTTATATGTCATTCCGCAAGAGTGACATTTGTTGTTGAAGGGTTAA
CTAAGGCACCAATTATTAAACCATTATGGAAAGACCAGAAAAAGGTTTACCAAGTTCAATTGTTA
ATGAAGGTGCTGCTGGTAGAGTGAGTTGGTTTGTGATGATGATGCATTGAATGATTTGTTTGATA
TACTAAAAAGAAATACAAATATTTATCTATACCTGAACCAAGTCATTAA

YCR073WA_homolog 131aa (SEQ ID NO 310)

VKLPLFDLFLGAPDGHIALFPNHGEQLREKLAWVLPVSNAPSGPENRITLSIPVICH SARVTF
VVEGLTKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWFVDDDALNDLFDITKKKYKYL SIPEPSH

YDL010W_homolog 1190bp PathoSeq: 1..1190; CDS: 501..1187 (SEQ ID NO 311)

TGTTACAAAACATTCTGTTGGAGAGATAATTGAATTCAAAATTAACGTGTTGAATCCAACATTGAA
CAATGAATACACGTCCAAGAAAAATTTGACATGATTAGAATCGCGGTCAATTACATTCCCGGAACG
TCTTGGACTACTTGGATACAACAATGGAAAATGAGGAAAATGAGGAAAATGAGGAAAACGAGGAAA
ACGAGGAAAATATTTACCGAAGAGTAATTATATTACAAGCATTGAAAGAGGAGAAGTGAACGCCCC
AAACAGAAAACAATACCGAACATCACAAAAAAGACAACAGCTAAAAATTTTGGTCAGAA
CACAACCTTGGAAAGAAAGAAAAAACCAGAAAAAGAAATTCATCTAAAAACATACACAAATATAT
ATATATATATATAAATATATCCATATACATATGCTTTAATTTAACCTTCCCGCCTTTCTTTTCTTC
TTTTTGAATTATATCGATTTTAAAACTACACTTCATCATGGCTGGAGTTAGACAATTAAGAATAA
TAGCATTAAACGGCCTTTGTCTTGGTTAATTTTACTTTACATAAAGTTGGATCCAACGCTGCAT
CCTTGGTTTCATGCACAAGCATCAGACCAACAACCAACAAACATAACACCAAAAGTACTACATATA
CCGCCACTAATGACGAATCAGTTGCCAATCTCATTGATTCTAAAAATGATCCTCAAACCTGATGACA
AAATAAATCAAAAAATATCACAAAGATCAAGATGAAGCCATCAATGGTAATAAAGACACTAATAAAG
ACACCACCAAGTCAAACCAGATAATGGTGAATATGATCCAATATCTGATTTGATAAAAAATTAGAT
CATTATACCAATGACAATTTTCAGTAAATCATATTGTCCATATTCAAAAAAGATTAAACAATTGT

TATTAGAAAAATATGATATAACACCAGCACCAAATGTTGTTGAATTAGATCGATATGAATATGGAG
CTGAATTACAAAGTTATTTGACAGAGAAGAGTGGGAGAAGAACTGTGCCAAACGTATTGGTTGGTA
AATCATTTGAAAGTAGGGGTGGTTGTGATGAATTTGAAAACTTCATAAAGATAATGATTTGATTA
AATTGTTAGTTGAATGGGGTCTGGTCGTTTACAAGTTGCAAAGAAGAAATACCCCATCAAATGCCT
AA

YDL010W_homolog 229aa (SEQ ID NO 312)

MAGVRQLRIIALTAFVLGLIFTLHKVGSNAASLVHAQASDQPNKHNTKSTTYTATNDESVANLID
SKNDPQTDDKINQKISQDQDEAINGNKTNTKDTTKVKPDNGEYDPIISDLIKIRSLSPMTIFSKSYC
PYSKKIKQLLLEKYDITPAPNVVELDRYEYGAELQSYLTEKSGRRTPVNVLVGKSFESRGGCDEFE
KLHKDNDLIKLLVIEWGSGRLQVAKNTPSNA

YDL083C_YMR143W_homolog 1256bp PathoSeq: 1..1256; exon 1:

501..521, intron 1: 522..848, exon 2: 849..1253 (SEQ ID NO 313)

AGTGGTTGTTCAATAATGGTAAGTTCCTGGAAATAGCCATTGTTGCTTTCTGGTGGTTAGACTTGT
AGGAAGTAGAACTGTTTCCAAATGAAAAGTAGTTTTAATTAGAAAAATTTTCAAAGTGCGTGAAGC
CCAGTCTGAATGTGCGAGGAAGCCAGTCAGTTAGTAGTGTCTTCCCTCCACTGTCTGTAATACA
AAATTTCCCTTAGTGAAAATGCGAAATATATCTGTACTGGGAACCCCCCGGAAAAAACCCTA
TGCTCAAAACTATATGTACTGTACACAATCTAGGGCTATAGCCCTAATATTGTACAGGAAGAACTT
TAACTATGGTGCGAAGAGCGTTTCCAAATTTTTTTTTTTTCAGGTGTAGTCTGTTCTATGGCAATAC
TGTTGTTAGTAGAGAGTGTCTCGCACTAACAGAACATTTTTTTTCAGAACAGGAAAAATTTTGAAAT
CTAACATCTTTTACTGAAAGCCAGCATCAACACAATAATGTCAACCCAATCTGTTCAAGTATGTA
AACGAATTGAAATAAAGAGATAGAGAGATGTTTTATTATCAAAAATACGAAAGGAAAGGCAATTAAA
AAAGGAAATCAAAAAGTCCCAACCTTGCAGTAGAAGAATTGAGGTATATGAATTTGATAGATAGCC
AGAACGGTGTTACATAAATGGGATATAGAACAAACTATACGAGGAGTTTGTTCACCGATCATTC
AATAACCAGAAAACGATAATATTTTAGCGACCATTAATGACACTTGAAGGCTCACTGGGCCAATA
GAATATCTCCATATACACTTTTGAATATTTACTAACAATTTACTTTTGTCTTAGACTTTTGGA
AAAAGAAGACTGCCACTGCCGTTGCTCATGTTAAAGCCGGTAAAGGTTAATTTAAATTAACGGTT
CCCCAATCACCTTGGTCCAACCAGAAATCTTAAGATTCAAAGTTACGAACCATGGGACTTTGGTTG
GTTTAGATAAAATCCAAGGTATCGACATCAGAGTTAAAGTCACTGGTGGTGGTCACTGTTCTCAAG
TCTACGCCATCAGACAAGCTATGCTAAAGGTTGGTTGCTTACCACCAAAAATACGTTGACGAAG
CTTCTAAGAACGAATTAAGAAAAATTTTCGCTTCTTACGATAAGACCTTGTTAGTTGCCGACTCAA
GAAGAATGGAACCAAAGAAATTCGGTGGTCTGTTGTCAGAGCAAGATTCCAAAAATCTTACCGTT
AA

YDL083C_YMR143W_homolog 142aa (SEQ ID NO 314)

MSTQSVQTFGKKKTATAVAHVKAGKGLIKINGSPITLVQPEILRFKVEPLTLVGLDKFQGIDIRV
KVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEASKNELKKIFASYDKTLLVADSRRMEPKKFGGRG
ARARFQKSYR

YDL125C_homolog 959bp public: 1..959; CDS: 501..956 (SEQ ID NO 315)

GTGGTAAGATATAGAAAGCTTACCACCTTTGACAAAGTTTGAAATAGGATGGGTGAAAATTTGGACAT
CTTGAATACTTAAAATTTCTGAACCTTGATCACCAGATCCTTTTCTTTTACATAAATTAGATATGATGG
ATAGGTTAGAATCGTCTTTAAAGAGAAGGTATAATATCTAACTGATTTGGCGAGGTGTTGGAAG
TCACTCCACTGTATATATTCTCGGAGTTTAAAGTACTACAGTTCACTGGGGTGAATACCTAAATAG
GGGGGTAGAATACGAACCTCTACAAATTTTAAAGGAGACTATGACCCGAAAAGAGAAGAAAAATTTA
TTACTCTAAGAATTTTATATACCTCCACAACCTCACTTTTTCTTTAGTTTCATTCTGCTTTTTTTTT
CTTACACATCTTAAGGTCAAACAATTTAACTTATTAGCTTGTGAAAATCTCACTTCAATTCAAGTT
CTCTTTCAATTGACATTATAGTATTTCCCAATTTCAATTATGGCTTCTCATGCTTCTGTATATTCT
GTAAAATTATCAAAGGTGAAATTCCTTCTTTCAAGTTAATTGAAACTGCAAAGACTTATTCCTTCT
TGGACATTCAACCAATTGCTGAAGCCACGTTTAAATTATCCCTAAACACCATGGGGCAAAGTTCG
ACAACATTCCAGACGACTACCTTAGTGACATTTTACCAGTTGTCAAAAAATTGACAAAAGTCTTGA
AATTGGACGAAAATAATACTCCAGAAGGTGAAGGTTATAACGTTTTACAGAACAACGGAAGAATTG
CTCATCAAGTTGTTGATCACGTTCACTTCCATTTGATTCCCTAAAAGGATGAGGCTACAGGTTTAG

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GTGTTGGTTGGCCTGCTGAAGCCACTGATTTTGATAAAATTAGGAAAATTGCATGAGAAAATTAAAGG
AAGAATTGGCTAAGGTAGATAATGAAAAATTATAA

YDL125C_homolog 152aa (SEQ ID NO 316)
MASHASCIFCKIIEGIPSFKLIETAKTYSFLDIQPIAEAHVLIIPKHHGAKLHNIPDDYLSLILP
VVKKLTKVLKLDENNTPEGEGYNVLQNNGRIAHQVVDHVHFHLIPKKDEATGLGVGWPAEATDFDK
LGKLHEKLKEELAKVDNEKL

YDL133CA_YDL184C_homolog 297bp PathoSeq: 1..297; CDS: 220..294
(SEQ ID NO 317)
CATAATTATTACATATAAACTCGCACTATAATTTTTTTTTTTCTATTCTGTGTGTGTGTGTGTGT
GAGAGCCAGAGAAACCAAACTGACTGAGTGATCGTCTCTCAACAATTTATTTCTCCTCGTCTTATT
TTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTA
CCAAAACACTAGTATTTCAACATGAGAGATAAGTGAGAAAAAAGAGAGTTAGAAGATTAAAGAGA
AAGAGACGGAAGGTTAGAGCTAGATCCAAGTAA

YDL133CA_YDL184C_homolog 25aa (SEQ ID NO 318)
MRDKWRKKRVRLKRRKRRKVRARSK

YDL136W_YDL191W_homolog 1303bp PathoSeq: 1..1303; exon 1:
501..503, intron 1: 504..943, exon 2: 944..1300 (SEQ ID NO 319)
TATTGTCTGATGCTATACGGAATGGGCGTTACAAATATACAAACTTATATTTGAAAGTAAATCTTA
TTATTTTCTTCTATCGTATGCATACCGATTATTATCACAAGGACAATTGCCTATTGTTGTGTGGAA
TAAATTTTAAATCCTTCTTATTGGTGCTAGACTTTTGCTTTTTGTGGTGATTAGGGCTTTAGCCCT
ATCACGTGAAATACTGTATATAAAAAATTCTTTATAGCGCGATAAAACATATTTTTTTTCCGTATT
AACAAATATGTGTGAAGTTTTGTCTGCTGTTTCTCACTGTTTTTCTTTTCTGCTAGTAT
CAATTAACGCTTAGATCCAATACAGTTTTGGTAACTTGACACGAACAAAATCTCAAATTTGTTAC
TGTGTGAACCAACAAGGAAGAGAAAAAAACCATACAAAAATTTTTTCAAGTATCAAGGAATTAGA
AGAGACGTTTAAATCAACAAAGTTCAAATCTATCAACAATGGTATGTTTAAATATCGATATTATCCA
TAGATGTACATGTATCCTAATGGGTTTCATTATTTGGAAAGTTATGTTTATGGGAGTTCTATTTAT
TAAGATATGGGATAAGAATTAAAGTATTGGATGAGTAGTACAAGACCAACAAAGAGAAATAGCCCC
CTTTCCCTCCACTATTCAATATACTCAACAACATTATCAAGTTAAAAGTTCAGAAGATACACGTAA
ATGAAAAGTTAATACCAAGAAGAATACAAATTACCAGTCCATACCGTGTGTTGGGTTTAGATTACTA
TATTTTACAAGAAACATATTATATGAAATGATACCCAATCCACAGCGACTTTTCAGATAGCCAAAT
AACTAAGCAACTCAAGATAACATAGGATCATGCATCAATCACAATGAAACATTAATACTAACTAA
CTTTTTTTTTTATTATTAGGCCGGTGTAAAACTTTTGAATTAAGAACTAAATCTAAGGAACAATT
AGAATCTCAATTGGTTGAATTGAAACAAGAATTGGCCACTTTAAAAGTTCAAAAATTACAAAGACC
AAGTTTACCAAGAATTCACACTGTTTCGTAAAAACATTGCTAGAGTATTGACTGTTATTAAGTTGAA
TCAAAGAGAAAATGTTTCGTGCCTTTTACGCTGGTAAAAAATACATTCCAAAAGATTTAAGAGCTAA
AAAGACTAGAGCTTTAAGAAGAAAATTGACTAAATTTGAAGCTTCTCAAGAACTGAAAAAGCTAG
AAAACAAGAATTGCTTTTCCACAAGAATAATTGCTATTAAAGCTTAA

YDL136W_YDL191W_homolog 120aa (SEQ ID NO 320)
MAGVKTFELRTKSKEQLESQLELQELATLKVQKLQRPSPRIHTVRKNIAARVLTVINLNQRENV
RAFYAGKKYIPKDLRAKTRALRRKLTKFEASQETEKARKQRIAFPQRKFAIKA

YDL167C_homolog 2690bp PathoSeq: 1..1640, public: 1641..2690; CDS:
501..2687 (SEQ ID NO 321)
CTCTGTGTAAATTGATGAAATCCACACAATAAAAAATTTCTTTCTTTCTTTTAAAGAACCTAAAAACA
GAATCAACATTATTTGCCCCATACATATCCAAGAATTAAATACTTATTAGTTCTAAGTGGAAATAGA
AGAGAATCAAACCTTAACATTACTGTTACGCAACGTCAAGAGGGCATTTTTTTTAGTTTAAATTTGT
TTCATTTCAATTGAATCTTTAAGAATCACCGAGTATACATACTTTCTTTTGTATTTTATCAGGGAA
GCCACATCCAACCAAGTTACATCCCACAAAATCCCTTAATCTTGTTCTTAGTTGTATTATTAATTA
CTATTGAATTTAAGTTTGATATGCGAGAGAATATTGTGGATTGTATAAGTTTGAAGTTGAGCTTGA
ATACTTTGAGGGGCTTAATCATATATTGCATTTTATACCCTACTCGCGGTGTTGCTTACCACACTG
ACTAGTATGATCTTTCTGAGATTTCTAGCCAATAAATTATGAGTGATATTTATATTATTATTATCATA

TTTCTACTACCTGTGATGACTCGCCGACATTTGTCTACTAAGGATTCTTCCGAGTTAATTGAATTTG
CTTGGGAAACAGTCGATAGTGTCACTTTGGAAACTTTATACAAAGGATCAAACCTTGGTTCGTCCAA
CCAACACACCTATCACACCTTACTGCTCGAAGATTTCATAGAATAACATGGGACAATGTCAAAAATG
CTGGGTCGTTCAAAGACGCCATCACAACTTTGATCAATACGTACAAGAACACATAATTTCCAAGA
AAAAGGAGTTTTCATTTGTGATGTTTGACATTTCCAAATTGAGAGTTTCAGTTGGTTTCGTGAAGCTA
GAGACAAATCCGTGGTTTTACCTTCGTATCTACAACATCCAAGGATTTTGTATTTACCAAGAGAAT
ATTTAAATTGGCAATCTAGCCACCTGAAACATTATCATACCCCCCAACTTCTTTAACTAATATTA
TTACTGCATTAGAAGTTGAGGTTGAGAATATATCTGAATATGTGCGACTTGCCAAACTTTTCTTCCA
CACCATCACCATCAAAAAGCTTCAGCAACAACGACGACGACAACTGCAAAATGTACAGCCATTGACG
TCCTTTCCAGTGAAACAGAACCAGTAAAGTCAATTGCAATTTGCACGCCAAAATTTGCCAAAC
AATTGATCAAAAAATCCATCCCTGTTGAGAATCACCTAATGTATTTACAAGACCTTTTGATTCGG
CTCAAGATATCACTGCTTTTACATCAGAAAAGATCAAAAGTACTCTATCTTTCCAACCTTGCCAAACG
ACACCACACAATCAGAGTTGGAATCATGGTTCCTCAGTATGGTGAAGACCAGGTGGGTTTGGGA
CTTTTAAAGTCTGCAGATGATAACAATAATAACAACAACAATAGCAATGGCGGAAAGGATATC
AGAATGCGAGAAAATATGGTATTTTCAGGGTTTGTGGCCTTTAATACTCATGAGGAAGCAGTTGATT
GTTTAGCTTTGAATGGGAGAGTGTGAATGATCGTCTATTGAAGTTCAAGCGTCTTCTAGTAAAG
TGTTTGATATGGCCATGGATAAATGTTGTTGACTCTGTTCCTCACTCTCAAAGAACAGACCTAGAC
CCGGGGATTGGACTTGTTTATCTGTGGGTTTTCATTTCCAGAGAAGAACACACTGTTTCAGGT
GCTCTTTTGGCGCAGTGGCGTTTCAGGATGTTTTTAACAGTAATACAGGCAATGCCAACGGTAATG
GCAATGTTAGCGGCAACCACAACCACAACCAATAGTGGAGCTCGCCGTGGCATGAATTTACAGC
CTGCTCAAGCTAATGAGAAAATTTGGAACAGGCAATATTAGTATTCCTTCTTACAACGATCCAATCA
AGGGTCCAACAGGTAATGTCACTAATCACCTCAACAATTTCTGAGACCAATTTACTGAACAACACTA
ATCTTAACAACAACAATCATCATAGTAATAATTATCACAAATAACTACCATCACCACAACAACAATA
ATAACAATCATGGGAATAGCAATGGTAACACCATAACATGGTTCCTTCCATTATAACAATAGTGTTT
CATTTAGAGCAGGTGACTGGAATGTGAAAATTTGCATGTATCACAATTTGCCAAAAATTTGTGTT
GTTTAAAATGTGGTGTGCGCCAAACCTGCTATTAACAATCAACAAAATAATACAATTCATTCGGTGA
ATTCACGGCCGCTGCCATAGCTGCAGCAACAGCCAGTGGTCAACCTTTAACTTTGAATAATAATG
CATTTTGAACCTTCAGCAACAACAGTCTCAGTCACAACCCCAAGGTCAGCACCATTACAACCAAC
ATCTTCGTAACAACAATGCTTCTGGGGCATCAAAGTTCAACAATGGCTACAACCCAAAGAATCAGT
ATTACAATAATAATAGCAAGAATCTTAGCAACAATTTTGGTCTTAATGGTATGCATCAGCAAAACC
AAAATCAAATTTTGTATGTTTACAACAATTTGAACAACAACAGCAACAACAACAGCAACAACAGC
AACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACATGATTTAA
ATGGAAGTAGCTCTTCCCATCAACTGAACTTCAATTGAATAATACTTGA

YDL167C_homolog 729aa (SEQ ID NO 322)

MSDIYIIHISTTCDDSPFTVKDSSELIEFAWETVDSVTLETLYKGSNLVRPTNTPITPYCSKIH
RITWDNVKNAGSFKDAITNFDQYVQEHIIISKKEFSIVMFDISKLRVQLVREARDKSVVLPYSLQH
PRIFDLPREYLNWQSSHPETLSYPPTSLTNIITALEVEVENISEYVDLPNFSSTPSPSKASATTTT
TTANVTAIDVLSSETEPNKQVIANLHAKIAKQLIKKSIPVENHPNVFTRPFDQAQDITAFTSERSK
VLYLSNLPNDTTQSELESWFTQYGGRPGGFWTFKSADDNNNNNNNSNGGKGYNARKYGISGFVA
FNTHEEAVDCLALNGRVLNDRPIEVQASSKVFDMAMDKLLLSFPLSKNRPRPGDWTCCLSCGFSN
FQRRTHCFRCFSFAAVAFQDVFNSTGNANGNGNVSGNHNHNHNSGARRGMNLQPAQANEKIGTGN
SIPSYNDPIKGPTGNVTNHLNNSETNLSNNTNLNNNNHHSNNYHNHNNHNNNNHNSGNTI
GRSHYNNVFPFRAGDWKCENCMYHNFKNLCCLKCGVAKPAINNQQNNTIHSVNSTAAAIAAATAS
GQPLNLNNNAFLNLQQQQSQSOPQGHYHNQHSRNNNASGASKFNNGYNPKNQYNNMNSKNLSNNT
GLNGMHQONQNIILMYSQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQHDLNGSSSSSHQSKLQL
NNT

YDR238C_homolog 3359bp public: 1..1467/1469..3040/3042..3359,

PathoSeq: 1468/3041; CDS: 501..3356 (SEQ ID NO 323)

AATAGCATTGAACAAGAAGAAGAGGACAACGATAGACCAAGGTTGGTTTTAGCCAATCCTGATTAT
GATAGTGATGACAGTTCATAGACAATTTACAGCCTTAAATGGATATATATGTATATTTAATAATAA
AGGACTTGTTTTTTTAGTAAGTGTGATGCTCTTTTCTGGGTGTACATTTCCGATGACCAACCA
GGTTATATTTTAGCAGTTTATAGACAGTGTATCGATGGGTAATATAAAATAAAAGCTCATTGAATA
CTATCTAGTGAAAAGTCGTGTGTAATCGATTTGAAAAATATAAAACCATACACGTAATGAAATG
TGTGTGAAAGTACAACCAACAACGAAAAAGAACAAAAAATGTTGTCCGCCAAAAAAGG

AGAACAACAAATCAAAGTTTCAAGACTATCTCAAATCTTGTGTCACCATAACTATCAATTGTTCA
CCTCTTGAACCAACATCAAATTGAATAAACATAGGATCATGAGTGACAGTGGTTATACATTAATCT
ATGAGCCTAATACGGCTACGAAAGTATCTGTCAATGAATTTAAAAATTTGTTGGAAAAGGGTAAAG
ATGATGTGAAAGTAGATACCATGAAGAAGATTTTGATTACCATATTAAATGGAGACCCCTTACCTG
ACTTGTGATGCATATAATCAGATTTGTTCATGCCTTCCAGAAATAAAGAATTGAAAAAGTTGTTGT
ATCATTATTGGGAGGTTTGTCCAAAAATGGATGAATCAGGTAAAAATGAGACATGAAATGATTCCTTG
TGTGTAATGCCATCCAACGTGATTTACAGCATCCAAATGAATATATTTCGAGGCAATACTTTGAGAT
ATTTGACGAAATTGAAAGAGCCAGAATTATTGGAACTTTAGTTCCTAATGTCCGTCAATGTTTAG
AACACCGTCATGCCTATGTCAGAAAAAATGCTGTTTTCGCATTATGGTCTATTCATAAAGTCAGTG
ATCATTTAGCTCCTGATGCTGACGAGTTAATTTACAGATTTTGTATGAGGAAAAACGATTCTGTTT
GTAAAAGAAATGCTTTTGTGTTGCTTGGAGACTTGAATAGAGAAGCTGCTTTGCAATATATTCAAG
ATAATATTTTTCAGTTATTGAGACTTTGGATCCATTGATACAATTTGGCTTTTATTGAGTTTATCAAAA
AGGACTCTATTCAAATCCAGCTTTAAAGCAACAATATGCCCAATTAATGACAGAAATTATTGAAA
GCTCTTCAAATGTTGTTATGTATGAAGCTGCTAACACGTTGACTGTTTTGACTTCAAACCCACAAT
CAATTTTGTGTCAGGAAACAAGTTTGTGTAATTGGCTACTAGAGAGTCTGATAATAACGTTAAAA
TTATCACTTTAGAGAGAATAAATCAATTACACAAGCAACATCCTGGTGTGTTACAAGACTTGTTCAT
TAGAAATTTTACGAGGTTTATCTTCCCAAGATTTGGATGTTAAAAAGAAAGCTCTTGATGTTACTT
TACAATTTATCACCACCAGAAATGTTGAAGATGTTGTTAAGTTATTGAAGAAAGAATTGCACTCTA
CAGCTTTATCCAATGATGACAAGAATGCAGATTATAGACAGTTGTTAATTAATGCCATCCATCAAT
TGGCTATTAAATTTGTGGAGGTTGCTGCCAATGTCATTGATTTATTGTTGGATTCTATAGCCGATT
TGAATACCACTGCCGCTACGAGGTTATCACATTTGTTAAAGAAGTTGTTGAGAAATTTCCAGATT
TAAGGGACGCTATTTTGAGAAGATTGATTTTGGCTTTGCCACATGTGAAAAGTGGTAAAGTTTCC
GTGGTGCATTATGGGTTATTGGTGAGTATGCCTTAGAGGAATCATTAAACAAGAATCTTGGAAT
ATATTAGAGGAAGTATTGGTGAAGTACCAATTATTGCTAGTGAATTGAAACTGAAAAAGCGTGATG
ATACTGAGGAATCACAAGAGGAAGAAACCGAGTATGATGGTAAACCTCGCAGAAAGGGTCCAGTTG
TATTGCCAGATGGTACCTACGCTACTGAGTCAGCATTGACAAGCGAAACAACACTGACTCTTTGGAAA
GTGACAGCAAGACTCCTATCAGAAAGCAAATTTCTGCTGGTGATTTCTACTTAGGTGCTGTATTAG
CATCAACTTTGGTGAAATTGATTCTCCGATTGCAAAGTTTGAACAAACTCAAGAAAAAATTTTGA
ACGGATAAAGCAGAAAGCATTGTTGATTATGGTTTCGATTTTAAAGAGTTGGGGAATCTAGCTTGG
TTTCTAAGAAATTTGATGAGGATTTCTGCTGACAGAATTTTGTCTTACATCAAGATTTTGAACGATG
AAGAAGACCTTCAGGAAATCAAGACAAGCTTCTTGAAGATACTAAAGATGCATTTAAAGCACAAA
TTAATAATGCTGAATTGAAGAAAGCAGAAAGCATTGGCTAAGGATTTGCATGATAACGCTGAACAAA
TTGACGATGCAATTGTTTATGACAGTTGGATAAAGATAACAAAAAGAGTAAAGCTTCTGTGGATG
ATGTTGCTGCTGCGTCAGGAAGCAATGAATTAAGAAAGAAAATTTGTCGTCGAGATTGAACAAAA
TTATACAATTGACTGGGTTTTCCGATCCTATTTACGCAGAGGCATTGTCAAAGTTTATCAATACG
ATGTTGTGTTAGATGCTTGTCTAGTGAATCAAAACCAACTACTTTAAGAAACTTATCAGTTGAAT
TTGCTACATTGGGTGATTTGAAAGTGGTTGATAAACCAACTACCGCAAATATTGGACCTCATGGTT
TCTACAAAGTTCAAACAACCTATTAAAGTTACTTCCGCTGATACTGGTGTCTATCTTTGGTAACATAG
TGTATGACGGTCAACACTCGGACGATTACGTATAGTTATTTTGAATGACGTTACGTTGACATTA
TGGATTACATTAAGCCAGCCACTTGTTCAGAAAGTCAATTCGTAATGTGGAACGAATTTGAAT
GGGAGAATAAGATAACCATTAAATCACCTATTGAAACATTGAAAGAGTACTTGGATGAATTAATGA
AGGGTACAAATATGCAATGCTTGACACCGGGTCCGTAATTGGAGAAGAATGTCAATTTTATCAG
CAAACCTGTACTCAAGGTCAAGCTTTGGTGAAGATGCATTGGCTAATTTATGTATAGAGAAACAGA
GTGATGGACCAATAATTGGTCATGTGAGAATAAGATCAAAGGTCAAGGTTTGGCTTTGTCTATTG
GTGATAGAGTAGCTTCCATTTCAAGAAAAGGTAAGAAGGCAACTATTGCTCGTGTTTAA

YDR238C_homolog 952aa (SEQ ID NO 324)

MSDSGYTLIYEPNTATKVSNEFKNLLEKGDVVKVDTMKKILITILNGDPLPDLLMHIIIRFVMP
RNKELKKLLYHYWEVCPKMDSESGMRHEMILVCNAIQRDQLQHPNEYIRGNTLRYLTKLKEPELLE
LVPNVRQCLEHRHAYVRKNAVFALWSIHKVSDDLAPDAELIYRFLYEENDSVCKRNAFVCLGDLN
REAALQYIQDNISVIETLDPLIQLAFIEFIKKDSIQNPALKQQAQLMTEIISSSNVVMYEAANT
LTVLTSNPQSILLAGNKFVELATRESNMVVKIITLERINQLHKQHPGVLQDLSLEILRGLSSQDLD
VKKKALDVTLLQFITRNVEDVVKLLKKELSTALSNDDKNADYRQLLINAIHQALIKFVEVAANVI
DLLLDSIADLNTTAAYEVITFVKEVVEKFPDLRDAILRLILALPHVKSGKVFRLGALWVIGEYALE
ESLIQESWKYIRGSIGEVPIIASSELKSKKRDDTEESQEEETEYDGKPRRKGPVVLPGDGYATESAL
TSETTDSLESDDSKTPIRKQILAGDFYLGAVLASTLVKLILRLQSLKQTQEKILNGLKAEALLIMVS

ILRVGESSLVSKKIDEDSADRILSYIKILNDEEDLQEIKTSFLEDTKDAFKAQINNAELKKAEALA
KDLHDNAEQIDDAIVFRQLDKDNKSKASVDDVAAASGSNELKKENLSSRLNKIIQLTGFS DPIYA
EAFVKVHQYDVVLDVLLVNQTTTTLRNLSVEFATLGLKVDKPTTANIGPHGFYKVQTTIKVTS
DTGVIFGNIVYDQHSDDSRIVILNDVHVDIMDYIKPATCSESQFRKMWNEFEWENKITIKSPIET
LKEYLDELMMKGTMMQCLTPGAVIGECCQFLSANLYSRSSFGEALANLCIEKQSDGPIIGHVRIRS
KQGLLALSLGDRVASISRKGKKATIARV

YDR294C_homolog 2270bp public: 1..278/280..2270, PathoSeq: 279;
CDS: 501..2267 (SEQ ID NO 325)

GTTTGATCACATGTGTTGTGAACACTCGGGTAATACAAAATAGTGAGAGAGAAGAAGGGGAAAAA
AAAAGCAGAACACAAAACATGGAATTTGAAAACAAATTTGTAATTCATCGATCCGAGACTTCCAT
AGCAAAGTTAACAAGCACAAATGTCTTTTAACTTAATTTGGTGGATTAATCGGGATCAATCTGAAT
TGTTTCCCGTATTGTTTAAACCAAGAAAAAGGATAATCAAACTAAATCTTTCATATTAACACT
ACCATTTTGTAGTGGTCAGTTTATATAATTTATCCTGTTCTCTTACAAATTAATAAAAAA
AAAGAAAAAAGAAAGCTCTCTCTCCCCAAAAGAAAAAGCAAAGGTAATTCCTTCATACACACCTT
TGATATCTTTTCTCTTAGACTTTTCTTTTAACTTGCATCAATTGGAATATTACTTGTTCATACT
GGAGTTTTCATTGAACTAAATATTATTAATAATATTATTATGCTTGAATTGAATTCATTTACGATTC
CTCGGAATTTCACTGAATTCCAACTCACAGCATTAAGATCTACTATCAACTTAAGATTTTATTTT
TTGCCACATACTGTGCTCAAGGATCATTTGGCTTGAACGGTTCACTGTGTTTAGCAAGAGATATTT
TTGTTGGCTATGTTGTATACACTCAATTTATTAAGCTTTATCGAGTATTAAGAGGGTACGGTATTG
TAGATTCTATTGGAAGGTTATACCTATATGTTAGTTCTACGGTGTCTCAATCTTTTCACTAC
CATTTATTAAATCCAAAATTGACAAGGAATTCGAAGCGACTATTGGCAAAGTAGAAGAAGAGATTA
TGAAAAACGATCCACAGTTATTACAGTTTCCCGAATTGCCAGAACAGGGTATTGACGCTGACAATG
TTTCTTGGAGTTGGATAAATTACAAAACCTTGAACATTCTGACTGGATCAATGGAAGAGTCAGTG
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TGGCAATCAATTGCATCCCGATGTTTCCCGAGGTGTGCGTAAGATGGAGGCCGAAGTAGTTCCATA
TGGTTTTGGATATCTTTAATGCTCCGAGTGACGGGTGTGGATCGACAACTTCGGGAGGTACTGAGT
CGTTATTGTTAGCCGGGTGTGCTAGAGAAATATGGGAAGAAATATCGTGAATAACTGAGCCTG
AAGTCATTGCCCCGTGACAATACATGCGGGAATTGAAAAAGCCTGTTTTATTTTTGAATGAAAT
TACATAAAGTTGACTTAGATCCGGTTACCTTTCAAGTTGACGTTAAGAAAGTAGAAAGATTGATCA
ATAGTAATACAGTTTAACTGTGGATCAGCCCCAAATTTATCCTCATGGAATAATTGATGATATAG
AGTCTTATCCAAGTTGGCAGTCAAGTATAATATCCCGTTGCACGTTGATGCATGTTTGGGGTCAT
TTATTGTTTCGTTTTTAGAAAAATCAAAAGTACATGGCGATAGGAAATTGCCCATATTTGATTTTC
GATTACCAGGTGTACGTCAATCTCATGTGATACTACAAATATGGGTTTGCTCCCAAGGGGTGAT
CAATAATTATGTACCGTTCCGCAAAATTTACGTGAGTGTCAATACTATATTGCAAGTGATTGGACGG
GTGGAATGTATGTTCTCCAACCTTTGGCTGGTTCTAGGCCAGGTGCTCTTGTAGTTGGATGCTGGG
CTACATTAATCAATATTGGGAAACAAGGATACACCAAGTTTGTGTTACGATATTGCTGGCGTCAA
TGAAAGTTAAACGAGCAATTGAACTGACCCGATACTATCCAAACATTTACAAATTTATGGTGATC
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TTAGTGATTTGTTGACCAAAAAAGGTGGCATTTTGCACCTTTACAAAACCCATCAGCATTTACATT
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AAGAAGCGGTGGCAATTGCCGAGGAACACAAAAGAATGGAGTGACCAAAGCTCCAGGTGATACTG
CTGCGTTATATGGTATAGCTGGCAGTGTACATACAGCAGGGTTGGCTGATAGATTAATTGTTGCAT
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YDR294C_homolog 589aa (SEQ ID NO 326)

MLELNSITIPRNFTEFLTALKIYYQLKILFLATYCAQGSFGLNGSVCLARDIFVGVVYVYQLLKL
YRVLRGYGIVDSIRRLYLYVSSVSSQIFSLPFIKSKIDKELQATIGKVEEIMKNDPQLLQFP
PEQGLIDADNLSLELDKLNKHSWDWINGRVSGAVYHGGENLLSLQVEAYKKYSVANQLHPDVP
RKMEAEEVHMLVDIFNAPSDGCGSTTSGGTESLLLAGLSAREYGKKYRGITEPEVIAPVTIHAG
KACFYFGMKLHKVLDLPVTFQVDVKKVERLINSNTVLICGSAPNYPHGIIDDIESLSKLAVKYNIP
LHVDACLGSIIVSFLEKSKVHGDRKLPIDFRLPGVTSISCDTHKYGFAPKSSIIIMYRSPKLR
QYYIASDWTGMYGSPTLAGSRPGALVVGWATLINIGKQGYTKFCYDIVSASMVKVRAIETDPIL
SKHLQIIGDPIGSVISFQLAPQQSGNLSIYEISDLLTKKGWHFATLQNPALHFAFTRLVTPVVD
LIADLVEATKEAVAIAEEHKKNVTKAPGDTAALYGIAGSVHTAGLADRLIVAFLDLTLYKI

YDR430C_homolog 3605bp PathoSeq: 1..330/1927, public:
331..1926/1928..3605; CDS: 501..3602 (SEQ ID NO 327)
TTCAATTTTTTTTAAAAAATAGCAAAAAGGTATTTCTTAGAAATGAAAAAATCACAATAA
AATTTATAAAACCGGATAGGGCCGTTATCGCAGGACGTGTCCCATGATCAATCTACAATGAAATGA
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GCATGATATACTATCGATAATATCTTTTCGATAAGAACTTAAATGTAGCAACGTGAAATTTTAAAT
AAAACCTCCTTTTCTGGTGATAAATTTTGACTTTGAAGCATAAAGAAGACAGAGCTAAAAAATA
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ACCCAGTTGGTCTAAAAATTGCATGGTTACGAAGTTACCCAAACATCACCTATCCCAGAAATTTCCC
TCACTGCTGTATCATTTAAACACACAGAGAGTGGTGCAACTCACTTACATTTGGATTCCCTTAATG
ACAGTAATAATGTATTTCTGATTGCTTCAAAACAAATCCTCCAGATAATACTGGGGTCTCCCAT
TTTTAGAACATACAACCTTTGTGTGGTAGTAAAAAGTTTCCGGTCCGTGATCCATTTTAAAAATGA
CCAACAGGTCGTTGAGTAACCTTTATGAATGCAATGACAGGCCATGATTACACATTTTATCCATTTG
CTACCACCAATTCAAAGGATTTTGAACCTAATGGATGTGTATTTATCGTCAGTGTGTAACCGC
AATTAACCATAACCGATTTCTTGCAAGAAGGATGGAGAATAGAAAATCAAAATGTTTCATGACATAT
CGTCCAAGCTTGAATTCAGGGAGTTGTATATAATGAAATGAAGGGCCAGTATTCGAACTCTGCAT
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ATGAATCATTCGAAAAAAGGTGTCTTCAGTTGACGTCAAACAACCTATATTTTCTACAGATAAAT
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GCCAAGTAAATAAGAAAGTTGTACATGAAAGGGTAGTTGATACCAATGGCTTGGTTTATGCCAACG
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TGACGAACCTTGCTGGAACAGAAAACACACCCATTACGGAGTTGGAAACTAAAATACAAATGTTAA
CTGGCGGGATAACATTTAGTTCTAAAATATCGACTGACCCCTATAATATTGAGCAACTAAAATTAC
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CACTGAAATTGACACCGCTGAAATACATCAGTGACATCGTTTTCAGTTTGGAGTCAAGATTCAATTTG
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TATTGCAAGAAATACAAAAGTATGTATTGCAAGGTGAATTCAGGTATAGACTAGTTGGAAATCAAG
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GTGAAAATGTCTTAGTTAACTTACCATTCAAGTGGGATACTCTTCATTAGGTAAGATTGGCTCTT
CGTATTATCAAGGATGGTGCTTCTTTACAAATATTATCTCAGTTATATTCTTTAAAAATCTAC
ATTCCAAAATAAGAGAAAGCAATGGTGCATATGGAGGTGGTTTGCATATGATGGGTTGAACGGGA
CATTAAACTTTTATTCGTATCGTGATCCTAATCCTGTTAAGTCGATTCAAACCTTTAGAGATTCTT
TACTGTATGGACTTGATGCTAATTGGAACGATAAGGATTTACAAGAGGCTAAGTTGCGGGTTTTCC
AAAGCGTCGATGCTCCAATTAATATCTCTCTCAGGGTGCTAGTGCCTTCTTTGAAAATATAGATG
ATTACTTGAGACAGGAAAGAAGAGAAAACTTTTTGGGTACCATTTAAAGGATCTCAGAGATGTGA

CTGAAAAGTATCTTGTGATAACCAAAACAACCTTGTCACTGTTATTGGTGACAATGAAATTTTAA
ATGTCGATAATAAATGGCAAATTAGAAATTTTCAAGTATAG

YDR430C_homolog 1034aa (SEQ ID NO 328)

MLKTRLKQSR AISRVVRRYACSHPI SPNLDKYPVGLKLHGYEVTQTSP IPEFSLTAVSLKHTE SGA
THLHLDSPND SNNVFSIAFKTNPPDNTGVPHILEHTTLCGSKKFPVRDPFFKMTNRSLSNFMNAMT
GHDYTFYPFATTNSKDFENLMDVYLSSVFEPQLNHTDFLQEGWRIENQNVHDISSKLEFKGVVYNE
MKGQYSNSAYFYIKFLES IYPSLNNSGGDPKKIVDL SYEGLLEFHSKNYHPSNAKTFTY GKLPLE
DSL SKISKYYESFEKKVSSVDVKQPIFSTDKSEIFDVTIPGPVDTMNGKETSEQYCTSI TWNLGNP
LDPNMQYDIFKWKILSSLLFDGHNSPFYQELIESGYGDDFSANTGLDSTTALLSFTVGLNLYLTKQK
VDNFNEKVM EI INNKI IPELSNEESSSYHGRIDAILHQIEIGFKRHKPDFGFGLLSSIVPSWVNGV
DPIDTLQVEKILSHFKEDYKQNGLRIFKELLEKTLCNPHSQKFKTMEPREDFTKQLVKDENLMIE
KRVSELTEDNKKAIYEQNLELAKLQLEDQNTTEVLPTLTIDDI PKRGDFY AIDLQVNNKVVHERVV
DTNGLVYANALKDISYLP TKLYKYLPLFNNCLTNLAGTENTPITELETKIQMLTGGITFSSKISTD
PYNIEQLKLQYVLSGMALKEKSSSVYDLWLEILTTTKFDT SDEVLEKLSVL IKNMGNQ INNIADR
GHSYAAAVSSSKLTPSKYISDIVSGLSQVQFVMELNSKLESEGKEYLAKEI IPILQEI QKYVLQGE
FRYRLVGNQEI IVENEK LIEKFDKDISSNRPTLSLTVTDGLSALLNSFNYNHTSENVLVNLPFQVG
YSSLGKIGSSYSSKDGASLQILSQLYSFKNLHHSK IRESNGAYGGGLTYDGLNGTLNFYSYRDPNPV
KSIQTFRDSLSYGLDANWNDKDLQEA KLRV FQSVDAPINISSQGASAFFENIDYLRQERRENFLG
TTLKDLRDVTEKYLVDNQNNLVTVIGDNEILNV DNKWQIRNFQV

YDR450W_YML026C_homolog 1366bp public: 1..1366; exon 1: 501..548,
intron 1: 549..976, exon 2: 977..1363 (SEQ ID NO 329)

TTAAGAACTAGCAGATGTAAAATGTTTTATGTCAATTATATAATTTGTTAATACATGTATATAGATT
TTTTAATGAATGTATTCCCTAAATAGAACAGAATTATGATGCTGTTACAGCAAAAACCTGGTTTGAG
TATTGGAGAATGTTATAAACTGAAATTTGATTTACAACCAAACCCGTGTCACGTGTAAGTAATTA
GGGCTTTTAGGGCTTTCTATATACAGGCACCAGAATTTTTTTTTTATGGGCGATAGAAATAATGTAT
GCGCGCGATTCTTCTCTGCTAGAGGTTTTCTTTTTTGATGTCTGTAACAGTGCGACTCACATAGTT
AAGTAATTTTAAAGCCAGAGATTGTGTACAGTCGACGCCCCCTAATCACATAGTTAATTCTCAAA
CTTCTCTCTCTTCTCTCTTTGCTTTTCTCCTAAGGAAAAAATTTATTTCATTTGTTGAAAAT
TTTTGTATAGTTTCAAGTAAACACACAGTAATCAACATGCCATTAGTTGTCCAAGAACAAGGTT
CATTCCAACACATTTTACGGTATGTGAGTGTATTATAAGATTATTTGAATGAGATAGAAAAGGGTT
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TTTCCCTGTTTAAAGTATTCGATTTACTAACATTATGAATTATTATTATAGTTTGTAAACACCAA
CATTGATGGTAGAATCAAGATCATGTACGCCCTTGACCAAGATCAGAGGTGTCGGTAGAAGATATGC
CAACTTGGTTTGTA AAAAAGCCGATGTTGAATTAACCAAAGAGCTGGTGAATTGACCCAAGAAGA
ATTGGAAGAAGATTGTCACCATTATGCAAAACCAACCAACTATAAAATCCCAGCTTGGTTCTTGAA
CAGACAAAAGATCAAGTTGATGGTAAAGATTACCATGTTT TAGCTAACAACCTTGAATCTAAATT
GAGAGATGATTTGGAAGATTGAAGAAAATCAGATCTCACAGAGGTATTAGACACTTCTGGGGATT
GAAAGTTAGAGGTCAACATACTAAACTACTTCTCGTGGTCTGTTAA

YDR450W_YML026C_homolog 145aa (SEQ ID NO 330)

MPLVVQE QSGFQHILRLNTNIDGR IKIMYALTKIRGVGRRYANLVCKKADVELTKRAGELTQEEL
ERIVTIMQNPTNYKIPAWFLNRQKDQVDGKDYHVLANNLESKL RDDLERLKKIRSHRGIRHFWGLK
VRGQHTKTTSRGR

YDR471W_YHR010W_homolog 1327bp PathoSeq: 1..1327; exon 1:

501..530, intron 1: 531..946, exon 2: 947..1324 (SEQ ID NO 331)
ATAGTTATTACAATATAATAAAGCAAATAAAAGAAATGATAAAGAACCATATTAACAAAGTT
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GTAATACCTAATTCATTTGGTGTGGTGCATCAGCTGCTAGGGCTATAGCCCTAATAGTATATGCA
GTCGCATACATTAATTGGTCATCTCATAAGTAAATTATATAATGTATAGTGTGCGCGCACTGTAAT

TTTTCACTAAGTTAAGGAGAGTGCAGAAAAATTTAGTACTAACAAAAATTGTATTGTGTTGTGTGT
GGCTATTGGGCAGAGCGAAAAATTCACCCCTACTGAGAGGAACTGTGAGGGAGAGAGATACACAC
AACTCTGTGCGCAAGAAGAAAGACAAAAATTTTTTTGAAAAAAGAGACAACCAACCTT
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TGTGAAACCCACATGATGAAGGTACCAAATCTCACCATTCCCACATGCCATTGTTGCTGGTATTGA
AAGAGCTCCATTGAAGGTTACCAAGAAGATGGATGCTAAAAAAGTTACCAAAAGAACTAAAGTCAA
GCCATTTGTTAAATTAGTAAACTACAACCATTTAATGCCAACTAGATACTCATTAGATGTTGAATC
ATTCAAATCTGCTGTCACTTCTGAAGCTTTAGAAGAACCATCTCAAAGAGAAGAAGCTAAAAAAGT
TGTCAAGAAGGCTTTTGAAGAAAAACATCAAGCTGGTAAGAACAAATGGTTCCTCCAAAAATTACA
CTTTTAA

YDR471W_YHR010W_homolog 136aa (SEQ ID NO 332)

MAKFIKSGKVAIVVRGRYAGKKVVIVKPHDEGTSHPFPHAIVAGIERAPLKVTKKMDAKKVKTKRT
KVKPFVKLVNYNHLMPTRYSLDVESFKSAVTSEALEEPSQREEAKKVVKAFEEKHQAGKNKWWFFQ
KLHF

YDR486C_homolog 1157bp PathoSeq: 1..1157; CDS: 501..1154 (SEQ ID NO 333)

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ATTCTTTTTTCAGCATCATTCGTATCTTTAAGCACAGGGAATAGCAATGGATCATGTAACAAATTC
CTTTCGTGATTTCGAAAGCCCAAAATGTTTCGTTTTAACAACGCACACACATGTGAAACCTAAACCG
AGTTAGTCGTCAAGAAAATAATTCAGTGTAAAGTCTGTACCTTAAGCGTCAAACGTAATCTGTCA
ACCTCTGGCATTGAGTGTAATTTAAATATTCATGATAATCTGGAACCTACAAGCTACGAAAAA
GAAAAAGAAAAATAGTACGAGTTCTTGGTGAGATAAATAATGGAGAACACTTTTTTTTTTCTCTTT
GGAGGTTTTAGAAGGCAAAACCAATCTAGACAAGGAGATGAACAGATTATTCGGAACGAAAAGCA
CTGCGCCCAACCATCTTTGAATGATGCAATCAAGGGAATCGATGAAAGAGTGGGGTCTTTGGATG
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CTCAAAAGGATCAGTTAGAGAATCAATCTTGGAATATGACACAAGCTTCCATGACAACAGATAACT
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ATGAACTACAGGAGGCACTTCTGACGAGCTATGATGTACCCGATGACATCAGTGAGCTGGAGTTGG
ATGCTGAATTAGAAGCTCTTGGCGAAGAAATTGATTTTGAAATGAAATGGCAGAGAGTGGGATAG
GTGCACCTAGTTACTTAAATGATACAGAACCTACAGCAGCAGATAAATTGCCTACATTTATTGACG
AACCAACCAGAAGAAGCTCAAAAAATCGCAAACTAG

YDR486C_homolog 218aa (SEQ ID NO 334)

MNRLFGTKSTAPKPSLNDAIKGIDERVGSLDVKLSKINSELSTYQQKISRMRDGPGRSALKQKAIK
LLRQRKQIEAQKDQLENQSWNMTQASMTTNDLQNTMVTINAMKTANKSLKQTYGKINIDELEDLQD
EMLDLIDKSNEALQALSTSYDVPDDISESELDALAEALGEEIDFENEMAESGIGAPSYLNDTEPTA
ADKLPTFIDEQPEEAQKIAN

YDR507C_homolog 4550bp PathoSeq: 1..1424, public: 1524..4550; CDS: 501..4547 (SEQ ID NO 335)

GAATGAGATTTTTTTTTTACTAAGGGTGCACTACTACTAGTTATTTGTTTTGTTGTTGACGATCA
TTAAAGAGAAAAATTTACAGTATACACAAAACACTTTACTTCTGCTGTTTTTTTTTTATTTTAGTTT
TTGGTTTCATAAATTATTAAAAAGAAAGCAATAATTATTGAAATAAATTTTATATTTTTGGTTTTT
TTTTCTTTGGTTTCTTTGAATTTTGCAACCAATCCAAATTTTTTTTTGAAAATTTTTCTTCTCTCT

TCATTGTTGACTTTTGAAAGTTTATTTCATCCATATTCTTCAAGTTAAAAAGTGTTCATATCT
GTCCAACCAAGAAGAAAACCAATAAAACAACATCAATTCCAACCTTTGTTTACATCAAACAGAAACAA
AAAACAGATAATTTATAGACACCTTCATTCATTCGTTATTTTTTTTCCAAGTACTACACGTCTTTAT
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TGAGAAGAATATCTACTGAAAAATCTTAAGACACCCATTGTTAACCAAATACCCAATGTCAAACG
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CAACTGTGGAAGATTCCAACCTGACTGATGACTACATGACAGAAATCAGAAAATCAAGACTTTTGA
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CGGTATTGCTCTATGTATTCAACAAAGGAATCATACCGTGATTGTAATTCTATAATTAACACCAG
ATGAAAACCCCGAACAGCATCAAAACATGAACAAGCCAGCGTTACGAACCAGTATTGCTGATCGTT
TGGATAAAGCTGGATTGGCTGAACCAGAATATGAACTGAGACTGATGGTGAAGATAAAGTGTCTG
TTATTGATTGGATGATCATTTAGCTGATAGAAGGACTTCTATTATGATGGATCTGGAAAGAGAG
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AAGTTCCTGATTTGCCAAAGAATGATTATGATGACACATTTGTCTAGTAATAGTGATGAAGTTTATA
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AATTACCAGTGGTAAATCAACTAAATCTTCCATTGATGAATTTGGCTAACGGCAGCTCTACAAGTG
GTCATAGAAAACCAAGATAAGACATTTCTCAACCGGGCCAGAAATGTTGATTCTCTATTGTAATG
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MPHSRQPSISSSIMSQSNHNHPQKIGPWKLGKTLGRGATGRVLLATHQTGTGQKAAVKVSVKSELQD
EETEKNGDGLPYGIEREIIIMKLLTHPNVLRLYDVWETSKALYLVLEYVEGGELFDLLVERGPLPE
VEAIKYFRQIILGTAYCHALGICHRDLKPENLLLDSQLNVKLADFGMAALESNGKLLTSCGSPHY
AAPEIVSGLKYHGAASDVWSCGVILFALLTGRLPFDDENIRNLLLKVQAGNFEMPVDEVREARDI
IARMLEVDPMRRISTEKILRHPLLTKYPMNSNEDLISEKSLPHPHGTGYKSLGSVRNIDKQILSNLTI
LWNRPEEEIVDCLLKDGSLNPEKTFYALLMRKYHKNQDDNTNNNSPKKSTSFNKNVVRSGSKYSLNG
TPRRKRASHISVSRPTSFQYKSNPGAGATANRNSVARHSVASSANNSPRKSYPKSPYRSPYRSPYK
SPSKRYSYNQSPTKSPYGRRSNSQRQFENEPLKAKPRNIYNEIVDAQSNFSLPPLPPLPSKDSR
YMIDEPNQPQLQPPALSQVPENFIVDESPDLMQSAKISSGKRNSIIIGNNNNSNSNKRMSKRKSIR
ASMTTGLKRNSITMKLLSTYAKLSGDDDDWEYMDKQTKRTSATFAALCDKIFNQEDYDEEDEQLVDP
EEKEAKEYERLMELERKKHEAELKARRELEKTKRRQKRRSILSSKKLSIIVKNDADPNNSEQELVD
EGIKQPKRQSKNLTALRALSEGHNASEELTEKDVENLKKRASASQVPVKRRQTPLVTRRPVSRDLPL
WQAHENEQLDRAKDALEQEWDRSQKRSSSTVSRKKVNRESMISVMDIIVEEDQGRVNRNSTRNTYYE
RERDYELPEPTVEDSNLTDYDMTEIRKSRLNLSQLNVDRDPLNEKRKSEPKTILSNVQIPSVTRKSR
NFTTSNKRLSVLSMYSTKESYRDLNSIINSPDENPEQHQNMMKPALRTSIADRLDKAGLAEPEYET
ETDGEDKVSVIDLDDHLADRRTSYDGSGBKRASRASTTKRYNVHSSSEKRPKSKVPDLPKNDYDDT
FVSNSDEVHKRQYKSMVSDASSDDVFDKIKLPDGKSTKSSIDELANGTSTSGHRKPKIRHSQPG
PEMLIPLHNGGIESSQPMASKVRGNMSSGHDDSVPPPPPAHKVNKKPLDDKTNFPPEVDPKRKGSF
FRKLSWGSKKTIENTNTAATNTTTQQQLVSPAESKEEKPKSSFFRWFSSSNTPSAAEIRKFNTILP
KHEMSTLALLNLSWSNFGKLDLRNDQGVGYITGAISKHNSFNLKSKCFRIKINQRDFNQKSEIVC
VRVKGSKVTTDTLFCIEKVLLKEGGLDK

ACAATACTAGGCACTGTTGAGTGAGTGAGCATTCTGTTTCTCACTCAGTTAACAAAATAAAA
AAAAATTTTCATAATTTAGAAGTTTCATTTACAGTCTTTTTTCAATTAACAGTGATACAAGAGTGTA
TGTAAGACACATGTACTAGCAACTATAATATGATTTACCAATGATTGGGATCACAAATAATGTG
TTAATATGAATGAGAGAAGGATAGTGAATAAGAGATTACGAAAGAATAGATTCAACAAGTTCAGAA
TGGTATACAACATAAAATGGAATTTTCAAATATGCAACTATCATTATGACTACGACAACAA
TTTTAATCGAGAGAAGATCATTAGATCAAGAGTTGGGAAACTAATACCAAGGAAATATCATTAAGA
ATTAATAGCTTTGCAAAAATTGGTTTTACTCATATTATTTGTTTTAGTTGGAAGCGATTACATCA
TGGAACAAAGTTTACTAACAACATTGTTATAGGTAAAAATGGGTATTTCTAGAGATTACGCTCACA
AAGAGTCCGCCACTGGTGCCAAAAAGAGCCCAATTGAGAAAGAAGAGAAAGTTTGAATTAGGTAGAC
AACCAGACCAACCAAGATTGGTCCAAAAAGAATTCACTCTGCAGAAAGCAGGTTGGTAACCAAA
AATTCAGAGCTTTGAGAGTTGAAACCGGTAACCTCTCTTGGGGTTCCGAAGGTTGTTCCGAAAAA
CCAGAATTGCTGGTGTCGTTTACCATCCATCTAATAACGAATTGGTTAGAACCAACACCTTGACCA
AATCTGCTGTTGTTCAAATTGATGCTACTCCATTAGACAATGGTACGAAAACCACTACGGTGCTA
CTTTAGGTAAAAAGAAGGGTGGTGCTCATGCTGCTCAGCTGCTGAAGTTGCCGATGCCAAGAGAT
CAAGAAAAAGTCGAAAAGAAAATTGGCTGCTAGATCTGGTGCTGCCATTGAATCCCGCTGTGTGACT
CTCAATTCGGTTCTGGTAGATTATACGCTGATCTATTCTTCAAGACCAGGTCAATCTGGTAGATGTG
ATGGTTACATCTTGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAACTGCTAAGAAATAA

MGISRDSRHKRSATGAKRAQFRKKRKFLGRQPANTKIGPKRIHSVTRGGNQKFRALRVETGNFS
WGSEGVSRKTTRIAGVVYHPSNNELVRTNTLTSAVVOIDATPFROWYENHYGATLGKKKGGAAAH

118/161

AAEVADAKRSRKVERKLAARSGAAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFY
LRRLTAKK

YFL014W_homolog_1 819bp PathoSeq: 1..819; CDS: 419..816 (SEQ ID NO 339)

TTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTGTG
TACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTTCGTCCA
AATTGAGACCCTCAATTACATTTTGTCAAAAAAATTTGGTCCCTAGTGTGCTATCGATAACGAAGG
TGAAGGCAGTTTAGCTTGGAGACATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAAAT
CGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACCACAGCAATATAGCAA
TCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTCCTTTGAATCTTGTTTTTT
TCGACATACACCATAAATCCCATAGAAAACGCAAAATGTCTGACGCCGGAAGAAAAACATTTCT
ACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAACAA
GTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTCAA
ACTGTTGCAGACAGCGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCGAA
CAAGCAGAGGGCGAACAAGACCCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAACCTG
AAATTGGAAAGGCTGCTGAATACGTGA

YFL014W_homolog_1 106aa (SEQ ID NO 340)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSLDKAVGSNVPDNQKSFTQTVADSVQQGSDN
AKADLKKQSEQAEGEQRPLSKQLKNMSRLPKSKLERSNT

YFL014W_homolog_2 884bp public: 1..884; CDS: 501..881 (SEQ ID NO 341)

CCTTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTGTG
TGTACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTTCGTG
CAAATTGAGACCCTCAATTACATTTTGTCAAAAAAATTTGGTCCCTAGTGTGCTATCGATAACGAA
GGTGAAGGCAGTTTAGCTTGGAGGCATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAA
ATCGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACCACAGCAATATAGC
AATCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCTCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTCCTTTGAATCTTGTTTTT
TTTCGACAAACACCATAAATCCCATAGAAAACGCAAAATGTCTGACGCCGGAAGAAAAACATTT
CTACTAAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAAC
AAGTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTC
AAACTGTTGCAGACAACGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCG
AACAAGCAGAGGGCGAAGCAAGACCCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAA
CTGAAATTGGAAAGGCTGCTGAATACGTGAGTGGAGTTGTCACCGGTGCTACCGAAGGTGCCAAAA
CCGGCGCTGATAGTACTAAAAAATAG

YFL014W_homolog_2 127aa (SEQ ID NO 342)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSLDKAVGSNVPDNQKSFTQTVADNVQQGSDN
AKADLKKQSEQAEGEAKTLAETAQEYVEVAKTEIGKAAEYVSGVVTGATEGAKTGADSTKK

YGL011C_homolog 1244bp PathoSeq: 1..1244; CDS: 501..1241 (SEQ ID NO 343)

GAAGGGCACCATAATGAAATCGACTCACTTCAGGATTATAATGGTATGAAACATTGTACTTGTATT
TAGTGCCAGGATGATTAGGATCATATATTGGGGTGTCTTCGAGTCTTGGTATCGGTTGTAAACG
TATCTGTTTCACTTATCAGTATCGTCATTTATATTAATACTTTTCTCCTATGGTTATATATTGGT
AAACAAAGAAACAAAACAACAAAAAGAAGTAGTAGTTTTGAAAATTGTCAATAAAAGAAACAAAG
AATGAAAGAATGATTGAATGAAAGAAAAAAAATATGAAAGTGAGTCCGACATAATGTAGAAAAA
TGTCGAATGTCTTGAACTTTACCCATTGAGTAGTTGTTGTAGTGTAGGAGGAAGAAAACAACAGAA
AGAAAGAGAGAAAGAAAAATTTGCCCACTACAAATATTCAACAAGTTTCATATAGTAATATAATCC
CAATTGATCATTTTATTTCCACACAATTATACCAATGTCCAATTCAGCAGGTTTGTATAGAC
ATATCACTATTTTTTCTCCTGAAGGTAGATTATACCAAGTAGAATATGCTTTTAAAGCTATCAATT
CAGCAATATCACCAGTTTAGGAATCACAGGTCAAGATTCTGCCGTTATTATATCACAAAAGAAGA

TCCAGATAAGTTATTAGATCCTAAAACCGTGTCATATATTTTTTAAAATCACTCCTAGTATAGGAA
TGGTTGCCACTGGATCAATTGCTGATGCTAGAGCTCAAGCCATGAGAGCAAGATCTGAAGCTACAG
AATTTAGATATAAATATGGTTACGAAATGCCGGTGAAAGTTTATCAAGAAGAATGGCGAATATAT
CTCAATTGTATACTCAAAGAGCTTATATGAGACCATTGGGTGTTGCTTTAACTTTTATTCAAGTTG
ATTTTGCTGATGAAGGTAGAGGTCCACAAATTTTTAAATGTGATCCTGCTGGATATTTCACTGGGG
TGAAAGCCGTGGCCACTGGTCCAAAACAAGAAGCAACGACTTATTTAGAGAAAAAATTCAAAA
AAACCGATGCTGTTAAAGGAGATTGGCAAAAACTGTTGAATTTGCAATAATTGCCTTGAGTTCG
TGATTGGAATGAATTCAGAAAAATGATATTGAAATTGGTGTGGCCACTGAAGGAGAATTTAGAA
TTTTGACACCAGAAGAAATAGACGAAAGATTGATTTCAATAGCTGAACAAGATTAG

YGL011C_homolog 247aa (SEQ ID NO 344)

MSNSAGFDRHITIFSPEGRLYQVEYAFKAINSANITSLGITGQDSAVIISQKKIPDKLLDPKTVSY
IFKITPSIGMVATGSIADARAQAMRRARSEATEFRYKYGYEMPVESLSRRMANISQLYTQRAYMRPL
GVALTFIQVDFADEGRGPQIFKCDPAGYFTGVKAVATGPKQOEATTYLEKKFKKTDVKGWQKTV
EFAIIALSSVIGTEFRKNDIEIGVATEGEFRILTPEEIDERLISIAEQD

YGL031C_YGR148C_homolog 968bp PathoSeq: 1..968; CDS: 501..965 (SEQ ID NO 345)

CATTGTAGGTACACCTGTTTTTGCTCAATGTACACACACACGCACCAGCAGTAGGAAAAAAACAA
AATTAAATGAAAAATCATTTTCGTTCAATATTAAGCTTCTTAAGATAACCAACCAATTAATATGTA
TGTGACATACCATATAAATAAAGCTACAAATGGGGATAACTATGTATTTAATGATAAATGAATGGA
AGACCAGAATGTATAATGTTATAAGATAGTGATTTATATTGAAAACACCCTTAAAAAATCAACCA
CCCATCTAACCGTCGAATTGGAATGTCAATTTAGTTAGCATCGAAAATCAACAAAGACATGGGGA
ATCATTTACATATAAAATAATGAGAGAGAATTACAAACTGCTACGTTATGTTTTGTTTCATTATGTC
TTGTTTCATTATGTCTTGTTTCATTATGTCAAAAAATCTATAGTTACCTACCTACATCAATTTATG
GTCTGAAATACTAACATTTTTTTTTTATTTATAGTGAAAAATGAAGATTGAAGTTGACTCCTTTTCAG
GTTCTAAAATCTACCCAGGTAGAGGTACTTTATTTGTGAGAGGTGACTCTAAAATTTTTAGATTCC
AATCCTCAAAATCTGCTTCTTTATTCCAACAAAGAAAGAACCAAGAAGAATTTCTTGGACTGTTT
TGTAACAAGACACCACAAAAAGGTATTTCTGAAGAAGCTGCTAAAAAGAGAACCAGAAAGACCG
TCAAGCACCAAAGAGCTATTGTGCGGTGCTTCTTTGGAATTGATCAAAGAAAGAAGAAGTCAAAAC
CATCTGACAGAAAAGCTGCTAGAGACTCTAAATTAGCTAAAGACAAAGAAGCTAAAAAAGCTGCTA
AAGCTGCCAGAAAAGCTGAAAAGGCTAAGGCTGTTGCTTCTGGTGCTTCTGTTGTTTCTAAACAAC
AAGCTAAAGGTTCTTTCCAAGTTAAAGCTACCTCCCGTTAA

YGL031C_YGR148C_homolog 155aa (SEQ ID NO 346)

MKIEVDVSFGSKIYPGRGTLFVRGDSKIFRFQSSKSASLFQQRKNPRRISWTVLYRRHHKKGISEE
AAKRRTRKTVKHQRAIVGASLELIKERRSQKPSDRKAARDSKLAKDKEAKKAARKAEKAKAVA
SGASVVSQQAQKGSFQKVKATSR

YGL043W_homolog 1418bp public: 1..436, PathoSeq: 437..1418; CDS: 501..1415 (SEQ ID NO 347)

AATCTACCATTAGGCAATGTCATATAATTTAGATTACGAACAGCTGATGACGCAGTTTCATTATCT
CCATAATTTATAATGGCATACCTTTGGATTACCTGTTAATTCATCAAATAATAACTTCACATCT
AATACTGGTCCAACCTGATCTTGCAATATCCCGCACCTGTTCTTCAGTGTAATCAAATGGAAATTTA
CCTATTGAAACACAAGTGCTTTTACTATCCATATTTAGTTTGAGCTGCCTAGTTTTCTTGATTCTT
GGTAACAAAAAATATAATTTAACAATTTATCGATAGAATCTCTTCCAAAGTACAACCAATTT
CGATACATTTTTTTCTATGAGATGTTTTTTTCCCTTTGTCTTTAACTAATGTATTTGGGTACACT
ACCTGAACCTACCAGTTCAGTTCAGTCTAAAAAATTTTTATTTATTGTGTTGTTTATACTACCC
TTTGATATATTACTAATATTTATCTTACCTTTTCATCATGGATACAAAGGAAATAAGATTACCG
TATCTAATCTTGAAAAAGCAGTAGATGACACCACCATTTTAAAGTTGTTGAATATCTTGAATGATG
GGGTTAAACCATCCGAAAACTCTTGAGAGAAACCAAGTAGGTGTAGCTGTCAACAAATTCAGAA
GTCACGACAGTGCCGAAATCAACGGTTTAGTTAAAAAATGATCAGAAATTGGAGAGATGCCGTGC
AAGCCGAAAAGAACAACAAAAAGAAGTTAGCAATAGCAGCTGGAACAGGAACAGGAACACCTTCAA
GCTCAGCAATTTGCCATCATCATCGGTTCTGGAAGTACAACACCAAAACCATCAGAGTCAACCA
CATTATCGGCTGCCCGTAAAGGTCCAAGAAATCCAAGAACTGACGGTGTAATACTCAATTTATACG
AAAATGATACCAGAAATGCATCGGTTAGTGCTTTATACACGTCGTTAGCAGTTGATCGTGACGATT

CACCAAAACACATTTTGAAGAATAGCTATTGAAATCGAGGCTGAAGTATACAAGAGCGAATACCTGA
AAGTAAGTGACAGTTATAGAAATAGGTTAAGAAGCTTTACCATGAATCTTCGAAATAAGAAAAACC
CAGAATTAAGAGAAAGAATCTTATCGAAACAAATTTTACCTGCTGCGTTTATTAAATGACCCCTA
ATGAAATGGCTCCTGAGGCATTGAAAAAGGAAATTGAAAAATTGCACAAACAFAAATTGTTTGATG
CTCAAGGTGCTACTGAAAAGAGAGCAGTGACCGATAGATTCACTTGTGGCAAGTGTAAAGCACAAGA
AGGTCAGTTATTATCAAATGCAAACCAGATCAGCGGATGAGCCTTTAACTACATTTTGTACTTGTG
AAAATTGTGGCAATAGATGGAAGTTTTCATAA

YGL043W_homolog 305aa (SEQ ID NO 348)

MDTKEIRSTVSNLEKAVDDTTILKLLNILNDGVKPSKLLRETKVGVAVNKFRRSHDSAEINGLVKK
MIRNWRDAVQAENNNKKLAIAAGTGTGTPSSSAISPSSSGSGSTTPKPSESTTPSAARKGPRNPK
TDGVNTQLYENDTRNASVSALYTS LAVDRDDSPKHILRIAIEIEAEVYKSEYSKVSDSYRNRLRSF
TMNLRNKKNPRLRERILSKQILPAAFIKMTNEMAPEALKKEIEKLHKQNLFDQAQGATEKRAVTD
FTCGKCKHKKVSYYQMOTRSADDEPLTTFCTCENCGNRWKFS

YGL103W_homolog 1301bp public: 1..688, PathoSeq: 689..1301; exon
1: 501..548, intron 1: 549..899, exon 2: 900..1298 (SEQ ID NO 349)
ACATTTATTGTTGGCTATACCTTTCCAGTTTAAAGGAATGGTTAGGCGGGTCAGTCTACTTTATT
TTTACTGTAATGTGTTGTGCCAGTGTATGGTTTATCAAGACTAAAGTTCCTGAGACAAAGGGTAAG
CATTCGTACCAGGAAGTCTGGAATTAACGGTAGTTACTTCCAGTATATATGGTGTTCATTGTGTT
TTGTGTCTAAAGTTGCGTTAGGGCTAAAGCCCTAATCAATAGTAGTGTACTTTGTTTGAAGAAAAAT
AATACATGCAAAATACCTGCATATTAGAATTATAAGGGAATGAAATGAAAAAAGGAATAATTT
TGTAAGATCGCATAGTGTGAGCGCGCACACACACAACTTTGTAGTGCTACAGTTTCTCTCTTCT
CCATACACTCTCGCAGTCGCACGCTTGACAAAAGTTAATTAGAAATAGAAAAATTTCTCATTCTCTT
TTGAGTTTTCACCATAATCAACTAGTAATAACCAACAAATGCCTACTAGATTAACTAAAACCAGAA
AACACAGAGGTAATGTTTCTGGTATGTACAATTTCACTAAAGTTTAAACGGATGAAAGAGTATTGA
ATGTTCAAGGACATATGGAGATTTAGAGAAAACATGGAAAACATAATCGAAAATGAATAATGAATGG
AAAATTTTTTAACTGAATATCAGAATAGACACAACACACAGATCCAGAGTCATTATCACATTGA
TCATACAACCAAGCAATGAATATGAGTAGTTTGGGAAACCACAACATACGAGTTATTTTTCAGAA
CAATCAAGTTTATCATTTACAGAAGACAGTTCCATCAATATGTCCAAAATACTCTTTGAAGTCAAT
TAAAGTCAAATGAACGAATTACTAATTATTTTTTTTCTTTAGCCGGTAAGGGTAGAATTGGTAAAC
ACAGAAAGCACCCGGGTGGTAGAGGTAAAGCTGGTGGTCAACATCATCACAGAACCAACTTGGATA
AATACCATCCAGGTACTTTCGGTAAAGTTGGTATGAGATACTTCCACAAACAACAAAACCACTTCT
GGAGACCAGAAATCAACTTGGACAAATTGTGGACTTTGGTTGATTCTGAAAAGAAAGACGAATACT
TGAGCAAATCATCTGCTTCTGCTGCTCCAGTCATCGACACCTTGGCTCACGGTTACGGTAAAGTTT
TGGGTAAAGGTAGATTACCAGAAGTTCCAGTCATTGTCAAAGCCAGATTGTTTCTAAATTAGCTG
AAGAAAAATCAGAGCTGTTGGTGGTGTGTGCAATTAGTTGCTTAA

YGL103W_homolog 149aa (SEQ ID NO 350)

MPTRLTKTRKHRGNVSAGKGRIGKHKHPGGRGKAGGQHHRTNLDKYHPGYFGKVGMRYPFHKKQN
HFWRPEINLDKLWTLVDSEKKDEYLSKSSASAAPVIDTLAHGYGKVLGKGRLEPEVPVIVKARFVSK
LAEEKIRAVGGVVELVA

YGL147C_homolog 423bp PathoSeq: 1..423; CDS: <1..420 (SEQ ID NO 351)

GCTATCAAAATCACTGTTTACAATGGTGACAGAAAACACGTTGCTGCTTTAAGAACTGTCAAATCT
TTGATTGCTTAACCTGATCACTGGTGTCACTAAAGGTTACAAATACAAGATGAGATTTGTTTATGCG
CATTTCCCAATTAACGTTAACATTATTAAAAAAGATGGTCAAGATTACGTTGAAATTAGAAATTTT
TTGGGTGAAAAAGAGTTAGAGAAGTTAAATCCATGAAGGTGTCACCATGGAAATTTCTTCTACT
CAAAAGGATGAATTGATTGTTTCTGGTAACTCTTGGAAAGCTGTTTCTCAAATGCTGCTGATATT
CAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTAAATCTTGGATGGTATTTATGTTTCTGAA
AGAGGTACCATTTGTTGAAGAAATCTAA

YGL147C_homolog 140aa (SEQ ID NO 352)

121/161

AIKITVHNGDRKHVAALRTVKSLIANLITGVTKGYKYKMRFFVYAHFPINVNIKKDQDYVEIRNF
LGEKRVREVKIHEGVTMEISSSTQKDELIVSGNSLEAVSQNAADIQQICRVRNKDIRKFLDGIYVSE
RGTIVEEI

YGL213C_homolog 1655bp PathoSeq: 1..1655; CDS: 501..1652 (SEQ ID NO 353)

GATGATCGCTAACAGGTACCCGATTTATTCATCAACAAAGAAGCTACTTCATAGAATTGATTCTC
AACCTTAAATAGCTTGTAGTTTATGATTGGGACTAATTGTGCAGCATCGAACAATATTGCCAGT
TGCATAGAATAAATCGGTATTTATACGGCATAACCAATCGATTGTAGGGGGTTGAAGCTGGTGCATA
TTCTGGGGTTGTTGCATTTCCAGTCCATAAACGTTGAAACACAAATTTGCTGTGTAATTTGGTGAAT
GAATTGATCAGATGATCCTATGGGTGGCATTTGTTAAGGTTGTTTCGCTACGATGTATTTCTAGGATA
ATGAAGGTAAGTACGAACCTTATGAGTTTGTATTTCTTCTGATGTTTTTTTTCTTGTTTTCTT
TTGTCTGTGTAGCAAGAAGAAAAAAGTGTCTTCAAGTCTTGGACTCAATTTTCAACCCCT
CCACAAACTCAATTTCAATTAACTATCAATAATCCAATATGGGTAAACAGTATATATCTACCGTCA
GTGCATCTCAGGCTCATAAGCTGGATATTTCTTGGTGTAGCTATTACCAATAAGTTCATGTATCCG
TGTCTAGTGATGGATATGCGAAATTTTGGGACAACAAGCAAGACGAAGTTCATCTGCCCTAAAGAAT
TTGTCCAACCTGGTATTTATAGATAAAAGCGGAATCCATGCGGTGGCTGCTTACGAAAATGTTTTC
CAAGCTCTACATTTGAAAGTGACATTATTAGCATTTGCATGTTTCAATGGATCTATCATCTTCAGAT
ATTATATCAATGATGACTTTTCAACTATCGAAAGTCTAACTGATGATATAAAATTTGAAAGCA
ATTGTTGGACCCCTGGCTTTTATCGCGATCCAGAATCCAAACAAGACTATTTTATTACAACCAAGA
CCAATGGCACTACAGAGGTTTCAATTTATGAATATTGTTGATGAAAATGAGAAGGCTGTAATCACAT
TTGAAAAGTTTGGGCAATTTAAAAGGAACTCTTCTTCTTCCCAAATTTCTTGGCTATATGTCCAA
CAGAGAATAAAAAATGTGCTGTGGGTACATCAATGGTGATGCTTTGTTATATGACTTTGTTAGCT
TGAAATTGATATACACATTTCTGTTTCGAGTGATTTGGTGACCAGTAGAAATTTCCAATCGACGTCTA
TACCTAGGGTGTGGCATTTTCCCTGGTGGAACCTTGTGCTGTGGCAAGAGACAATCAAGCTG
CTGGGTCAATTACATTATACGACGTTGAGCATGGTGAGAAATGTGGGGTCTTTGGCCACACCCCTCAC
ACTCGGCCAAATCTGTTGTTGGTGGGTTTGCACATCAAGGCTGGATTTTGGGGTTGAGTTTGTATG
AGGAAGGTAAGCACTTGGCTAGTTGTGGATTGACAAATGCATAAGAGTCTGGAATTTAGAAAACAA
GCGAAAGGGAAGCAACAATTAGTATATCTATATCAGACTTAGATGATACTACACATAATGATCAAG
ACGAGAGTGTCGCTTCTGGTGTGCTTTTATTAAGGGGGTTAGAGGTGGCTCTGGTGGTGACA
GCAATGAAGGATTATGTGTCGTGAGTTTCGATAGAGGAATAAGATGGTACCGAGAGGCAGGAGGAA
TATAG

YGL213C_homolog 384aa (SEQ ID NO 354)

MGKQYISTVSASQAHKSDILGVAITNKFTVSVSSDGYAKFWDNKQDEVHSPKEFVQSVFIDKSGIH
AVAAYENVLPSSTLKVTLLAFACFNGSIIFRYIINDDFSTIESLTDDIKSFESNCWTPGFYRDPES
KQDYFITTKTNGTTEVHLLNIIVDENEKAVITFEKFGQLKGNSSSFNLSLAICPTENKKCAVGYING
DVLLYDFVSLKLIYTFRSSDLVTSRNSQSTSIPRVLAFSPGGTLLAVARDNQAAGSITLYDVEHGE
NVGSLATPSSHAKSVVGGFAHQGWILGLSFDEEGKHLASCGFDKICIRVWNLETSEREATISISISD
LDDTTTHNDQDESVASGVAFIKKGVRRGSGGDSNEGLCVVSFDRGIRWYREAGGI

YGR085C_YPR102C_homolog 1418bp public: 1..1418; exon 1: 501..503,
intron 1: 504..896, exon 2: 897..1415 (SEQ ID NO 355)

ATAGAGATGCTTATTCTGGTGGTTCAGTTAATTTATATCATGTCACTGAACAAGGTTGGACTTATC
ATGGTAATTTCAATGTTGGTGATCTCTTTTGGGAAGTTAAAGAAAAGGAACAATCATTTGTAAATG
TAGATGGATAAAGTAAGTTGATTGTATAAAAAAAGAAATGGATTCAATTAATATAAATTTACAAATCT
GATAATAAACTACAGTAACTATTATGCAACAATTGAAAGTATCCTGTGTACCGTGATTAGGGCTCA
AAGCCCTAACAGGTTGCACGTGATGTTGATTATTATCCCTGCACACATTGAGTTTTTTTCTA
TGGTGAAAATTTATTAGTGAGACGATGTTGTTTCGATTTTACCACACACTCTCACACTGAGTGTAGT
CATACTAACAATCTTCTCACACTATACACAAAAAAATCTTTTCGTTTGAAGGTTTGAAGGTTTC
GTTTTCTCAATAGTATATCCATACAATAACTGCCAAAGATGGTATGTTCAAGTGTTTAAAGAGATC
GAAATGTTTTGTTTTAATTGGAAGTGATATCATAATGAGAAAATATGGGAAATAGAGATAGGACCG
AATTAATTGAAAGAGTTTTCTTTTGGGGAAATGGGTTCAATAAGATTTTTCAAGATTTGGAATCAAA
TTATGTCAGATGTGAAGAAGAGTAAATATAACAAGAGTTCAAATCATTAATAATTTTATGTAAAT
ACAACGATTTACATTAACGAATAGAATAAAAAACAAGCCAGCATATAACAGATACCAAGT
GATTCATCCAGTGATATAAATAATGATATTCAATTAATAACAATATTAAGACATTTTTTTATTTAT

GTATCAACAAAATACTAACTTATCTTTCTTTTAATTAGTCTGACAAATCCCAAAATGTTATGCGTG
AATTACGTATTGAAAAATTAGTTTTAAACATTTGTGTTGGTGAATCCGGTGATAGATTAACCAGAG
CCGCCAAAGTTTTAGAACAAATTATCTGGTCAAACCCAGTTCAATCTAAAGCTAGATACACTGTCA
GAACTTTCGGTATTAGAAGAAATGAAAAAATTGCCGTCCACGTTACTGTGTCAGAGGTCCTCAAAAGCTG
AAGAAATCTTGAAAGAGGTTTGAAAGTTAAAGAATATCAATTAAGATCTAAAAACTTCTCTGCTA
CCGGTAACTTTGGTTTCGGTATTGATGAACATATTGATTTAGGTATCAAATATGATCCATCTATTG
GTATTTACGGTATGGATTCTACGTTGTTATGGGTAGAGCCGGTGCTAGAGTCACCAGAAGAAAGA
GAGCTAGATCCACTATTGGTAACTCTCACAAAACCAACAAAGAAGATACCATCCAATGGTTCAAGA
CCAGATACGATGCTGAAGTTTTGGATAAATAA

YGR085C_YPR102C_homolog 174aa (SEQ ID NO 356)

MSDKSQNMRELRIEKLVLNICVGESGDRLTRAARKVLEQLSGQTPVQSKARYTVRTFGIRRNEKIA
VHVTVRGPKAEIILERGLKVKEYQLRSKNFSATGNFGFGIDEHIDLGKIDPSIGIYGMDFVVMG
RAGARVTRKRARSTIGNSHKTNKEDTIQWFKTRYDAEVLDK

YGR118W_YPR132W_homolog 919bp PathoSeq: 1..919; CDS: 482..916 (SEQ ID NO 357)

TATTGCGTAATCGTTATCAATGTTTGGATTGTTGCAACGCTGGGTTGTGTGTATATGCGAGAAATG
AGTAATTGTTTAAAAATAATCGATGCAGCAGTCTGCCACTAAATAAAATAAATGTCATATTGACAT
GATAAGGATTTATCAATACTGTTAGGTCTATAGCCCTAACTTTAATCATTTACACGTGATACAAAA
AAGTTGTTTGATCCCGCAGCACTATGAGTACGCACTCACTAATTATAGCCTGAAAAAAAATTTTC
CACATAGTAAGGGGATTTGTATGGTGGTGCGCTCGCCTAAGACGCTGTCATACATTTTCTAAAGT
CACACTGATATAGGGATGTTGTGGTAGTGATTGTGTGTTCCCAACAAATAACTTTGCGGACACTCT
CATATACTCAATTTTTTCTTACAAAAATTTTTTTCTTCTACTTTTTTCAAGAATTCTTCTTTTA
CAATTCAACAACATCAATCATGGGTAAAGGTAAACCAAGAGGGCTTAACTCTGCTAGAAAAATTAAG
AGTTCACAGAAGAAACAACAGATGGGCTGATCAAGCTTATAAGCTAGATTATTAGGTACCGCTTT
CAAATCTTCTCCATTTGGTGGTTCATCTCAGCCAAAGGTATCGTTTTTGAAAAAATTTGGTATTGA
ATCTAAACAACCAAACTCTGCTATCAGAAAAATGTGTCAGAGTCCAATTAATCAAAAACGGTAAGAA
AGTCACTGCTTTTCGTTCCAAACGATGGTTGTTTGAACCTTTGTTGACGAAAATGACGAAGTCTTGT
GGCTGGTTTTCGGTAGAAGAGGTAAAGCTAAGGGGGATATTCCAGGGGTAGATTCAAGTTGTTTAA
AGTTTTCCGGTGTCTCTTTATTAGCTTTATGGAAAGAAAAGAAAAGAAAGCCCAAGATCATAG

YGR118W_YPR132W_homolog 145aa (SEQ ID NO 358)

MGKGKPRGLNSARKLRVHRRNMRWADQAYKARLLGTAFKSSPFGGSSSHAKGIVLEKIGIESKQPN
AIRKCVRVQLIKNGKKVTAFFVNDGCLNFVDENDEVLLAGFGRRGKAKGDIPGVRFKVVKVSGVSL
LALWKEKKEKPRS

YGR277C_homolog 1164bp PathoSeq: 1..724, public: 724..1164; CDS: 196..1161 (SEQ ID NO 359)

AATTCATTTGATCTCTAAGAAGATGAACAGGCCTTGAATGGGAGGGGTTGGTTGACTTCCACGAA
ATGTGGTTGGAAAACTTGAGTCCTCAAAAAGGTTCTCTCGTAAAAGGCCAGAGAAAGAAAAAAC
ACCAAACCCCAACCAACCTAACCTTTTCTTCCATCCATTCTCTTTCTTACTTTGCAAAATG
TTGAATCCAGTTATATTCAATTAAGATCCTATAAAATACGATTATTCACAATTTATTATATCTTTA
CTCCCGAAATTCATTAATTGTAATCGTATTGATTTAGTTATACTTTGTCAAATCACCGAATCAAAT
CAATTGAATGAAATTTTATGTTTTTATTATCAATTAATTCGTAATCATAAGAATAATGGAGATACT
GATGGAGATACCGACAGTTTGCCATGTTTGATTATCGATTTGAAATTAATATATTATTTAATTTA
TCAACAAAAAATTGAATCAATTATGTTTAAATAATTGGAATCATGGATATATTGCGGAAGGTGAT
AATGATAACAGTACTAACTTGTCATCTTTGCCATTGTCAATAACACAAAATATCAAAACATTGAAAT
CCAACAATCCAATCAAGAGCAAAATAGTAGTAGTGCTTATAATGATGAGGATGATAAAATTA
AGTCGGCAATATCAACAATTTAAACTACTGCTGTAGGTGGAACATTTGATCATTTACATGATGGT
CATAAAATTTTATTATCAATGGCAATTTTTTTAACTTCAAATAAAATTAATTATTGGTATAACTGGT
TCTAATTTATTAATTAATAAAAAATTTAAATCTCAATTACAAACTTTTAATCAAAGACAAAAATTTA
GTTATTCAATTCATAAATTTATTATTATTGAGTGAAACCAAGTGTATTTTTTTTGAATTTATGAA
ATTAATGATGTTTGGTCCAACTGGTTATATTAATTAATGATATTGATAATTTAATAATATCTCAAGAA
ACTAAATCTGGTGGTGAATTTGTTAAACAAATTTCTGTAAGATCATGGATTTAAATTTATTAGATATT
ACAATAATTAAAGTGATTGGTGGAATATTGAAGAAAATTCATGGAAAGGTAAATTAAGTTCAA

CTGATATTAGAGAACAAGAATATAATCGATTATTAAATCAATAA

YGR277C_homolog 322aa (SEQ ID NO 360)

MLNPVIFIKDPIKYDYSQFIISLLPKFINCNRIDLVILCQITESNQLNEILCFYYQLIRNHKNNGD
TDGDTDSLPMFDYRFEINILFNLSKLNQLCLNNWNHGYIAEGDNDNSTNLSSLPLSITQISNIE
IPTIQSRANSSSAYNDEDDKITTSRQYQFKTTAVGGTFDHLHDGHKILLSMAIFLTSNKLIIGIT
GSNLLINKKFKSQLOTFNQRONLVIQFINLLLLSETSVIFFEIEINDVCGPTGYINDIDNLIISQ
ETKSGGEFVNKFRKDHGFKLLDITIIVIGGNIEENSWKGLSSTDIREQEYNRLNQ

YGR284C_homolog 1427bp public: 1..1427; CDS: 501..1424 (SEQ ID NO 361)

CAAGAGTAAAATCTAAATCGTTCCAATGATTTTGGACAGCTCATAGGTTAAGAGGTCTACATGTGT
TGGTGGCAGTAGTATTGGTATTAAAGTGGGTGGGTCATGGTATTAGAGAGTGGGTGTTATAAAGAA
GGTTGTGATTTTTTTTTTTTCCACTGGTGGTGGTGCTGATTGCTACTGCTGTTTACATTTTATTGTTT
CGTTTCGTTTTTCCTTTTGTTTTGTTGACGTTGACATTTTTTTTTTGTCTGTTGTTGTTGTATGGGAATT
TTTGTATTAGTTGTTCTTTTTTGTTTTTTTTTTACTTGTTCAAAGTTTCATATAATAATAATATTCT
TGTTTTTCATATTTTTTTTTTTCAGAACAAAGAACAAATACAACCTATATAATTTGATCTTACTCTTAT
CCCCAGGTTTTTCTATTGTTTTTGGGTTTGCCATTTCATATATATATATCTATTATTCAAATCAAT
TTGAGGAGTATCATTAAATTTAAATTTATATCAGTTAAACAATGTCGTATCGTGGTCCTAATCAATTTG
GTAATCAACCTCCACATCATGGAATACCTTCTCAACCTCAACCACATATTGGTCCAATATCTTCCA
GCAAAAGTCCCTTAGAACAAATTTGAAGATGTTGCTAAAAAAGTTGAAGATTGGATCGATGATTATT
TTAAAGTCTTGAAACCATAACGTCCTCCAGCAATGGTAGAGCATTTTTTGGTGGCCACTTTCTATGAGG
ATACTTTAAGAACTTCTCACTCAATGGAATGAACAAGTTTATTACTTGCACAACCTATAGACACTATT
GGCGTTGGTTGACCGTTTTATTCTTGATCAATAATATGGTGGTTATGACAGTTGCATCCACTTTAG
TAATTTGCCAGAAAAAAGAATAACATTTGCTACTATTGCAATGATCGTTGTTGTTATTATACAAGGTA
TTGGGTATGGTTTATTGTTTGTATGCTCAATTTGTTTTTGAGAACTTGTCCGTTGTTGGAGGGTTAG
TATTAGCATTTTCCGATAGTATTGTTAGAGATAAAAGATCCCTTAAACATGCCAGGTTTACCGATGT
TGAACAATCAAGACAACAAAAAGTATTTCCTTTTAGCTGGTAGAATTTTGTATTAGTATTATTATTTT
TGGGATTCGCTTTTTCTCTGATTGGTCAATGGGTAGAGTTTTTCATTATTATAATCGGGTTAACTT
CTTGTGCTTCAATTGTTGTTGGTTACAAGACAAAGTTTTTCAGCTGCTATCATGCTTATTGTTTTAT
TCTTATACAATGTGTTCACTAACCAATTCGGGCTTATGCATCTCAAGATGCTAGACGTGACTTTT
TGAGATATGAATTCCTCCAAGTTTTGTCAATTTGTGGGAGGATTATTGTTAGTGGTTAATGCAGGTG
CTGGTGAATTTCTCCATCGATGAAAAGAAAAAGATTATTAA

YGR284C_homolog 308aa (SEQ ID NO 362)

MSYRGPNQFGNQPPHHGIPSPQPHIGPISSSKSPLQFEDVAKKVEDWIDDYFKVLKPYVPAIGR
AFLVATFYEDTLRIFTQWNEQVYYLHNYRHYWRWLTVLFLINNMVMTVASTLVIARKKNNIATIA
LIVVVIQIGYGLLFDAQFVLRNLSVVGGLVLAFTSDSIVRDKRSLNMPGLPMLNNQDNKKYFLLA
GRILLVLLFLGPFVSSDWSLGRVFIIIGLTSCASIVVGKTKFSAAIMLIVLFLYNVFTNQFWAY
ASQDARRDFLRYEFFQVLSIVGGLLVVNAGAGEFSIDEKKKIY

YGR285C_homolog 1876bp PathoSeq: 1..1215, public: 1216..1876; CDS: 501..1781 (SEQ ID NO 363)

AATTATTAGTTGAAAAACAAATCATACCTATTGCCAGAGCTCAAATGAAAGTGAGAATTACGTTAT
CTAAAAAAGCATACTTAAAGACTTTTCAAGATGAAATAAAACCTGTTATTGATCAAATTTGTGGAGG
AAGATAACAATGGGAAACAATATGAGATTGTTGGGATTATAGATCCTATAAATTATAGAGTCTTGG
TCACATTAAATTGAAAATACAGATGGAAGCAACAAAGTCGCTAAAGGAGAAGGGTCTATAGAAGTAT
TAGATATGCTCTGCCATAAAAGAAATAAACTAACTAGACAAGTGTATAGAATCTTTTTTTATTAATA
GATGCTTATCTTAGTTATGTTCCAGAACAAATTCATGTTAGGAGAGAGAGAAACGCAATCACTCAAT
TTTTGCACAAACAAAAACGAGAAGATGAAGAAGCAAAAAAGAAAAATTTTTTTTTTCTCAACCATCT
TAAATCCTCCTACAATTAATTTTCATACCAATAAAGAACATGTCTATTGTATTACCATCAGGAACCTA
CTGACGGATTTAAAGCCGTCTCCAAATACCTCTGCCCCAGTGGCTCGTCCAATTTGAACCAGTTGGTC
GTTACTTCTTAGCCACCGCTCAAGAATTTGCGTGGACACACTTGGTCTGAATTTGAAAAATTGG
AAGCTGAAAAGAAATGTTAAACAAATCGAAGTCAACGAAGATGAGGATTTGGGAGATGAAGAACAA
GTGAAGATTTATTAGAACACGATCCAAGAGAATGGAAGACTGCCAATTTATATGCTGTTTTAGGTT
TATCTCATTTTGAGAAGTAAAGCCACTGAAGATCAAATCAGAAAGAGCCACAGAAACAGGTTTTTGA

AACATCATCCAGATAAAAAATCCGCTAGTGGTGGATTAGAAAAACGATGGATTTTTTCAAAATTATTC
AAAAAGCCTTTGAAGTTATGTTGGACCCAGTCAAGAGAAGACAATACGATTCTATTGATGTTGAAA
ATGATCCAAAACCACCAGCTCCAAAATCCAAATACGATTCTTTGAAGCTTGGGGTCCAGTATTTG
AAAGTGAAGCAAGATTTTCTACTAAACAACAGTTCCATTGTTGGGAAATTTAGAAAGCACCAAAG
AAGAAGTTGATGCTTTCTACAGTTTCTGGGGAAGATTTGACTCTTGGAAGACTTTTGAATTCAAAAG
ATGAAGATGTTCCAGATGACACTGCCAACAGAGATCACAACGTTATATTGAACGTAAGAATATTG
CCCAACAGAAAGAAATTGAAGCAAGAAGATCACAAGAGATTATCGAATTGGTCGAAAGAGCTCATG
CTGAAGATCCAAGAATTAAATTGTTCAAAGAAAAAGCCAAGAAAGAAAAGGCTGCTAAGAAATGGG
AAAAAGAATCTGGATCAAGAAAAGCTGCTGAAGAGGCTGCTGCCAAAAGGCTGCTGAAGAGGCCG
CTGCTAAGAAAGCCGCCGAAGAAGCCGCCGCTTTGAAAGCCAACCTCTAAAAAGCTAAAGAAGCTG
CTAAAGCTGCTAAAAAGAAAAACAAGAGAAACATCAGAGCTGCTGTTAAAGACAATAATTACTTTG
GTGACTCAGCTAAATCTGCCGACATTGATGCTGATGTCGATTTGTTAATCGAAAAATTCGACGATG
TCAAATTAGGTGAAGTTGCTGATAAAGTTAAAGATGCTGATGCTGCTTCAGTGAAATCTACTTTTG
TTGAAGTTGCAAAGGAATTGGTTGGAGCTGGTTCTTTAGATGCTTCCTATTTGAAATATTTTAACT
AGATTTTTTTTTTTGTAGGAAAATAATATATATAGAATGTAACTATCAAAAACAATTATACAGAAG
CTGAACCTCAACAAGACTAAACAGCAAG

YGR285C_homolog 427aa (SEQ ID NO 364)

MSIVLPSGTTDGFKAISKYSAPVRRPIEPVGRYFLAHASRTLGRHTWSEFEKLEAEKNVKQIEVNE
DEDLGDEEQSEELLEHDPREWKNTANLYAVLGLSHLRSKATEDQIRRAHRKQVLKHHDPDKKSASGGL
ENDGFFKIIQKAFEVMLDPVKRRQYDSIDVENDPKPPAPKSKYDFEAWGPVFSEARFSTKQPV
LLGNLESTKEEVDAFYFSGFRFDSWKTFFKDEDPDDTANRDHKRYIERKNIAQQKEIEARRSQE
IIELVERAHAEDPRIKLFKEKAKKEKAACKWEKESGSRKAAEEAAKKAEEAAAKKAAEEAAALK
ANSKKAKEAKAAKKKNKRNIRAAVKDNFYFGDSAKSADIDADVLLIEKFDDVKLGEVADKVKDA
DAASVKSTFVEVAKELVGAGSLDASYLKYN

YHR021C_homolog 1178bp public: 1..537/917..1178, PathoSeq:
538..916; exon 1: 501..503, intron 1: 504..932, exon 2: 933..1175
(SEQ ID NO 365)

TTTCATTTGTAGGCATTGTGTAGAATGTGGACTGTAGGAAGGTGCAAAATATATATCCAATAAGTC
ACATCTCAAATTTGGTAGTAGAAGAAATCAACCTTGGGACAGTATTCTCTGCTTAAATAGATTTTAC
TGATCAAATAAAATATTGGCTCAACCATTTGAAAAGCTATTCTTGACACTTTTTCAGTTTGTAGTTT
TGGTTGTTTCACAATTGAAAAAAAATGTTGAGCCCTAATAGCCCTAATTGTTTGCACGTGATGT
ATTGCTTTGAGTGAAAAGTGTACATTTGTACACACACAAAAAATACTAATCTTCCCCCA
ATATGCTGCGTATAGTGAGAAATCTTCTTCTCTCTTGCCATACTATCGCATTTTTTTTTTTGGTAA
CTCAGGAAACCTAATTGGAAAGAAGAAAAGAGAAAAAATAATTTTCAGTTTCAATAGATTTT
AGTTTTTTGAATTATACATATTAGAGAAACAAGTTAACAATGGTATGTTTCATTAGATTACCATGAG
TTATGGAGGGATATTCTGGATGATCAGAATATCATAATATAGGAGTATACTATTTTACTGGAATC
AAGATATAATTGAATTGAAATAAAAAATTGAATAAGAGGAAGCATAGAATACGGAATGATGATTAAC
AAATCAGAAAACATTGTACTACCGAATAATGAATTAGGATCAACATATTAATATCAACTACTACTT
TAAAGAAGCAGGAAAATGAGAAGAGAATCAGCATGAAAGTTACCACCTCAGAAAACGTCAAAGAAA
TATACTTTTGGTGTGGATCCATGTGTTATTACTGAAATCATCGAAACGAATATAACCTCCTTTTC
CCACATTGACATAAATCAGACACAATCTTTCAAATAAAACATGTAATACTAATATTTTCTTTT
TCGTATAGGTTTGTAGTTCAAGATTTATTACATCCATCTCCAGCCACTGAAGCTAAACAACACAAAT
TGAAAACCTTTAGTTCAACAACCAAGATCTTTCTTTATGGACGTTAAATGTCAAGGATGTCTTAATA
TCACCACTGTTTTTCAGTCACGCTCAAACTGCTGTCACTTGTGACTCTTGTCTACTGTTTGTGTA
CCCCAACTGGTGGTAAAGCTAAATTGACTGAAGGTTGTTTCAATTCAGAAGAAAGTAA

YHR021C_homolog 82aa (SEQ ID NO 366)

MVLVQDLLHSPATEAKQHKLKTLVQQPSFFMDVKCQGLNITTVFSHAQTAVTCDSCSTVLCTP
TGGKAKLTEGCSFRK

YHR141C_YNL162W_homolog 1179bp PathoSeq: 1..1179; xon 1:
501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367)
TTTATATTGTTTTTTGTTTCTATGTATAGTAATTATTTAATTTGATGTTCCATTATTCATGTAATT
GTGATGTATTTTTTTTGTGGTCTTCTTTGTGTTTTGATATTTTGCAGCTGGTCCGATCATACAA
ATTTGGAAGGAGCTACCAAAGCAGAAATGATAGCAAAAAAAAAACAGGAGACTTTTGGAATTTCTTG
GTTTAGGGCTCTAGCCCTAATGCCTGTATATAATTGATTGATGCTTTAAATTTGTGCGGTGAAAA
ACAGAAGCGAAAAAAAAAGAGCTGGAAGTGTGATTAAACAACAACGAGGGAAGAAAAAAAAACTTAA
TTAGGTGAACAAAAATTAATGTGTGAGCGTGTACATGCACAATTTTCAATTGGTTATTCTCAGCA
CTAACAACTCAACCTCCATTGTGAGAAAAGAGATTTTCTTTGAAAAAAAAATTTACATACATATC
TTAGTTCACTAGTAACCTTTCGAAGACAACATAGACAAGATGGGTATGTTCCAGTATAGCAATATTC
AACAAATGAGATACAAGATATTCCTCCAATACAAAGAGATTAATGGTGTTTTTGATAGAGTGTAAG
CCATGTGTTTAAATAAGAATGATTTGTCAAGGGATAAGATGAAAAGTGGAAATGTCCAAACAACAT
TGAAACGAATTTTCTGGGATAGCGTTCAAAACAATCAAACTATCCAGGTTTCTTATGACAATTAAG
AAAACAAGTCAATATTATCAAAGATGGAGTTTATAAGGAGAGATATTGAAACATCAAATGTTGA
AAGAAATAGCCAATTTTGGCACCATTCTCTGTGATCATAGAAATACTAACAATCCTCTTGTGTT
ATAGTTAACGTTCCAAAACTAGAAAAGACCTACTGTAAAGGTAAAGAATGCCGTAAACATACCCAA
CACAAAGTTACCCAATACAAAGCTGGTAAAGCTTCTTGTTCGCTCAAGGTAAAAGAAGATATGAC
AGAAAACAATCCGGTTATGGTGGTCAAACCAAAACAATTTTCCACAAGAAAGCCAAGACTACCAAA
AAAGTTGTTTTGAGATTGGAATGTGTTGTCTGTAAAACCAAGGCTCAATTACCATTGAAAAGATGT
AAACATTTTGAATTTGGGTGGTGACAAAAAACAAAAGGTCAAGCTTTACAATTTTAA

YHR141C_YNL162W_homolog 106aa (SEQ ID NO 368)
MVNVPKTRKTYCKGKECRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGYGGQTKQIFHKKAKTKK
KVVLRLECVCKTKAQLPLKRCCKHFELGGDKKQKGQALQF

YIL112W_homolog 3583bp PathoSeq: 1..3583; CDS: 365..3580 (SEQ ID
NO 369)
GTGCGAATAATACAAGCGATCGTTTTGAATAATCCAATGATTAGCTCTGATCAACGAATTCAAAATT
TTCCCCCTCAAGGACGTAGTACAACAAGAGATGAGAAGGGGTTTGAAGTGTGTTGATTTCAGAGGAGA
TGACGGTGCAAAAAGATCTACCACCAAAGAAGCACATAATTTTTTTGAATGATTTCAGGAAAGAGTTC
CATTAGTGATATCTCAAGCCAAAAATTTTCAAGGGAAAGTCCCGTAATGTTTCACGGGAAAGCAG
CAGGCGAAGTTCAATAATAAAAATTGATCATCATACTAATGTGGACGTGTCAACGAAACCGGAAAA
TATAAATAGCAGAGATAACAAAACCTGAGAAGAATATGACTTTGAGTTTCAGAGTCAACCAACCGAG
TGTCGAAGAAGTTAGTAAATCTTTGAAACCAACAATTACCAAGAAAACCTCATTCACTGATTACTT
AAAATCTGCCAAAACTAAGGCTAAAGAAGAAAGTTAAACAATCGAAAAAGTGACAAAAAGATTAA
TTCAGAAGAACGAAAAACGGAACCAATTCAACAAGCGAGCACTTTTAAACGGACAAAAAGGATAA
TAACTGGAACCCAATAGTGAAGTAAATTTGAAAGACAATAATGACGACCTGAAAGCTACAGCTGG
CTGTGCCCTAGGACCTGATAAGAATACTGGAACCAACGATTTCAGATAAATCAGAAACGACTCAACC
AAAATTTGCCCGCTCAGAATCATTGTCGATACATCATTATTGTCTCCAGTTAATGAAAGTGATAC
TGATTTCAATTTCAATGAGTTAGCAGAGATACCGGAAGCAAAGGATGGTTCAAGTTGTGGCAGCAAA
TGTGCTGGAGAACATTGATGAGAATGAAAATATTTTCAAGCTGAACTGTTATAGCAGATGACCT
TCCACGTCTCGATGAAGGAAAGAACTTTTACGTGAACAAAACAGCAGATGTAAAGAGACATAAATT
GAAGAAAACAAAATTGAATACTATTTTTAGTTCCGATGAAGAGGAGGAGGAGATTCAAGAACCAGA
TTTCAAACCTCCAAGAACCAGAAAACTACCAGAAGATGACCAACATCCTGATTTTCAAATTTCAAA
AGCAACAACAGAAATCAGTAACGATAAAAACAGAAGTAAATAAGCCAGAAGTGAAAGAGGTTGGCGA
GAAAGAGAGAAATCACCAACTAGAAGATAGATTACCAATTAAAAAGAGAAAAATGCGGTCCGAGAA
TGCAAGACATCTGAAAACGGTGTGAGTTCAAATCAGAATCTAAGATTTCAAAGTCGAAGAACT
ACCTTACAAAGTTAAACGTGATTCAAGTGGTTCGATCATTATTACAACGAGCTTGCAAGAAGGGTAA
TTTTGCAGATGTCCAAGATTACATAGAGAGGGGTGCTAGTGCCAATGAAAGGATTTCTGTGGATT
CACATGCTTGCATGAGGCAGCATTGGAAGGTATACACAAATTTGTGAAATATCTCATCGAAAATGG
TGCTAATGTAAATGCGAAAGCTGATGAAGCTGGTGATTCCGAGACACCATTGATCGATGCAGCTGA
AAACGAACATCTTGATTGTGTTAAAGTGTACTAGAAAATGATGCTGATCCTACTATTTTCAATAT
TGATGGATTACCGCTTTTAACTAAGATTTATAATGAACATGAAGGAGAAGAAGGATATGATGAAT
TATTCAAGTTCTAGAAGAAGCAACTGCAAACTATAACAGTCGTTTACCAAGAGAAGTTCAAGTTGT

ATCAGATGCTCCTATTGGTAGTGGACCAATCATGGAGGATCCAAATGACAACTATTTTGCAGAGCT
AATTAAAGGTAAGGGAATATATAAAATACGCTGCAGAGAATTCAAAGAGAAAAACAGCAGAATATTT
TGTTGCTGGTCATAATTTAGAAGGAAAACAGATATTTTAATTTTAGCTGCTAGAAACGGCCACAC
AGAACTTGTTGATATTATACTAGGGCTAAACCCTACACCTTTTAATATTGATACCGAGTCAAGTTG
TGGTGTACTGCATTATTGGCCAGTATTGGACGCGGTCAATTTGAAGTTGTCGATTCTTTGTTGTC
CAAAGGTGCTGATCCATTCAAGACAAGAAAAAAGATGGGTGAATGCTTTAGAAATTGCACAACA
CTCGCCACATTTTGATTACAGGGAAGTTAGTGTAAATGAAATTCATGGAGAAGAAGAGTGGAAAC
CAAAATTTTGTCTGGTATTCCGTCAAGGGTAGTATCTCGTGCAACATCTCGTGACCTTCTGTTCC
CGTATCATCAGACGAAGATGACGTAGTGAAGAAAAAGAAATTACAGCACACACAGAAAAATAAAG
TGCTGAAAAGAAGCTGGAGGATAAAATCACGAAAACAGTTAATGAGCATGTCAGCAATCGGAAACC
CCACGAGTCTACAGGTCGAAAACCTTGAAAAGACTCATAGCAATGAGGAAAGAAAGCGGAAACGTGA
ATGGTCAGACGATGAACCTAAAGAACCACATCTTTTGAAGAAGTCAAAGTCTGATTTGAAATTGAA
ATCACTACATAGAGAATTCACCTTCTGATGATCACCACACCAGTGAAGCCATTGAGATTTCTTTTGC
AGAAAAAGAAAAACATTTATCGGCAACGCCACCTGCTCCTCCGCCACCACCACCACCACCCTTC
TCAAGCAGTTTATCAAGGCACAAGAAGAACAATAAATCAAAGATGCTGAAGAAGCTAGATTGTGGCA
AGAAAAGGTGCAAGCTAAAAAGAGGGCTCGAAGAGAAATGTTTTTAAAGTCCGAGAAAGAGAAAGA
GCAGAAACGGAAAGAAGAAGAATTGCGAGCACAGAAGAAAAACGAATTGCCAAAGCAAAACA
GGAAGAACAGGAGAGACTTGCTAGAGAAGCAGAAGAGAAATCGAAAGAACTAGAAGAAAAGAAAGT
GGGGTTGCGACAACAGTTGACATTAGATCATTTATCCGGTTGGATTGCGTTATTGCAAGTTTGATGG
AAACCCAAATATCTCGGCTGTTGATAAATTTTGGCTTTCTATGTATTTGTAATCGACGATAAAAA
GTATGCTGTTGATTGCAAGTCTCCTTGATCAGCTCAACGGTTGTCAGCAAGGTTATCAATACGT
ACAACCTCATCAGAAGAGAGAAATAAATGCAACTGAAAAAGCAAATTTGTGGAAGCTCTTTTCAA
GTTTATTGGTATTGATCCTAGGAATCCAAATTTGTGATCAAAGAAGCTCAATAACAAATGGTCAAAA
ACAGTTTCAAATTTGTTGCTTCATTTTGTGGAGGTAGATTTAGCTGAAGAATTTTAAAGGAATT
TCCAGAAGTACACTCAAAGCAAAGATAACCAAAATTGATGTTAGTTTAGAGTCTTTGAGTGGGTT
TTCTGATTGCGTCAAGGATGATATAATAGTTGATGGAAATCTTGAATTGATATTGATTCCAAGAA
AATCGAAAAGTTTATTCCTCCTCATTTGAATACTAGGAAAGACATTATTAGGACTGTGAGTACTTT
AGCACACCCACTATGGTGA

YIL112W_homolog 1072aa (SEQ ID NO 370)

MTLSSESTKPSVEEVSKSLKPTITKKTSTFDYLSAKTKAKEEKVTIEKSDKTINSEERKTEPIQQ
SEQLLTDKDKDNKSEPNSEVNLDKNDSDKATAGCALGPKDNTGKNDSDKSETTQPKLARSESFADT
SLLSPVNESDTDNFNLAELIPEAKDGSVVAANVSENIDENENISEAETVIADDLPRLDEGKKLLR
EQTADVVRHKLKKTCLNTIFSSDEEEIEQEPDFKLQEPEKLPEDDQHPDFQNSKATTEISNDKTE
VNKPEVKEVGEKERNHQLEDRLPIKKEKMRSENAKTSSENGVSSKSESKI SKSKLPYKVRDSSGR
SLLQRACKKGNFADVQDYIERGASANEKDFCGFTCLHEAALEGHTQIVKYLIENGANVNAKADEAG
DSETPLIDAAENKHLDCVKVLENDADPTIFNIDGFTALTKIYNEHEGEEGYDEIIQVLEEATANY
NSRLPREVQFVSDAPIGSGPIMEDPNDNYFAELIKGKGIYKYAAENSKEKTAEFYVAGHNLEGKPD
ILILAARNGHTELVDIILGLNPTPFNIDTESSCGVTALLASIGRGHFEVVDLSLSKGADPFKTRKK
DGLNALEIAQHSPHFDREVSVIMKFMEKKSGTKILSGIPSRVSRATSRAPSVPVSSDEDDVVEE
KEITAHATENKSAEKKSEDKITKTVNEHVSNRKPHESTGRKLEKTHSNEERKRKREWSDDPEKPHL
LKSKSDLKLSLHREFTSDDHHTSESHDSFAEKRKHLSATPPAPPPPPPPPSQAVIKAQEEQK
IKDAEEARLWQEKVEAKKRARREMLKSEKEKEQKRKEEELRAQEEKRIAKAQEEQERLAREAE
EKSKELEEKVGLRQQLTLDHYPVGLRYCKFDGNPNISAVDKFLPFYVFVIDDKKYAVDLQVSLIT
STVVSKVINTVQPHQKREINATEKSKLWKLFFKFIGIDPRNPNCQDRSSITNGQKQFQNLHLHVE
VDLAEFLKEFPVHSAKDNQIDVSLESLSGSDCVKDDIIVDGNLEIDIDSKKIEKFI PPHLNT
RKDIIRTVSTLAHPLW

YIL148W_YKR094C_homolog 659bp PathoSeq: 1..659; CDS: 501..656 (SEQ ID NO 371)

TAGTTTCTTTTGGCGGTATATCCTCACTCATGATTGATGTATTTGCCCACTAAAAAGAAAACCAAT
GAAACAATAAGATTGATTGATAGATTTGGTTGTAATTAATCTGATGCTTTCAACATTTGTTTTTGT
TCGTGCTCGGTCAATTGAGGTTGGGTAAATGTTTTTCTTTTGAGAATTGTGAGCATGCAATGTGCG
CATGCAAATATGATGTCGCTCAATTGCGACATACTACTTAGGGCTATAGACCTATTGCACGTGCGT

127/161

TAGTTTTAAACCTAAAAACAATTTTGTGCAGTCGTGCACCATTTCGTTCTATTTTCTACTGTGA
TTGACGTACAAACCTTCACAGTTCACGCACACTTTTGTGCTTCCTCAAACCTCTCTCACAGGCTTG
GTAGGAATGAAAAAATTTTGGTAAAGCGGAAAAAATAAACTTGAATATTTTGGAAATC
CCCTTTTGTATTACTACAATAGATTAAAGTAACTAAAGATGATTGAACCATCCTTGAAAGCTTTAG
CTTCAAAATACAACCTGTGAAAAATCCATTTGTGCTAAATGTTACGCTAGATTGCCACCAAGAGCCA
CCAACCTGTCGTAAGAGAAAGTGTGGTCACACCAATCAATTGAGACCAAGAAGAAATTGAAGTAG

YIL148W_YKR094C_homolog 52aa (SEQ ID NO 372)

MIEPSLKALASKYNCEKSICRKCYARLPFRATNCRKRKCGHTNQLRPKKKLK

YIL150C_homolog 2297bp PathoSeq: 1..1162, public: 1163..2297; CDS:
501..2294 (SEQ ID NO 373)

ACTCAGCCTTTTGAAATTCACCTTTTGGTAAAAGGATATGTAATTGAATCCGCATAATGGACTTTCT
CTAACTCCATATTGTTGTTCTACCTCTTGGGATAGAGACTTTGATCGTGACATTTTGTAAAGTGG
TAGAGGTATGGGTAAGATTATTTTACCACCGTTTTCCTTTAGCAAATAGTCTAAAGCATTTTCTG
AATTGTTGAGTTTCGGTACATCATTTAGCTATCTTTTGTACAATTGATTGCTTCTACCTCTAGTCA
TGGAATAACAAGTTAACAGCGTGTGTTTGGTGGTTGTTGGAACAAATAAAATTTGTGGTGTGTAAT
GTGTGTGTTTGTGTTTTTTTTTTTACCAGCATTTTGTCTTGTCTAAAAATGAAACAGCGCAATGAT
TCTTTTTCATAGTTTTTTTTTTTCCATACATAAATTCTGACGCGTGCACTATATCTGCTAACATACTC
GGCAACAACAAAGAAAGAGAATTTGAACTAATCCGAAGATGAACGACCCAGAGATGAACAAATTG
ACTCCGATGATGATTAAACAGAAGATTCATCTGATGAATTGAAGGACTTGGTGCAGGAGTTTGAAT
TGAAATATGCAGAATTAAAGAAGAACAAAGCCTTGAAAAAACGTCGTTTACAGTCACCACTGGAAG
ACATGCTGAATAAACAGAAACCCATCAACCGGAGGTCCCAGAACCCAGAAAAAGCTAAAGTCC
ATTTGGATAAGGTAGTAGAAGAACCAGCAAGAAATTTTACCAAGAAGGAGCCTCGGGATTCCA
AGATAAAAGAATCAAACCTTCTTAAACAAACTCTACGAGACAAGTAATAAGCATGATAAAGAAGATG
CCCATAAAATAGATTTTCACTAAAAGAAGGTTTGAAGTTTCAATTGGATAAGTATACTTTTACGCCAA
AAGACGTTGTTGATGATTTAGAACCAGATATCAAGCTTTTACTTGGCAGAGAATACCTTGCCCAAC
TGCAAAATTGCCGACATTATTGCCGAAACTGATGAAACATGAAATTCCTTAAATTTGACAAGTTTT
TAGCGAAAACCCATAAATCAAACAACATGCTGAACCCAAGTATTGTAATTGGTGTCTTGTGTCCT
TTGTGGTGCAGCAAGGACCCAGTGCAGGTTGCTGCCAACAACTCTAAATACATCAAGTTGAAGGTTG
GAAATTTTATGAATTCGTAGACTTGATGCTTTTGTGATAAGGCTTTTCAGAAAAACGGGAAAAATCC
AACCGGTTGATTTATTATTCATTTTGAATCCATTGATCAACAAGTATGAAATACAAGTTGGCAAGG
GCCAGTTTTCAGTCTGGGTTCAATTTGAAAGTAGAAAAACACCAATGTGTCAAGTATTTAGAGATAG
GATCGTTAAGAGATTTTGGGTTTTCAGGTTTACTAGAAAGCTAGATAATAGCATGCAAGGAGG
CCATCAACACAAGGACGCAAGAATTCTGCGATATACATTTGGATATGAAGTTTAAAGTCTAGTACAA
GAATGGAATTAAATGGAAGTGTTCGATTAGATCCCGCAAAAAACAAGAAAAAGATGTACATGA
ATAAAATGGGTCTGGCTTTATTAAGCAATATAACGAGGAGAGTACTGTTATAGGAACAAGCTACG
GTTCTCCTCTTGATCCAAAAAGGTACCAAGACCCGAAAGTACTCCAGAACCAATCAAGCGGCGCA
AACTAATAGACGACAAGGCAAGGAGATGCTTGAACAAAAGCTATCGAACTAGGTTTCGGCTTCAT
TATTGAACAATTTACAATTATCTAAGAAAGAAGCAACAGATAAACTTGCAGTGATCGTCTGAAGA
GCAAGGATTACCAACACAATGATTTACATATTGGGTTTGTATCCAACAGGTACATCTTTGAACC
AAAATAGTACCCTGCTTGGCAGCAAGCTGATGGAATAATCTCGAGCACGGGAATTGCATGATTTGA
GTGTTGAAACATCTGGTCATAAGTCGTTGTCTTCGTCTAAACAAGATCGCCAGTCGAAAGTTGCAA
AATGGAACACGAATATCAGAACTTTACAAAATTACGATCGACGAGTTGCCAGCCACTCCTTGAGTA
CCTCTCGTCGGTTACAGAATCTTGTAGGAAAGCAACACACGCTACACTAGTAGATAAAAGGAAAA
GAGTGGTTGTCTCAGATGATGAACAACCGGGGATGGAAGAAGATGAAGAAGACATTGAAATCCAGT
TTGACGACGAAAAGTCTAAGATGTCCTACATGAAAATGACTGGAGCCAGGTAA

YIL150C_homolog 598aa (SEQ ID NO 374)

MNDPRDEQIDSDDLTEDSSDELKDLVQEFELKYAELKKNKALKKRRSQSPSEDMSNKQKPHQPEV
PRTPEKAKVHLDKVVEEPKQRIFTKKEPRDSKIKESNFKLNKLYETSNKHDKEDAHKIDFSKRRFEF
QLDKYTFTPKDVVDDLEPISKLYLRRRYLAQSQIADIIAETDSNMKFLKIDKFLAKTHKSMNYAEP
KYCNWCLVAFVVRKDPVQVAANNSKYIKLVGNFMNSVDLMLFDKAFQKNGKIQPGDLLFILNPLI
NKYEIQVGKGQFQSGFNLKVENTNVSSILEIGSLRDFGFCFKFTRKLDNSRCKRAINTRTQEFCDIH

LDMKFKSSTRMELNGSVSIRSPQKNKKKMYMNKNGSGFIKQYNEESTVIGTSYGSPLDPKRYQDPK
VLQNIKRRKLIDDKAKEMLEQKLSKLGASLNNLQLSKKEATDKLASDRSKSKGFTNTMISHIG
FDPGTGSLNQNSTSLGSKSMEKSRARELHDLVSETSGHKSLSSSKQDRQSKVAKWNTNIRTLQNYD
RRVASHSLSTRRLQNLVGKQTHATLVDKRKRVSDDDEQPGMEDEEDIEIQFDEKSKMSYMKM
TGAR

YIL167W_YIL168W_homolog 1499bp public: 1..1499; CDS: 501..1496
(SEQ ID NO 375)

TTTCTTCATCAACTTGCTCAAATGTCTTTGAAAGTGAAAGCTTACTTTTTTTGGTTTCGTTTAGGTG
GCATCAAGGTAAAGGAGGGAGTTTTGGGTATAGTTAGGTTTTTGACTTATTTCCTTTTTTGAGTAGA
TATAACAGAACTACCAAAGTGAGCCACATCTGTTAATCTTGAAAAGCAAATTGAGAAAACCAT
TTATGCAAGTCGTGTACTGGTGATATCTTGGTCAATTGCTACACTTTTGTAATGAATACTGTAAT
GTAGCCGACGTGGGTGAANAATATATATTTAAGTATATAGAATCAGGTCAATATAAAATGTTTGA
AATATAACAAAATGTTTCAATGTAAACGTATGGTTAAGGGATTATAAATCAAACGTAGTAGTGCTT
TTGTTCCATAAAAAACCCATCGTGGTGGTAACGTCAGGAGACCCGACATCAAATGGAATTCACACA
ATCAGTCTCCGAATTTATTACCCTTGAAACTTAACTTAATGAAAGAGCCTTCCATCACTACTACCT
TTGTTGAGGTTACAGACAAACTTCCACAAAGCCTCCGTGCAGGGTGTTTTTCAAGAATGAGTATG
AGCAGCCCTCCGGCAGTGTCAAATTAAGAGGCATGGGACACTTGGTTGGCCAGTCTATAGATGTGG
CCAGAAAACTTGGCAAATCGAACGTAGCAGTTTTTTTCGTCATCTGGTGGTAATGCAGGATTAGCAG
CTGCTTATGCCAGCCAGTTTTTTTGGAGTATCGTGCACCTGTGGTGTTCCTGAAAGTTCGAAGCCAA
CTGTTATAGAAAAGTTGAAATCCCTTGGGTGCAGATGTCATTATTCATGGGAAACATTGGGGAGAGG
CCGATAACTATTTAACTGATTTTTGTTATTAAAAATCTTGACAAAACAGTCTATCCGGTCTATTGTC
ACCTTTTTGATGACCCATTGTTGTGGGAGGGTCATAGTAAGATCATCACGGAAATCATCGATCAAA
AGCAATTACCCAACTTTGATAAAGTTAAGGGGGTCATTTGTTCCGTAGGAGGGGGTGGCTTATACA
ACGGAATAGTTGAAGGTTTGGAAAATCATAAGGAGATACCAGTGTGGAATGAACTAAACAAG
CGGCCACGTTTACGAGGCGGTCAAAGAAGGTAAAGTTGTTCAATTTACAAAAGTGCAAACTTTGG
CCACTTCTTTGGCTTCGCCGTACCTTTCTTCCAAGGCATTAGCAAACATATATTGAGCGTCTACAG
TTCTTGCTGAAATGATGACTTGGACGCTGTTAAAGGTGTTGTTGATGTATACGACCATTTCCGAT
ATATGGTTGAGCCTGCATGTGGTGCATCCGTTGCATCAGTGATGCACAGGCAAGATTTATTGAATA
AATTTGGTACATTAAAGTCCAGATGATATTATCATTGTTGTCATATGTGGTGGATCGGCTATCAACA
AGTATATTATAGACGAATATAGAAGTTTATTAGAAAAAGACTCTTGA

YIL167W_YIL168W_homolog 332aa (SEQ ID NO 376)

MKEPSITTTFVEVTDKLPKPPCRVFFKNEYEQPSGVKLGRMGHLVGQSIDVARKLGKSNVAVFS
SSGGNAGLAAAYASQFFGVSVCTVVLPESSKPTVIEKLKSLGADVIIHGKHWEADNYLTDFVIKNI
DKTVYPVYCHPFDPLLWEHGSKIITEIIDQKQLPNFDKVKGVICSVGGGGLYNGIVEGLENHKEI
PVLAIETKQAATFHEAVKEGKVVHLQKVQTLATSLASPYLSSKALANYIERPTVLAIEDDLDAVKG
VVDVYDHFGYMVEPACGASVASVMHRQDLLNKFGLTSPDDIIIVVICGSAINKYIIDEYRSLEK
DS

YJL034W_homolog 2564bp PathoSeq: 1..806/1401/2504, public:

807..1400/1402..2503/2505..2564; CDS: 501..2561 (SEQ ID NO 377)

TTTTTGAACAGAGAAATGAATGAACAATTGATGACCATAGAAATGAAGTGAGAACACATAAAATCT
GCGACACTTCACGTGATAACAACAAAGTGACATGAACAACAAATGTCGTTTGTATAATTTGCGACA
TTTGTGTTTCAAGCCAAAAAAGAAAGACAGAAACAGAAAAAAGAAAAATCTCAAAGTTGCCACGT
AAGCACAAATTAATCTTTTTATGGTTGTAACATTTCTAGTATATTCTACGTAATAGGTGAGGTCCCT
ATATGCAGTACACACAGGTTTTTTTACAGATGTTGACACAGTGTGAAAATTTATTCACGTTGATT
TATAAATATACAACCTTACCTTCCACGGTTTTTTTTTTGATTTTTGATTTTTGAATTTCTTCTTCT
TTTTTTGTCAATTTATTTATTAACAATTCTCTTGTAACTTTATTTGATAAATTTTACAAGATT
TAATTAGATCAATTAGATTATAGAAATCATTTCAATATAATGAGATCATCACAACTTCTTGGTTAC
CACGTATTGGTTTTATTATATGTGGCGTTAGTTATACCTATACCATTTTTTGGTTTCACCGAAGCACG
CATTTGCGGTTGCTGCAGTGAGCGATGATGAATCCTCGACAGATAATTATGGTACAGTCATTGGTA
TAGATTTGGGTACCACTTATTCCTGTGTTGGTGTATGAAAACGGTAAGGTTGAAATTTTGGCCA
ACGATCAAGGTAATAGAATCACTCCATCATACGTGTCGTTCAATGGCGATGAAAGATTGGTTGGAG

ACGCTGCCAAGAATCAAGCTTCCTCTAATGTCAACAACACTGTTTTTCGATATTAAAAGATTGATTG
GTTTGAAATATAATGATGACACTGTGCAAAAGGAACCTTAAACATTTGCCTTACAAAATTGAAAATA
AGGGTAACAAACCAGTTGTTAAAGTTGAATACCAAGGTGAAGAAAAAACTTTCTCCCTGAAGAAA
TTTCATCTATGGTTTTTGGGTAAATGAAGAGTATTGCTGAAGATTACCTTGGCAAAAAAGTTACTC
ATGCCGTGTCACTGTTCCAGCTTATTTCAACGATGCTCAAAGACAAGCTACTAAAGATGCCGGTA
CTATTGCTGGTTTTGAACGTTTTTGAGAAATTGTCAATGAACCTACTGCTGCCGCTATTGCCATGGAT
TAGACAAAGGCGACCAAGAAAAACAATTATTGTTTACGATTTGGGTGGTGGTACTTTTGATGTTT
CTTTATTGTCCATTGAAGGTGGTGTGTTTTCGAAGTCTTGGCTACTGCTGGTGATACTCACTTGGGTG
GTGAAGATTTTGATTTCAAGATTGTCAGATACTTGGCCAAACAATTCAAGAAGAAGCACAAATATTG
ATATCACTGCCAATTCTAAAGCCATTTCCAAATTGAAGAGAGAAGCCGAAAAAGGCCAAGAGAACCTT
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CTCTTTCAAGAGCCAAGTTTGAAGAATTGAACATTTGCTGCTTTTCAGAAAGACTTTGAAACCAGTTG
AACAAGTGTGGAAGGATGGTGGTGTCAAGAAATCCGATATTGATGATATTGTTTTGGTTGGTGGTT
CCACCAGAATTTCAAAAGTTCAAGAATTATTGGAAGGATTCTTTGATGGTAAAAAGGCTTCTAAAG
GTATTAACCCAGATGAAGCTGTTGCTTATGGTGGCCTGTTCAAGCAGGTGTTTGAGTGGTGAAG
AAGGTGTTGATGACATTGTTTTGTTGGATGTTAACCATTGACTTTAGGTATTGAAACTTCTGGTG
GGGTTATGACCACTTTGATCAAGAGAAACACTGCCATCCCAACCAAGAAATCTCAAATCTTCTCAA
CTGCTGCTGATAACCAACCAACTGTTTTGATCCAAGTCTATGAAGGTGAAAGAACCATGGCTAAAG
ACAACAACAGATTGGGCAAAATTCGAATTGACTGGTATTCCACCAGCTCCAAGAGGTGTCCACAAA
TTGAAGTCACTTTCTCATTGGATGCCAATGGTATCTTGAAAGTTGAAGCTGCTGATAAGGGAACCTG
GTAAATCTGAATCCATTACTATCACCAACGAAAAGGGTAGATTATCCAAGGATGAAATTGATAGAA
TGGTTGAAGAAGCTGAAAAATACGCTCAACAAGATCAAGAATTGAAAGAAAAAGATTGAAGCTAGAA
ACTCATTAGAAAATATGCTCATGTCTTGAGAGGTCAATTGAGTGATACTTCTGAAACCGGTTTAG
GTTCTAAATTGGATGACGATGACAAGGAACTTTGGATGACGCTATCAAGGAACTTTAGAATTTA
TTGAAGATAACTTTGATACTGCTACTGCTGAAGAATTTGAAGAACAAAAACAAAAATTAATTGACC
TTGATAACCCATCACAGCAAAATTATACGGTGGAGCTGCTGGTGAAGGTGCTGGTGGCGCTGGGG
ATGCCAAATTCGGTGATGATGATTGATGATGAATTCGATCACGATGAATTGTAG

YJL034W_homolog 687aa (SEQ ID NO 378)

MRSSQSSWLPRIGLLYVALVILIPFLVSPKHAFAVAASVDESSTDNYGTVIGIDLGTYSVCVGM
KNGKVEILANDQGNRITPSYVSFNGDERLVGDAAKNQASSNVNNTVFDIKRLIGLKYNDTQVKEL
KHLPYKIENKGNKPVVKVEYQGEKTFSP E EISSMVLGKMK SIAEDYLGKKVTHAVVTVPAYFNDA
QRQATKDAGTIAGLNLVLRIVNEPTAAAIAYGLDKGDQEKQIIIVYDLGGGTFDVSLLSIEGGVFEVL
ATAGDTHLGGEDDFDKIVRYLAKQFKKHNIDITANSKAISKLKREAEKAKRTLSSQMSTRVEIDS
FVDGIDFSETLSRAKFEELNIAAFRKTLPVEQVLKDCGVKSDIDDIVLVGGSTRIPKVQELLE
FFDGKKASKGINPDEAVAYGAAGVLSGEEGVDDIVLDDVNPLTLGIETSGGVMTTLIKRNTAI
PTKKSQIFSTAADNQPTVLIQVYEGERTMAKDNRLGKFELTGIPAPRGVPQIEVTFSLDANGIL
KVEAADKGTGKSESITITNEKGRLSKDEIDRMVEEAKEYAQDQELKEKIEARNSLENYAHVLRGQ
LSDTSETGLGSKLDDDDKETLDDAIKETLEFIEDNFDATAEEFEQKQKLIDVANPITAKLYGGA
AGEGAGGAGDAKFGDDSDDEFDHDEL

YJL035C_homolog 1346bp PathoSeq: 1..125, public: 126..1346; CDS:
501..1343 (SEQ ID NO 379)

GCCCCATGGTGACAGAAAAGTATTGATCCAGGTTTCTTTGAAGGTTTGTAATACGTTTTAACTTG
TGACCTAACTCATTTCATAAAATCTTGTATAAAATTGGTTTCTTTGAATTGTTGTAATCTCTT
AAGATTGTCTCGTCTTCAGTGTGTCAGTGGAGCTGCTATTGCCAGTCGGCGGCATAACAGCAGGT
TCTGGTATGTCTCTTCATCTACTAAGCCGGACAATCCCAAAGCCGTCTCTTGTCTTTTATTCTT
CTAAGGAATGCTTTATGTAGTTCTGACATTCTTGCCTAAAAGGAAGTACAGTATTAAAGCTCGAAA
CTCAATTGCAACAAAAGTCTTAATTTTTCTTCTATAAGTAATTGATCTTGGTCCCCCAACAAAA
AGATACAGAGGAGAAAAGGAGGCCCTTAGGCTGACAGAAAAAAAATTTAGTACCTGCCACACAG
TAGCTCCAAACCCATATATGATTGATAGAGTTGAAGTATGCTGACAGATCTTACTTCACACTTTC
AGTACATGGCTATAAGCTTGTGTCGGTTACAAAGCCTTACTAAATAATGAGACACCAGTGTCTAT
GTATAGTCGTGGATTCAAAATCAGATAAAATCATTAGCATAGGCTACAATTATACCAACCACTCTC
TAAATGGTACACAACACGCAGAATTTATTGCTTTACAACGATTTGGGGAACAAAACTGAGTATTG

ACTATAATGATTTAATTTTGTATGTGACAGTGGAGCCTTGTATTATGTGTGCATCTTATTTACGTC
AGTTGGGCATCAAAAAAGTAATATTTGGTTGTGGGAATGATAGATTCCGAGGAAATGGTACCATT
TATCAATACATAGTGACATCACCTTGCTAACGCAGCTTATTCAGTATCGGGGGTATATGTAGGA
CAGAAGGAATCCAATATTACGAAATTTTATATTCAACAAAATGAGTCGGCACCAAATCCAAAAA
TCAAAAAGAACACAGATATTGAGAGTAAGGAATACCCAGAGAATCAGTTTTGTAGCATTTCAAAGG
ATGAATTTATAGAGTTTTACGGAATGAAAGAGTGCATATTTACGATGGGAAGATTTTTGAAATCA
CTCCATTACAAAACAAGGGTTATGATATAAAAGAATTGATATCGTTGGATATGATGCAAAAAGTTC
CATTTCTAGAGGATGAGTTGGGACAAATTACAGATGAGCAAATAATTGAATTTCAAACTTATTTT
TCAACATAAATGATGATGGAACGGTTAATTATAAAAAACCAATAGGCAAATATAACAGTAAAAAGA
GACACTTTGCAAACGATGAAGAATAG

YJL035C_homolog 281aa (SEQ ID NO 380)

MSTDLTSHFQYMAISLFVGYKALLNNETPVSCIVVDSKSDKIISIGYNYTNHSLNGTQHAEFIALQ
RFGEQKSSIDYNDLILYVTVPEPCIMCASYLRQLGIKKVIFGCGNDRFGNGTILSIHSDITLPNAA
YSSIGGICRTEGIQLLRNFYIQNESAPNPKIKNTDIESKEYPENQFCSISKDEFIEFYGNERNVH
IYDGKIFEITPLQNKGYDIKELISLDMMQKVPFLEDELGQITDEQIIIEFHNLFNINDDGTVNYKK
PIGKYNSKKRHFANDEE

YJL180C_homolog 1504bp public: 1..938/940..1504, PathoSeq: 939;
CDS: 501..>1502 (SEQ ID NO 381)

CTTTATCTAATTGATTTAAATAATTATTAACATTAGTACCAATAAATGCTTTACCACAACCTTGCC
AACTTTTTTCATTTGATTGGGTATTACATATTTTATTTAATTTAGCATTTGTAGTATCAATTATTG
TTAAATTTGTCATGGCTCGATCAAGTTGTAAATTACCCATGGATAATTCGCTTGAGATTTATTTA
ATTGATTATCCATTTCAAGTAGGACTTTTTGTAAATGCTTCTTGATTCATGATTAAATGAGACGAGT
GTGTGTGTATGGGCGATGAAGCTGAAGGTTTTGCAGATGTGGTGTCTATAAGAGTAATTTGATGTG
AAAAATATACAATCTATAATCAGTATGTTTCAAGTTTGGAAATGGAAGCCCCAAGAAGAACAACAGGG
AAATTAATAAATAAAAAAGGTGTTGGAGAAAAAATAAATTTGAACAGAAAGATTCACTCTTTTAGA
TCAACGAAATATATCTTACCATCCCCCCCCCTCCAAAATGCTTAGATTTACTAGGACTACTGCCTT
GGAAATTAAGATCTATTCCAATTGCCACTATTCAATATAGACAATTTACTTATTCCTACTATATGTT
ATCAATTAATAAACCTTACTCCATCTTTAGGAATAAATAATACCATTGAATCCAATATACCTTCAG
AACTAATAGATTAGCTAAACCTGGTACTAGATTTTGGAAAAAAGGTGAAGTTAAATTCATAATG
AACTCAAAAATATGAAATTCATTTAGATGGGAAACTCTACGCACACCACTTGGATTCCCATTAG
AATTACCAATCAATAAAAAACAATTTGGCATATTTAATTGCTCATGAATGGACTCATTTACCTGATA
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AACATTTGAGTGATATGAAGACAGAAAAAGCTGAAGAAATGTTAGCATTTGGAAGATATTAATTTAC
AAATGTTAAGATATCTTGATACTGATACTTGTCTTATATTTGCTACCAACAAAGAATGTGATGGTA
AATTAAGAAAAAGACAAGAAGAAATTTATCGTCCATTAATTAATGAATTTAATGAATTTTTCACAA
TTTATGCTCATAATAAAAAATTTAATCCCTCGACAAAAATCTATTGAATTTGAAATATTTAGATTTGTG
AACTGATGGATTAAAGAGGTAATAAACAAGATGAAACCACTCAATTTAGTTGTATTGGATTGGTTAA
ATCAATTACCAATTTATGATTTAATTTGCCCTTGGAGAAAAACAATCTTAACCTACTAAATCATTTTAT
GTGAATTACTTTATTAAGATCAAATGTTAATGATATTGAAACTTTTAAAGAATTATATCAATTTA
ATAAAAAATCCATTGATGAAGATTATTATCATAAACCTTTAGAAGAATTAGTTGAATTAGGAAATT
TAGAACTATTTATCAAACTGAAGAATGGGGTGAAGTAGAAGATACTCATGA

YJL180C_homolog 334aa (SEQ ID NO 382)

MLRFRTRTAWKLRSIPIATIYQRYQFTYSTICYQLKTLTPSLGINNTIESNIPSETNRLAKTGTRFW
KKGEVKFNNETQKYEIQLDGKTLRTPLGFPLELPINKKQLAYLIAHEWTHLPDIKVKSSSTLPLTAL
ATRAIDLSSQHLSDMKTEKAEEMLALEDIKLQMLRYLDTDTCLIFATNKECDGKLKRQEEIYRPL
INEFNEFFTIYAHNKNLIPRQKSIELKYLDCEDTGLRGNKQDETTQLVVDLWNLPLIYDLIALEK
TILTTKSFLCGITLLRSNVNDIETLKLKYQFNKNSIDEDYHKTLEELVELGNLETIYQTEEWGEV
EDTH

YJL187C_homolog 3689bp public: 1..452/3414..3689, PathoSeq:
453..3413; CDS: 501..3686 (SEQ ID NO 383)

TATTTATATATAATCTAACAACAAGTACTATCCCTTAACCTATTAGCTCAATGTCATTCTTCATTA
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TTAAACTGCTGTTTTATTGTAAAAATTTATTGTCGCTTTCTTCATAACATTATTTGTAAACAGTCTC
TAACTGTATTGTTGGGCTGACAGTAGAGTATTGCGGTCATTTTTAGGAGTGATTATAATTCCTCTGT
GAGAAACGCAAGCAACAAAAAAGAACAAAGGAACACAATCATGATTAATTATATTAATAGTAGA
AACTCAAGGGTGAGCTAGATGACTGAGCGTGCGAGAAAAAACAATCATCCAAAGTTTAAA
CAAAGTATTCCTTTTTTTTTTTCAATTTTACAACCAAAGATAAAATACTACACAACACCCCAACATTA
CAGCCAAAACCATATCTGTGCAATATTTACGCTCCAATGGATTCAAACCCGTGTCAAGACGTAT
CGGGTGATACCAGTAGCACACCAATGGCCAACAATAATCCCCTAATGACAGCACAATCTCCTCTC
AGAACCATTCTAAAACTGGCTTGAGAAAAACCAACAACAACACTACCACCAACACCTGCACCTGC
AAATGCATTCTCATTCACAGCAGTCACCTTATATTAATCAATTGGAATACCTTTACCAATAACCAGT
TTTCACGCTCTTTCAATAGTTTAATTTTGGAGGATGCCAATGATGCCAACCAACAATAGTTCAA
CAACAACCTTAAATAAGAAAAACCATTAACAAGTCACCACCATTCAATATCAAGCAGGACTTATTAA
ACGATAGTATCGACACGTTTCTTGATAACTCCAACACGGAACGATAGAAGATGGAGACGTCACAA
CAACAGACGACGATCAGGATTTTGATGATGAAGATATTGAAGATCCTGAAGCAGTGACGTACACCC
CAACTTTGAATATCTTGAATCCAAAAAGTCGATAGCTTCAATATTATATCTAGCAAGCATAGAA
AGAGCAATAGTCAGATTACCTACAATCTGCAGTACGGAAGCCATCCGAAGAAGATACGTCATCAT
CGATGGCTACAATAAGGTTATCTAACAACCTCACAAGTTCAATTAAGAGATCGTCAAAGTATTTGA
ATTTATCTATTGATTCCAATTTGAAAACGGTTGATGGAGGTAAAATTCCTCGATGAAAATAGATGACA
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AGCCGGACATATTTGCTGCTATAACTGCAGCAAAACGGGAATTTCAATAATCAATTTAAAAGGCCAC
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CATCTTCGCCACAGTCTAACTTGCATTACCTTCCAAGTTGGGACTGAAAGGATTCAAATGTTTTA
AAAATGCAAAATAGAGACGCGATAATGTCTCAAGCAGAGTTATGACTCCAGAAAAACCGAAAATGG
TATCTAAAATATTTGGCAAGTCAGCAAAAATAAGGCGAGCTTATACCCCAACCCATACATCTACCC
CAATGGCTGTCTCATCACTCAACCTCCTTCATCATCTACACTGAATTCAACAACGGCAGCAATAA
CATCTACAAGTCCAGCAGCTGATGAGCATTATGATATTGACAATGACTGTGACAGTCCGTCAAAAA
ATAGAAAACGTCTAATATTTCTGCATCTTCAATTATTATTTATCAAGATGAAAATCATATCAAGT
CAATGAAATCAAAATCTAGTAATCCAATACCCTACCCCTCCGACCGAACCACTACCGACAAATA
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TCAATTCCTCGGGTTGGTCAAAAAGAATAGCATAAGTGGTCTGCTGGACAGGAACTACCTCCAG
AAACACCAATCAAAAGAAATCCATTAATGATTTTAAATACCAACAAAGTTGTACCTCCATATAGCA
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AAAATGCAAGCTTTTCTGGCAGCGTGAATCCCAACTACTACGAACAACAACACTCAACAGC
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TCAATAACACAAGTTATATCAAAATTTTCCCTTCTTCGGAATTGAAAAGGAGCAGGTGCTTCAGC
GACCACAAGAAGATTTAGAATTAGTTTTCAATTCTGACATTGAACTAGATGATAACATAATACCAG
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TAGATAAATCAAATGCAACTAAACGAGAAATTAGCGAACCCCTTCAACACCAATCAATATGTCAT
TTGCAAGAATAGTTTTAAGAAACCTATGAATAATGCTGAAAGAGGTGATGACCCTGATAGTATAA
TTGCTCAACGCATAGATATTATGCCATCGTTAGATGAAGTTGACTCAGTGTCTGTTTATCCTTCAA
AGATAGATGAACATTTAATTGAAAAGTTTGAATGAAGAATATCAAGTATATTGGATCGGGAGCAT
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TTAAAGAAGATGAAGCAACTAATATGCAAGAACAAGAAGGAAAGAGTATCTAGTTTATTTCAT
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TTGATTTCTTAGAGGAAAATAAACATTACAAAATTGATGAATTTAGAATTTGGAAGATCCTAATTG
AAATTTCTAAATGGGTTAAAATTTATTCATCTGAAAAATTATTTACATTTGGATTTAAAACAGCAA
ACATTTTTTATCACTTTTGAAGGGTCATTGAAAATTGGTGATTTTCGGATTGGCTACTAAATTGCCTA
TACTAGAAAAGGACTTTGATCTTGAAGGAGATCGTAATTATATTGCCCGGAATTGATTAATGACA
AAATTTATACTCCGTTTGCAGATATTTTCAGTCTTGGATTGATTATATTGGAGATCGTGCTGAATA
TAATTTTACCAGATAATGGAACGCCATGGCGTAAATTGAGAAGTGAGAGCTTGAGTGGTGGCC
GATTATCAAGTGATAATATTTCAATGTTTTTACAACACAATCCAAATACCAATAGCAATATCAGTG
GCAGTGGAAGTAGAAGTGGTAGTGGCAGTACAGGAGGCAATGGTAGTGCTGGTGATTGA

MDSNPCQDVSGDTSSTPMANNPTNDSTISSQNHSTGLRKHQQQHYHQSHSQMHSQSQQSPYIN
QLEYFTNNQFSRSFNSLILEDANDANTNNSSTTTLNKKKTINKSPFFNIKQDLLNDSIDTFLDNSNT
ETIEDGDVTTTDDDDHDFDDEDIEDPEAVQYTPTLNLIKSKKVDNFNISSKHKRSNSQITYNSHVR
KPSEEDTSSSMATIRLSNNSQSSIKRSSKYLNLSDSNLKTVDGGKIPDEIDDISLNEIDVAVAPN
DFSSPLSARKPDIFAAITAANGNSNNQFKRPHKLVSQSPSPSSKNKFRISSTTSSPQSNLHSPSK
LGSKGFKMFKNANRDAIMSSSRVMTPEKPKMVSKIFGKSAKIRRAYTPTHTSTPMAVSSLNPPSSS
TSNSTTAAITSTSPAADDEHYDIDNDCDPSKNRKSSNISASSIIYQDENHIKSNHARKSSNPIPY
PPTEPLPTNISASVAETGKGSTTTKSNLSKGCPLFDDKENKASYQFVKPLQTAFNSSGLVKKNSIS
GSSDRKLPPETPIKRNPLMILNTNKVVPYSSGFAEGKDVMGDQHDYSHIPCONQRFPGSVNPNT
TTNNNTQQHHDSDLSIEVGRNNSYDASSSTINNTSYIKIFPSELKKEQVLQRPQEDLELVFNSD
IELDDNIIPETPTKSLLPNQHHQHHLPLYTQSKSPLLKFDTEKDGRNLSIVLDKSNATKREISE
PPSTPINMSFAKNSFKKPMNAERGGDDPSIIAQRIDIMPSLDEVDSVSVYPSKIDIEHLIEKFGMK
NIKYIGSGAFSIAFECLFNNEKFAIKRTKKPLIGKLEKQTIKREIEALRVLTSEKEDATNMQEQE
EGKEYLVVYFIEAWDFNNYYYIMTEFCEGGTFLDFLEENKHYKIDEFRIWKILIEILNGLKFIHKN
YLHLDLKPANIFITFEGSLKIGDFGLATKLPILEKDFDLEGDNRNYIAPELINDKIYTPFADIFSLG
LIILEIAANIILPDNGTPWRKLRSGDLSDAGRLSSDNISMFLQHPNPTNSNISGSGSRSGSGSTGG
NGSAGD

YJL189W_homolog 887bp public: 1..666, PathoSeq: 667..887; exon 1:
501..506, intron 1: 507..737, exon 2: 738..884 (SEQ ID NO 385)
AGTCAAGAATTTTATGATGACTTTGGAGGATGGTCTGATTAAAGACTTGTCTTTTACCAGTTTTC
AGCATTGTTGATGGCGTTTAAAGCATCAGCTAAGACGGAGGTTCTAGTCATGGTTGAATTGTCTGT
TGATAAAAAGAAACCGTGAAAAGGAAGTATTGTGAAAAATCGATTGATATTTTTTTTTTTCCTCCT
TCCTCACTGTAACAGTAGTAAACACACTAGTTACAACCTGATGACCTGCATATTATAAATCTTTCTG
AAAAAATTTTTTCCCTGTATTTTTGTAAATCTTTTCGCTCTTTCTCACTCACTCACACTTATTAAT
GAATGAAAGGTTTGGTGTCTACAACTCCACTAACAAAAATCTCACTCCTGTGCCTAAACACACACA
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TGCTGGAACAAAGACGAGAGAACTAGACAACCTCAGATATAATAGAACATCCATACTAACTTCACTC
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YJL189W_homolog 51aa (SEQ ID NO 386)
MPSQKSFRTKQKLAKAQKQNRPLPQWIRLRTDNKIRYNAKRRHWRRTKLGI

YJL190C_YLR367W_homolog 893bp public: 1..893; CDS: 501..890 (SEQ
ID NO 387)
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CTTTTACGGTTTCTTTTATCAACAGACAATCAACCATGACTAGAACCTCCGTCTTAGCTGATG
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AACCAAGATTCAACGTCAAAATCAACGACATTGAAAGATGGACTGACAACCTGTTGCCAGCTAGAC
AATTCGGTTACGTTATCTTAACCACTTCTGCTGGTATCATGGACCACGAAGAAGCTAGAAGAAAGC
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YJL190C_YLR367W_homolog 130aa (SEQ ID NO 388)

MTRTSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLTMQKHGYIGEFYIDDHRSGKIVVQLN
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YJL197W_homolog 4619bp PathoSeq: 1..3041/3260..4619, public:
3042..3259; CDS: 501..4616 (SEQ ID NO 389)

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YJL197W_homolog 1372aa (SEQ ID NO 390)

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SPEVFQHLGEWFGILGQPIIRAIINPDTKEKQIERFPPLFWVHQLGKKTQPTYLRHRHNGSNHNH
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ISKKTIVSPNMLEDALKDHGIVASSYNIMVEAKEKHQTEFPIDQFILSHSNAYEEVSQGGHGLGLS
NMGNTCYMNSALQCLLHVPEINYYFFYNIYKKELNFDNPLGYHGDVANAFGSLLKQAFDHVKNSSS
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KLANTCWNQHKARNDSVIIDLFTGLYQSTLICPDGCKKSITFDPFNDLTLPLPISKWKYHTFTIVD
LSNQGVIPIPERIMKLEVLNKTNSFDDLLSYLSNFLNVPSTELFAYEIFQNAIYSDFLDYTKNKF
PISDIIIRDTDVIVYIVPHNPAVDIIIVPVFNAVEDADSSYQMVNFFGIPLFVVMNKEVDVNSFGFI
RKKLETVSLLSKIDLVDVEYEKIKRSNEDYVEKVFYKKSDFPALSQPLETSDCEKNNNNTSDNDD
EDADNDEGYDSEVSLANPYLGANFGFKIMYVHDYSPKLNSNLSRYNHDQTTKFKQTERVINVPTH
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YJL198W_homolog 2693bp PathoSeq: 1..899/1285..2693, public:
900..1284; CDS: <3..2690 (SEQ ID NO 391)

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YJL198W_homolog 896aa (SEQ ID NO 392)

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ELKSFIENLRIGFTKICKKFDKTCGYSIKQDFINEFLPQYSRVFENDTIEELDYKLNQIIKIYAFL
SNKLTQTSTTKEDLDNIKFELSRDHIHFERNVWVDLLSLEKKSYNIDLNSVQNNKMGDEG
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CLAVLVAAAMLWASEALPLYTTALLIPLLVTCKVCKTPGTDDPMDATKASQYIFGTMWNSTIMIL
IGGFTLAAALSKYNLAKILSSYILALAGTNPRNVLLAIMCVSLFLSMWISNVAAPVLCFSLIQPVL
RSIPTDSPVAKALVLGIALASDVAGMASPIASPQNVIALESMNPNPGWGKWFVAALPVAIISLILI
WVELFMTFKINNVKIKQFKPIKEKLTMKQWVFAVTITILLWCVMQKIDGTFGESGIITCPIVL
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YJR049C_homolog 2279bp PathoSeq: 1..839, public: 840..2279; CDS:
501..2276 (SEQ ID NO 393)

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YJR049C_homolog 592aa (SEQ ID NO 394)

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YLR048W_homolog EMBL_entry 1042bp public: 1..1042; CDS: 28..786
(SEQ ID NO 395)

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YLR048W_homolog SWISS-PROT_entry 253aa (SEQ ID NO 396)
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IKESSYVNIPVIALTDMQSPSEYVDVAIPCNNGKHKCIGLIWLLAREVLRRLRGIIPDRTTEWSVM
PDLYFYRDPEEIEQNAVEEAKTEGVEGAPVAEAEETWTGETEDVDWADSGATPSC

YLR088W_homolog 1335bp public: 1..80/494..776/821..1335, PathoSeq:
81..493/777..820; CDS: <1..1332 (SEQ ID NO 397)
TCGGGGCTACAAATTTTCGTCCATGAAAATTGGGTTGCCACCAATACTTTGTATGCGATTATGCAT
GCTCCACGAGGTGAAAATACCGAGGCAATGGCGTTGGTTGTGCCATGGACTAATTCTGACAACGAG
TACAATGAAGGTGCTATGAGTTTGGCGGTGGCTTTGGCACGGTACTTTACAAAGATGTCGATCTGG
TCGAAAAACATTATTTTGTATTTCTGTAGACGGGCCACAGACCGTTGAGGTCGTGGGTTGAGGCA
TACCATACGGTGTGGACGATACTGCGGGTTCGATTGAGGCGGCGATTATTATGGAGTACGGCAAG
AACGGTGATTATTTTGTAGTATTACGATATGTTCTACGAAGGGTTGAATGGGCAGTTGCCGAATTTG
GACTTGTGTAATACGGCCAATGTAATGACGTATCATGAACAGATCCCCTGTGCCATGCAAGGGATG
TCGGATAGGGTTATCAATTATAGCACCCGGTTGCAGACTTTGTTTAGGGGTATCCTCAAATTGACG
CTTGTCCGGTTGACTGATGAAGTTCATGGGTGTGAAGCATTTTCGGGGTGGCAGATCCAGGCATTT
ACGATCAAGGTAAGGGGGACTGAAGGGAAGATGTTACGCAGTTTGGCCGGATTGTGCGATTCTACG
TTTAGGTCGGTTAACAATTTGCTTGAAAAGTTTCACCAATCGTTTTTCTTTTACTTGATGTTGTCG
CCAAAACACTTTGTGTCTATTGGGACGTACTTGCCGTCGGCGATTTTGTGGCAGTATCGTATGCG
TTGAGCTCTGTGAGTGGGTGGTGGTTGCCGGTTTGATTTTCGAAAGCTATATTTTGTGGTGGTG
GTTGAAATTGCGTGTGCTATTTTGGCGTTTGTGCCGGTGAACCAGGTGATGCTTGTAGCGATTCTG
GCGGTGGTGTGTTGCCCGGCCAAGCCATCTTTTCCAAGCAGGCGGCGTTTTCGCTAATTTCTATT
GCGTTGTGGCAGTGGCATTACTTATTACCGCCCTCTTGATTGTACATTTTGCATTGGCGTTTAGT
ATTGGGATTTTAGCCCTTCCATTGACATTTGTCCCGACATTAATGAAGAACAAGTCTAGGCTAACA
GCTTTTGTGGCGGTGTGCAATCCGTTTTTGTGATTTTCGTTGCTGGGAAAGTGCTTGGCCAC
CCCAGCTATTTGACCGTTGGTCACTGCCTGGTCCGACATACAGTGTGGACATGGTTTATCGTT
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GAAAAAGTGAATAG

YLR088W_homolog 444aa (SEQ ID NO 398)
SGLQISSMKIGFATNTLYAIMHAPRGENTEAMALVVPWTNSDNEYNEGAMSLAVALARYFTKMSIW
SKNIIFVFPETGHRPLRSWVEAYHTVLDDTAGSIEAAIIMEYGKNGDYFEYYDMFYEGLNGQLPNL
DLLNTANVMTYHEQIPCAMQGMSTRVINYSTRLQTLFRGILKLTGLVLTDEVHGEAFSGWQIQAF
TIKVRGTEGKDVTFGRIVDSTFRSVNNLLEKFHQSFFFYLMSPKHVFSIGTYLPSAILLAVSYA
LSSVS AVVAGDFRKLIFV VVEIACAILAFVPVQVMLVAISAVVLLPRQAIFSKQAFLISL
ALLAVALLITALLIVHFALAFSIGILALPLTFVPTLMKNKSRLTAFCLAVSNPFFVIFVAGKVLGH
PELFDRLVTAWSDIQCWTWFIIVLWGFPAWVIITLSYCGYKPVKEKSE

YLR167W_homolog 1190bp public: 1..1190; CDS: 501..1187 (SEQ ID NO
399)
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TGACGCTGACGATTAATAATGTGAATTTCTTTTTTCTTTTGGTTGTAGTAATTGCTTTGTTTTGT
TGTCTAAATTAGGAAAATGTCGTGACCTTACGTACAGCACACATACCCTGTGCTGCACTGACC
AACAACAATGCGGTGTTAATCGATAACCAAAGATTATAAATAGGGGGTGAAGGTCGCCACTGTT
TGAATGAATCAACACAGTTTTTTTCTTCTTGCTTTTCTTCTATTATTACATTACAAATTCTGA
CAATCGTCAACTAACATATATATACAAATCTACAAGCAATGCAAATTTTCGTTAAACTTTGACTG
GTAAAACCATTACCTTAGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAG
ACAAAGAAGGTATTCCACCAGACCAACAAAGATTGATTTTCGCCGGTAAACAATTAGAAGATGGCA
GAACCTTGTCTGACTACAACATCCAAAAAGAATCTACTTTACATTTGGTTTTAAGATTGAGAGGTG
GTATGCAAATCTTTGTTAAACTTTAAGTGGTAAGACTATCACTTTGGAAGTCGAATCTTCTGACA

CCATCGATAACGTCAAATCCAAGATCCAAGACAAAGAAGGTATTCCACCAGACCAACAAAGATTGA
TTTTCGCCGGTAAACAATTGGAAGACGGTAGAACCTTGTCTGACTACAACATCCAAAAAGAATCTA
CTTTACATTTGGTTTTAAGATTGAGAGGTGGTATGCAAATCTTTGTTAAACTTTAACTGGTAAGA
CTATCACTTTGGAAGTCGAATCTTCTGACACCATCGATAACGTCAAATCCAAGATCCAAGACAAAG
AAGGTATTCCACCAGATCAACAAAGATTGATTTTTTGTCTGGTAACAATTAGAAGATGGCAGAACCT
TGTCTGACTACAACATCCAAAAAGAATCTACCTTGCACTTGGTCTTGAGATTGAGAGGTGGTTTCT
AA

YLR167W_homolog 229aa (SEQ ID NO 400)

MQIFVKLTGTGKITLEVESSDTIDNVKSKIQDKEGIPPDQRLIFAGKQLEDGRTLSDYNIQKEST
LHLVLRRLRGGMQIFVKLTGTGKITLEVESSDTIDNVKSKIQDKEGIPPDQRLIFAGKQLEDGRTL
SDYNIQKESTLHLVLRRLRGGMQIFVKLTGTGKITLEVESSDTIDNVKSKIQDKEGIPPDQRLIFA
GKQLEDGRTLSDYNIQKESTLHLVLRRLRGGF

YLR234W_homolog 2390bp public: 1..2390; CDS: 501..2387 (SEQ ID NO 401)

TCCAGAATAGTAATTAGGGACTTTAATTTTATTAGGAGTGGATTGCATAGAATATGCTATCTAATA
GATACATCTTATTATATTCTTATTTCATGGGAAAGCACCAGTATATGGAAATGCTGCCCAAGGTAGT
GCACACAACAACTAGTTTACAAAGTAAATTCGAAGTTACGTCAAAGCTTAGAATGGTTCTTATA
GTAGTTGTCTACTCTATCAAAAAACCCATAATTTGTCTATATAACGTAAGGATCACTATATGCTGT
TGAGTAAGAAATATGTTGCGAGCCGTACCGACAATGGATTGGCTGAACTTGTCTCATCAAACTT
GCAAAACACTTGGAGACGCGCGCGCGTTTCAACACACAATAAACAACACGAAAAATAAGGTAGAAA
ACAAAAAATAAAAGGAACCTTTAAACAAGAAGTAATCCCCATTAAAACTTGATCAACACTTTT
AGGGTTTCCGATTTCCCATTTTCTTGACTAAAATAATATGAGAATACTATGTGTTGCCGAAAAAC
CATCGATTTCAAAGAGGTGGCAAACATTTTGGGAGGAGGGCGAAAAAAGTAAGAACTCACGAG
AAAAATTCATCAAAACTACGATTTACCTTCACCTTCACTTCTGAAGATGGGCCATGTCAAGTAA
CCATGACTTCGGTGGCTGGACATATCACAGGACTTGATTTTGGGTCTGCCTTTTCGTGGGGAAATT
GTGTTCCCGGGCGACTATTTGAAGCAGACATCAAGACCATTATCACCAGAAATCTATTTATGAAA
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GTGGAGAATTTGGAACCATATCAAAAATAGAATCAAACCGGAAACCAATTTCCGTCCATTCCCAT
TGACAACCGTGGAGTTACAAAAAGATTGTGCTAGATTTTTTAAGATGTCTGCTAAGACCGCGTTGG
CAGCTGCTGAAAGACTTTATAACCTAGGGTATTTGTCTGATCCTAGAACTGAACTGACAGGTTTG
CCAAAGAAACCGATTTCAAGAGCTTACTAGAGGTGCACAAACAAGATCCGCGATGGGGAAGCTATA
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TGACTTTAAAAATGGGGAGATGAATTTTACCAGCAAGTGGATTAATGGTGCATGAAAAAATTATT
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ACAAAATAGAGACTAGGCATATATTAATAAATTGAAAAAGGGGAAAAATGAATATATTTCTTCTTA
CTCCTTTAGGAATGGGGCTTATAGAAGGCCTTGAAAAATGGAATTTGAAGATGTATCACTATCGA
AACCATTTTTCGGAAGTCGTTGGAACGATCACTTGAGGACATAGCAACCGGTTCCCGGCCAAAAG
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ATAATAATACGTAA

YLR234W_homolog 629aa (SEQ ID NO 402)

MRILCVAEKPSISKEVANILGGGRKKVRNSREKFIKNYDFTFTFNSDGPQVTMTSVAGHITGLD
FGSAFSGWNCVPGRLFADIKTIITKKSIIYENIAEEARNADKLMIWTDREGEYIGFEIMNAARK
YNRNLGLNNIWRARFSLERNHIIIRAAKNPVNLDMSAVSAVSCRMIDLRVGTSTFTRLLTDQLRQK
GIIKKNELASYGTCQFPFLGFVVDYKRVKSFTPEPFWYIEIETRKENKKTIFNWVRGHFFDKMYV
VMLYDRCKSKSGEFGTISKIESKRKPNFRPFPLTTVELQKDCARFFKMSAKTALAAERLYNLGYLS
YPRTEDRFAKETDFKSLLEVHKQDPRWGSYTTKLLNEGFETPRSGSHDDKAHPPIHPIKYVSLDT
LNTLDEKKVYEVVRRFIACCSKDAVGTQTVVTLKWGDEFFFTASGLMVHEKNYLEVYTYKKWESSK
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AYSVCSHQILVLCNECRRIILGNSSNNNNNNNNNT

YLR241W_homolog 3098bp public: 1..827/2190..3098, PathoSeq:

828..2189; CDS: 501..3095 (SEQ ID NO 403)

ATATATAGAATTATGGCTTAGTGCCCTTTATTAACATAAATTAGAGGTTACATTAATACAACCTTAAC
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CTATTGTAAAGTACATCGCCTAATGATAGATAGAGTACTGGCGACTCCTTACATGATGG
TAACGACAACAACATAACAACAAAAAATATTATCTTGACGGTATAATTAGTAGTGTGCGAGAGG
CACACGATAAGATTTATCAGTTTCTCTCGGTTGACCTTAATCTGTTTTGTATAGACTTTAT
TTTTTTTGTGTGTGACCACACCCACTTTTTAATATCACAAGATATTTAACTGATTATAGAAAACAA
CAACAATAACCCAAATACGTTAACCCTTTTATTACATATGATAGACAATATAATCAATAATTTGC
AAATCATACTACAGCAAAATGATGATAATTTACATCCCCTCACGACGATGTGATATATCGACCAC
ATTCTGCTCGTGTAGCAGATATCAAGTAATAATGCATCTACATTGGGACTCAGTCCCTATTAC
TATTTTCTATCTTACGATTAATAATATCCCAAAATATATGTGGCAAACCTTTAATCATTTGAATTTCA
GTCTACATTCGACCTCAAGAAGGAATTTACCTGAATTGCCTTCAAATTCATTATTTGGTTGGATTTC
CTACAGTTTACAAAATTACTGAGCAAGAAATTTTGAACATGCTGGATTAGATGCAGTTGTGTTTT
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CTGTGTTTGAATGTCAAGGAGTGGCAAAATCTAAACAAACTATTCAAAGAAGGAGAAGATAGTTTC
GAAATTAGAGGAAAGTTGGGTTGAATATTTTGAAAAAATGGGATAACCAATAAGAGCGATTGA
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AATCTGTTGAAGGAGATTCTTCTGACACTTTGAATCGCTTGTGAATGATGAAGTGAACAAGAC
CAAGTCTTCGGAAAGGTTGGTTCCGATTGTTTGGACCTAAAGTGGATTCAATAAACTACTACACCG
ATAAATTGGAGGTCATAGATAAAGAGATTACCAGGGCCAGAACTAGAGAATATCCCGCACTTCGA
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TTCTTTTTCAAATCACAATGGTTGGCACATTAGCATTACAAGATGCAATCACATGTGCTACTTTCT
TGGCACCATTTGCCGTTTTTGAACCTTTACTTTTGGTGGAGTTTCCATAAACAATATATTCCTTGT

140/161

CAACATTCATTGCCTTGAGAGCAATTGAAAGCAATGAAAATATCAACCCTACTGATTGGAGCAAA
TCATTGAAAACAATAATAAACTCTTGACGAAAGAAGGAATTGAACACTAAATACGAATACC
CCAATCTAGTTAATGATTTAGACGGGCCAATGATTGCATTGGATGGTGAAGATGTATTGATAGTTA
ATCGAGATGGTACAACCTGTACGGAACCACCTCAATATTTTCAGTTCAGAATGGGACTATTAA

YLR241W_homolog 865aa (SEQ ID NO 404)

MIDNIINNLOIILQONDDNFTSPHDDVIYRPHSARVARYQVIIASTLGLTALLLFSILRLKYPKIY
VANFNHNLFSLHSTSRRLPELPSNSLFGWIPTVYKITEQEILEHAGLDAVVFLEFFKMCIRIISI
CLVFATIIIIISPIRYKFTGRVDEDYPDDSDNDDDDGSNNNGTTIIKHIVSAGISVASKNNDGEQYQ
QFLWLTYTIFTYVFTFVTVYFLFKQTNRIISMRQKYLGSQNSVTDRTVKISGIPGSLRDEVALARHI
DRLNIGEVDVSLIVKEWQNLNKLFRRRRIRVRKLEESWVEYFEKNGITNKS DLI SLHPQVGESYRF
SNRYTDDAESPDWGSQNSNSAQASIIDQDSESVEGDSSDTLNRLLNDESRTPLSRKGFGLFGP
KVDSINYYTDKLEVIDKEITRARTREYPATSTAFITMKTVAEAQMLAQAVLDPKVNHLITNLAPAP
HDIRWDNLSLTRQDRNTKILAVTIFIGIMSLLLVYPVRFMASFLNTKSISKIWP SLGKAIESHKWA
ETLITGLLPYLFITILNIVIPFFYVWVISEKQGYLSHDEELSSVSKNFFYIFVNLFLVFTTFTGTAS
FVDTTKIAFDLARSRLRDLMSFYVDLIILQGLGIFPFKLLLVGNLLRFLVNSLFRCKTPRDYLNLYK
PPVFNFLGQLPQPIILIFITLVYSVMSSKILTAGLLYFIIGYFVSKYQLLYACVHPHSTGKWPPI
IFRRIILGLFLFQITMVGTALQDAITCATFLAPLPFLTLYFWWSFHKQYIPLSTFIALRAIESNE
NINPTDLEQIIENNNKTLDERRELNTKYEYPNLVNDLDGPMIALDGEDVLIVNRDGTTRKPPQY
FSSEWDY

YLR321C_homolog 1559bp public: 1..947/1189..1559, PathoSeq:
948..1188; CDS: 501..1556 (SEQ ID NO 405)

TTCCAGAAATTAGTAGATATTTCTGATATCAAGTTGGAGATAGGGATATCGAACTGGGATTCTATAT
TTTGTTTTATCTTGGAGAACCTGTGTGTTGTTGGCGTCTCTATCTCTTTATATATTTTCTCTATTA
ATTCAATTGAAACATTTGAAGGAAATCTTTCTTAAAGCATCTAGTGACACATGATCTCTAATCT
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GATACTGTGTGGTGTCTGGGATAATAATTATAATGTAAACAAAACAAAGTCGTGTCTAGTGATATTT
TTTCTTTTGTCAATTCATCTTTTTTTTTTTCTCTTGAGAAATGTATAACAGAGGATCCATCCATT
TGCTTGACAGAGAAATACAGAACACTAAACAAACATTTTTTTCATTCCTTTCTTGTTTTGTCTGTT
ATACCCCAAAAGTTTGAATAAGTCTTCAGATATCTAGCATGGCAACTTCTCAAGAATTGACAGCAG
ACATACAGCTCTTGCAACTAGTTTCCCAAGCGATTAGCTAATGATAGTGACAATTCATTACTTA
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ATAAGCTCAAAATAGAAGCACAAAGATATTCTCTTGCGAAAAACACACCAACGCCCAAGAGAATCT
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TTGAGAAATTTGAACACAAACCAAAAGTTGATTGATTCCCTTTATGTGGAACCTGAATGAAAGCTTGA
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AAATAGCAGACTCCATTAATCAACAGATTGAAGAGTATTCTTATGCATCTAATTTACAACTACCAA
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TGAGAAGATTAAAGAGAGAGAATATGAGAAGAGATTACGATGATCATAGTAGGAGAAGGCAAGCAG
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YLR321C_homolog 352aa (SEQ ID NO 406)

MATSQELTADIQALATSFPRKLANDSDNSLLINVAPTGRQAKRHIQQINYSSEFGDDLDFFDEFPSS
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FMWNLNESLITPTEFAEIVCSDLPLPFSMAAQIADSINQQIEEYSYASNLQLPNKGPYNVTIDLSV
NLNKQLYQDRFEWDMNQNEVTPEIFAEIVVADLGLSLEFKNAISHALHEIIRVKKEVIDGTFDNE
MHNHLHLVKGIMFEQGIRIFTENSQNGNDRWEPLVEVLTSSSEIERRENERVRNLRRLKRENMRD
DDHSRRRQAGKRRYDELEGAWV

YLR325C_homolog 737bp PathoSeq: 1..737; CDS: 501..734 (SEQ ID NO 407)

AAGAAAAGTATAGTCAAATTGTTATACAAGCTAAGGAGCCATAAACTTTCTTTGGACATGCTAATA
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AACTAAGTATCGGCAACGTCTGTTGGCCAATTGGGGTGGTCAATGTAGGTATTTCATGCAAGAAGT
GCAGCACTGAAAATAACCGGTGCCTCTAACGTCAGTAACATAATGCTAAGCGAGTCTACACGAAGA
TGGATTATAAGTATAAAGAGGTTGATTAGTTTAAAGAGAGAGTATATAATAATGCACGTGATTAG
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TCTCACGCACATAACGTGTAACCCACATAAAGAAAGAAAAAAATTTCTTTGAAAAAATTCACA
TCACGCTTTAACCCTTCAACCTATAACAACCTCAACCATGGCTAGAGAAATCAAGGATATCAAAG
AATTCGTCGAATTGGCTAGAAGATCAGACATCAAATCTGCTATTGTCAAAGTTAACGCCAAGGTCA
ATGCTAACGGTAAAAAATTCAAACAAACCAAATTCAGGTCAAGAGTTCAAGATACCAATACACTT
TAGTTGTCAACGATGCTTCTAAAGCTAAAAAATTACAACAATCTTTACCACCAACCTTAAAAATCA
CCAACCTGTAA

YLR325C_homolog 78aa (SEQ ID NO 408)

MAREIKDIKEFVELARRSDIKSAIVKVNKVNANGKKFKQTKFKVRGSRQYTLVVNDASKAKKLQ
QSLPPTLKITNL

YLR344W_homolog 1348bp PathoSeq: 1..1348, exon 1: 501..515, intron
1: 516..979, exon 2: 980..1345 (SEQ ID NO 409)

ATACCATGACAAGCAAGCTCAGGGTCGCGGGTTCGAGTCCCGCGGGGAGCTAATTATACCCTCATT
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CGTTTTATATTTTTTTAAGAAATTTGATGTTGATTGGTAAATGCCAAATTTTAAATGTGTGTTAG
GGCTATAGCCCTAATGTACTGTATATGCAGTATCAGAAATACTTTTGTACGCACAGTTTGTCTTA
CCAAATACATTATATATATATATATTTTTTTTTTTTTTTGAGTAGAGGAGCTACACTAGACCACAGTGGC
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CTTTTGGATCGATACTAGATAGCATATAATCATCAAAAATGGCCAAGATCAGTCAAGGTATGAAAT
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AGGAATATATACATTGAAAAGGAGATAGAACATCAACAACAACCATTAAGAATTAAGTTTAATAC
AGTTTCAATAAAGAGGGTTTTTTTCTCAGAACAACCATTTGACTGAAGTACTACACCAAGAAAGGTA
TAATGATTTTCAAGATTTTACCTGAATATAAAGAACATCCTTAATATTGAATTTCAATATTAAAAATA
CAATTTGGGGATATTGATGAAATTATGTATAGGAGATTCCATTTTTCAAACCTGTTGAATGGAAAA
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ATTGAAATTTGCTATTCAAGTTGATAAATTACAAAAAGAAAAATCAAATGGTGTCTCTGTTCCAAT
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TCAAAGAAAAGGTGGTAAAGCTGAATAA

YLR344W_homolog 127aa (SEQ ID NO 410)

MAKISIDVSSSRKARKAYFTASSVERRVLLSAPLSKELRQQYNVKSLEPIRQNDVLRVVRGSKKGS
EGKVN SVYRLKFAIQVDKLQKEKSN GASVPINIHPSKV VITKLHLDKDRKALIQRKGGKAE

YLR393W_homolog 1631bp public: 1..1207/1209..1631, PathoSeq: 1208;
CDS: 501..1628 (SEQ ID NO 411)

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GAATTTAGATAATGCTTCCCTGTGGGTCACCCCATTTCCAAATAAGCGGGCATTTCTCTAAAAATCTT
TGTAAGTGAACGTCTTCATCTTCATGCTTTGCAAATCGGGATTCACTGACGAACAAAGTCAGCATA
AAACCATTGTGCTTCCCTCAATCTGAAACATTATTCTTTCAATGGAAGATAAATCCTTCTCGGGAAC
ATTACACCAAATCTAACTAACAAATCTTCCAACACCCGATCTAGAGTTTGATTAGCTAAACCATT
CGGTAATTGGATCGACATATCTTGTATTCTTCTATGATTAATCTTTCTTTTTTCTTTCTTTTCTCAC

TGAATATTCGTAATTAAAAATTGATTCAAAATTGTATTGATGTTTGTATACTGGATAAAACAACTTGT
GTGAGATCATTCAATGTATTTGCTGGCGGAGAAGGAGGCAAGGACGAACCTTTTTTCTTCATACT
TTTTTTTTTCTCTCTCTCTTTTCTTTCAGTCACATTGTCTGAGTGTTAAAGGCTGGCTTTTCTGTG
CTGAACCTTGTGGACTGGTAAACGCACGACATAGAGTAATATTTGGAGAAACCAAAAGAATTTTGA
AAAACCGTGGTTTGAATTCGACCACAGATTGGTTGGACGACAAAATGCAAAGTGATTCATCCGGA
CTTTTGCTACCTCAAGAATAGAGTTCACGCGGTACCAGCCGCGTTTGTTAATACCATTAAAGAAA
CGGTCAAATCGGCACAAGAAAAGTCGTACAGTATTACTAGACCATTGGGGTTGTCAAAACCAGTTT
TGTTAAATCATAAATTGTCAGACACATACTCACTGTCCAAATATATACGAGGAGTTGTTTGGTCAAA
AATCCAAAGAAAAGAAGACAGAAACAACTAGACTACGATTTGAAACACTCGCCAATTTATGAAGTCA
AGTCATTTGAGAATACAAAGGGGAAAATATTTACTCCTCCTGTTTCGTACTTTTCGACAAGACAAAT
CTTTGTATTTCCCGGATTTTATAGCGAAAACATTGGCAGGTAATCAGAGAAGTTTGTACGACTCAT
TAGACAATAGATTAAAGCATAGTCAAATTTGTTTCTTCTGTTGCTGGTGAGCAGTGATCCCGTTCGT
ACTTTAAGGTTGAAAACAAAGATTACTATTCCCAGGATTATGATACCTTTGTGGAGGAATATCCCC
ATACCCAGATACTTGATGTGAATATGCCGCAAGTTGGATCAAGGGGTTTGTGACAACTTGAGCA
CAGGAAATTTAAGAAAGACTTTGAAGCCAGCTCTGAGATACGAGAATTATTTTCATCTTGCCCGCC
ACATAATGTGACGCGAAATTAGAGAACAGTTGTACTGTGATAATCAATGTTCCGGGTATATTTATA
TTGTTGATTGATGGGGAAGATAAGATGGGCGACAAGTGGGTATGCAACTCCTGAGGATTTGAAAT
TGATGTGGAAGGTTGTGAAAGGGGTGCAAAGAGAAATGACCAAGTAA

YLR393W_homolog 376aa (SEQ ID NO 412)

MFVYWINNLCEIIQCICWRRRRQGRITFFPSYFFSLSLFFQSHCSSVKWLFCAEPCGSVNARHRV
IFGETKRILKNRGLNSTTDWLDDKMVSFIRTFATSRIEFQRYQPRFVNTIKETVKSQEKSYST
RPLGLSKPVLNLNKLSDTYSLSNIYEELFGQKSKERRQKQLDYDLKHSPIYEVKSFENTKGKIFTP
PVSYFRQDKSLYFPDFIAKTLAGNQRSLYDSLNRSLIVKLFSSVAGEQCTRSYFKVENKDYYSQD
YDTFVEEYPHTQILDVNMPOQSWIKGFVTLSTGNLRKTLKPASRYENYFILPGHIMSAREIREQLYC
DNQCSGYIYIVDSMGKIRWATSGYATPEDLKLMMWVVKGVQREMTK

YML063W_homolog 1271bp PathoSeq: 1..773, public: 774..1271; CDS:
501..1268 (SEQ ID NO 413)

CCAGTGCCTTTTGTGTTTCCACATCATACTTCACTGAAACTAAATAAGTTTGTGTTACATTTT
GAGACTTCAGGTACGACCCAGGGTTGCGACAAAGTTTAGGTAGTTTGTCTGCTGAATGTGCAACA
AAATAGGGCTGTAGCCCTAGTCATGTGATGTGAATTAACATAACAAGAAGAATTGCTGGTGCGCAA
AAAGATTATGTGATTTTATGTGCGTTGTTATCCTGCACACTAAAATTGAGCAGTGACACACACA
CATATTGGGCTGTATTTTATTTCTGTTTTTCTGCTGTTCTCTCACTGTTAAGCTCTAAGTGAATT
TGTGTGTGCTGTAATAGTGTGTGTGTTCCAAGTCCCAGCTCTCACAGATACTCACGCACGCCATA
CTACTGAAAATTTCTGACTTTCTGTATCTAAAAATTTTTTACTAGGAATTTTTTTCTTTTACGTT
TTTCACTTGTTCATATAATCACCACCTCAAGTACAACATGGCTGTGCGTAAAAACAAGAGATTGT
CCAAAGGAAAGAAAGGATTAAAAAAGAAGGTCGTTGACCCATTACCAGAAAAGATTGGTTTGACA
TCAAAGCTCCAACCACTTTGAAAACAGAAATGTTGGTAAAACCTTGATCAACAGATCTACCGGTT
TAAAGAATGCCGCTGATGGCTTGAAAGGTAGAGTTTTCGAAGTTTGTGTTGGCCGACTTACAAGGTT
CCGAAGACCACTCTTACAGAAAAATCAAATTGAGAGTTGATGAAGTTCAAGGTAAAAACTTGTGTA
CCAATTCCATGGTTTGGATTTCACTTCTGACAAATTAAGATCATTGGTCAGAAAATGGCAATCAT
TAGTTGAAGCTAATGTCACGTGTTAAAACCTCCGACGATTACGTTTTGAGAGTTTTTGCCATTGCTT
TCACCAAAAGACAACCAAAACCAATCAAGAAAACCTACTTACGCTCAATCCTCTAAATTGAGAGAAG
TCAGAAAGAAGATGATTGAAATTATGCAAAGAGAAGTTTCCAAGTGTACTTTAGCTCAATTAACCTT
CCAAATTGATTCCAGAAGTCATTGGCCGTGAAATTGAAAAATCCACCCAAACCACTTTCCCATTTAC
AAAATGTCCACATCAGAAAAGTCAAATTGTTGAAACAACCAAAATTCGACTTGGGTTTCAATTATGG
CTTTGCACGGTGAAGGTTCAACCGAAGAAAAAGGTAAGAAAGTTTCTTCTGGTTTCAAAGATGTTG
TTTTAGAATCTGTTTAA

YML063W_homolog 256aa (SEQ ID NO 414)

MAVGKNKRLSKGKKGLKKKVVDPFTRKDWFDIKAPTTFENRNVGKTLINRSTGLKNAADGLKGRVF
EVCLADLQGSSEHSYRKIKLRVDEVQGNLLTNFHLDFTSKLRSLVRKWQSLVEANVTVKTSDD
YVLRVFAIAFTKRQPNQIKKTTYAQSSKLREVRKKMIEIMQREVSNCTLAQLTSKLIPEVIGREIE
KSTQTIFPLQNVHIRKVLLKQPKFDLGSLLALHGEGSTEEKGKKVSSGFKDVVLESV

YML128C_homolog 1517bp public: 1..1499, PathoSeq: 1500..1517; CDS: 501..1514 (SEQ ID NO 415)

TGATATGGATTTTTCAAACTAAGAAACAATACCAACTACAACAACAAGAAACATAAGTGTGCT
TAATTCAATGACCTCGAGTCATATTCCACGTTTTAAGTATGAGTGTGTTTACGAAGTTGTGGATCC
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ACATTGTTTCTTTCTTCCCACAGCAACCAATTTTATTTTATTTTCTTTTGGGACTTACCCACA
GTTGCTCAATTATGTATAACAAGGGTAGAAACTCTGTGGGATTCCCTCCTTAAAAATATAGCAATC
CTTTTCTTCAACAGATTGCTATATGACCCCCCCCCCTAAGCATTCAATTGCTTTTATATATATTTA
ATAATGTATTTCTCTTGTTCAGGATAATTATCATTATTGTGACGTTTAAATTTTACATTTCTTCT
TCTTCTTCTTCTTATTTCAACATTAAAGAACATTTAATATGTATTTCCCAATCATTGTATGGTTAT
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AATTTTAAAGAAGCTAAAGTTGCATTCAATGATGCCCTGGAGAATCCAAATTAATTAGTTTGG
CTAATGAAGAAGCTAAGAAATTAGAAAAAGGTTACAAGAAAGTTACTGAAGAATTAAATAACAATT
TGAATCCTCCAGATGATTCAATTAATGATTATTTGAATTTTGATTACTTATTTGGGAAAAGAAAAG
AAAATTATTCAATTAAAGAATGGATTTTGAAGTTGGCCAGTAACCAAGTTTGCAACTTTTAA
CTCAAAATAATATCCAATATAGTGCAAAGGATACCAAAGATGATTTAATCAATAAGGTTAAAGATC
AATTTGATTCTATTTCTAAGAAAAATCATGGGTCTAGTTTTATCCTGGCAATTGGTTATATGAAT
CTTGGTCAGAAAATGATTTGAAAGATTGGTTGAAATCTTATGGCATTGAATTTAATCCTAGTTCAA
CAAAGGATCAATTGGTTGAAAAATTAAGAATTTAGTTATCAAGCCACTCATTCAATTAGAGATT
CCAAAGAATCTTTATTTGATTCAATTGGATTTATTTGATAAAACCATTTTGTATAAAAAGGTCAAA
TTGAAGATGAATTTTCCAACTTGGTCATATCTCAATTACGTGAATGGCTTTATTTACATGGAT
TTATTGACACTAAACCAGGAATTTACGTTGAAGATTTGGATAAGGAAAAATTAGTCAAGATTGCC
AAAGTTATAAGAAATGTTTGTGAGTGACATTCATACTTGGTTGGCAAACACTGAAAAGAAGTCTC
AACCTTGGATCACAAAGGGAGAACAAAAGTCTCAGAAAAAGAAGGGTAGTAATTTGATTAAATGATA
CATCTTTTGTGGTATTAATAATTGGTCCAAGGATAAATTGCGTGAATTGGGCAATCTTGACTAA

YML128C_homolog 338aa (SEQ ID NO 416)

MYFPIIVWLYVSITFVVANYGFDQWINDDLKQFLKERKVFANDALENPKLISLANEEAKKLEKGYK
KVTEELNNLNPPDDSLNDYLNFDYLFGRKENYSIKEWIFESWPVTSLOTFLTQNNIQYSAKDTK
DDLINKVKDQFDSISKKNHGSSSFYPGNWLYESWSENDLKDWLKSYGIEFNPSSTKDQLVEKLKEFS
YQATHSIRDSKESLFDLDFDKTIFDKKGQIEDEFFQTWSYSQLREWLHLHGFIIDTKPGIYVEDL
DKEKLVKIAQSYKKCLLSDIHTWLANTEKKSQPWITKGEQKSQKKKGSNLINDTFFVGINNWSKDK
LRELGNLD

YML130C_homolog 2243bp public: 1..829, PathoSeq: 830..2243; CDS: 501..2240 (SEQ ID NO 417)

ATGAGTTCATAGATGATCTGTTTCACTTTCAAAATAACGTGTCAACAAAAATAAAGTTAGAGCATAG
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AACAAATTTCCGAAAAAGAAGAAAATCGAACACATTAGAAAAAGAAACGAACAAAAGAAAAAAAT
TTCAAATTTGATGTTGCATGTATATAAAATAATATAAAAGATATATCACCAGCACAACTGATTACTT
TTTATTTATATCACCTGTCAACAACAATTTCCAAATAAATACAACCTCAGAAAAAACACTTACTAT
CTTTTCTTAGTTTGGTTTCTATAATCTTATTAACATTCTTGCCTTTCATCCTTGATTATCATATT
AGATCTTATCTTTAATTTGTTTGAATAAATAATACCAATAATCTTCCCATTAGAACTTACAACACA
ACAACAAAAAACCCATTCTAAATCACTATTCTCCATTATGAAAATTTTCAGATTATTTTCACTAC
TAATCGTACAATTTATCATAAATACCACTGTTGCAGTATCACCTGTGTCAGCAGTTTACCAAAAC
TGAGTTTCAGTCCATTTGATTACCAGAATTTTGTTCACAGATCATAACTCCCACTTGTAATACAA
CTTTCACCTACATTGATGAATTGAATAAAGATATTCGTCCCTACTTGTCCGAATTAGTCAAGACCC
TGTATTTCCGTTATTTTAAAGTCAATTTAGATAAACAATGTCGTTTGTGAATGCTCAACATTTT
GTGCTAGTGAACCTGTGCTGTTGAAATATTGGAAGATTTCAATTGGAGTCAAGTCACCAATGAAA
GTTTGAACCTTCAGGATTAGGTAAGATTTCAATTACCTGACAAATCATCAATTGATAATTCCATTG
AAACCGAAGAAGTTCAAACCTGTGAAGATTAGATTATAGTGAAATAGATGATGACCATCATTTGTG
TTTATGTCAACTTGGTAATAAACCAGAAAGATTTACTGGGTATGGTGGTAATCAAAGTTTGTGATG
TTTGAAGGCTATTTACCTGGAATAATGTTTCCCTAATACTAATCCAATGTCAGTGACAAATGATG
CCGACAATGGTGGTGAACAATGTATCGAAAAGAACTTGTTTTATCGTGTGTTAGTGGTATGCATG
CTTCAATTGCAGTACATTTATCAAGAGAATATTTGAATTTCTGAACTGGTGAATTTTATCCTAATT
TAAAGGTGTTTATGGAAGAGTAGGTATGCATAATGACAGATTATCTAATATTTATTTCAATTATG

MKIFRLFSLILVQFIINTTVAVSPVSAVLPKSSFSFDFSPEFCSQIITPTCNTTFTYIDELNKDIR
 PYLSELVKTSYFRYFKVNLDKQCRFWNAQHFCASENCAVEILEDfnwsQVtNESLKPSGLGKISLP
 DKSSIDNSIETEEVQTCEDLDYSEIDDDHHCYVYNLVNNPERFTGYGGNQSFdVWKAiYSENCfPN
 TNPMsVTNDADNGGEQCIEKNLFYRVVSGMHASIAVHLSREYLNSETGEFYPNLKVFMERVGMHND
 RLSNIYfNYALVSQAIVKLSEILPLREFIqSGYDDITPAQKQHLLANNDVESVEVYDRLLLLDDIIP
 SLEANVVFENTsNLFdNSNLrDEFrsRFRNISAImDCVGCDCRCRMWGKIQTIGYGTALKILfEDDNY
 DNHNLKFRRIEIVALINTLFDRLSKSIEINfMKEMYLQHLKDIAEGLTPQGVYDKIqNNKPGNGFA
 PFFVSPPLPQKKPDQNTNTPKNQQQKQPQETDKKRLTLEEIAHTKKEPDRDTfIEDfRLSFDEVWQALRF
 VLTSYQRFPavLSRfTLVQLNEwWNKLLGKPTVYDYQSSFDVdALQYSQVLG

TGTGAAAAAAATTTGTGGTGTGGATGTTGTTGTCGTTGTTGCGTTGTCCACAACAAAAACAAGT
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GAGTATCCCCAGCAGTATTGACTTTCCCTAAAGATTACCCATTATCACCACCTACATTAAAGTTTG
ATCCACCATTGTTACATCCAAATATTTATGCTGATGGAACCGTTTGATTTTCGATTTTACATCCTC
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AGATCTTTGTTGAGTGTATGTCTATGCTTGCAGAACCTAATCCTGAAAGTGGGGCTAATATCGATG
CTTGTAATTTATGGAGAGATAATCGTGCTGAATATGACCGACAAATTAGACAACATGTCAAGGAGT
CATTAGGATTATGA

MPRSSTAQKRLLTEYQQLSRDPPPGIIAGPVSEDNLYKWECLLEGPSDTPYANGVSPAULTFPKDY
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NPESGANIDACKLWRDNRAEYDROIROHVKESLGL

CTACACAAAGCTTCGAGAGTTTTTTTTCGTTGCAGGGGTGGGACAGGTGAGTAACGAATAAAACGT
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ACGTGATATAATCTCCTATCGCTAGTAGTAAGTTTAAATTTTTTTGATCAAAAGTACACTCATCAG
TCTATTGTCGTAGATTTTCGCATACTTGTGATAATATCTGGTGTGTACACTACTTTTTTGGTTTGTGA

TTGTA AATTACAATTTTCTATTGGTTAAAATGATAATTGTTAACAAGTCTTTTTCCTCCCGGGA
TTGAATCCGGAAACTACCATTAATTCACCTACTCTACTCACCCTTACACCCCTCACTCACTCAA
ACAATTATATCAACCCAAAAAATAATCTTCACTACACCAATAACAAAGAACCAATAGTTCAAT
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GACCTACCGTGTCCACTTTAAACAACATATGTCAAATTACAATCGACATTAGCCCTTAAAAAGATACA
CATCAACCGTACCAGCAACTTCAAATCAAGAACAAGAAATATTGGTTGCCCAACGTAAAAATAGAC
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TCACTGGTGTGCTATGGCCGGTGCCTTTTATGCTTTAACTTGTGGATTGCTGCTACTTCAATTT
TAAATATTCCATTTGATACTACTACTTTAGTATCTGCATTACCCACATTACCAACATTTGCTCAAT
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TTTGGGATTTTGGTAAAGAATTAACCATCCCTGGTGTATATAGAACTGGGTATGCTGTTTGGCTG
CTACTGCTGTCATTGGAAGTTATTTAGCTTTCTTATGGTAA

YMR118C_homolog 176aa (SEQ ID NO 422)

MISRIGLLKRPTVSTLNNYVKLQSTLALKRYTSTVPATSNQEQEILVAQRKNRPTSPHLQIYEPQL
TWIMSSFHRITGVAMAGAFYALTCGFAATSILNIPFDTTTLVSAFTTLPFTAQYGIKICAYPFVY
HIGNGIRHLVWDFGKELTIPGVYRTGYAVLAATAVIGSYLAFLW

YMR230W_homolog 1176bp public: 1..1176; exon 1: 501..551, intron
1: 552..870, exon 2: 871..1173 (SEQ ID NO 423)

AAAAGCAAGAAGAGAAGGACTCGTTGGCCAATTTCTTCGGCAATTTCAAGAAGAAAAGAGTAGCTG
TTTAGAAGCTATATATATATGTACTCGCGCTTTAATGTTTATAGCAATAATGAAATGTTTAAATAAT
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ATGGTAGTTTCTTTGATTTTGTGTTTCTATTAGATTCTGTTTCTATTAGATTCCCGCTTTTTTTT
TTTTTGCAGACATTAACCTCAGGGCTATAGCCCTAATGGCAAAACATGCACGTGTATGTTTCTTG
ATTTTTCTACACTACTAGTAAAAAATTTTCTTTCCGCTCACTATTCACACATACACTCTTTTTTCG
CACAATTACAGTCTACCAACAGGAAAAGAAAAAAGGAATCTGGTAATTGAAAAATTGAAGTT
TGGTTCTTTTAAATACATCAATCAACTAGAGTCACAGCATGTTAATTTCCAAAAGAACAGAGAAAG
AGATCCACCAATACCTCTTCCAAGGTATGTAAATATGAATTATAAACTGGAACAGAAATATGGCATT
TCAAGGGATGCACGATAAGTCAAGAGTTTCAATGAAAAAGCACAGATTATAACAGTCTGTAAGAAAA
TTTCACTACCAACAACAATAAGAAGATATCAAAGAGATTGAGTAATCACTACTTACAAGAAACATA
TAACATCATGGAGAGTTTAAATTTGAAATACGAATGAATATACAAATGAACTATACCTTTTTATGG
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ACATGTATTATAGAGGTGTGCTGTTGTCTAAGAAAGACTTCAACCAACCAAGCACGATGAAAT
GATACTAGAACTTGTTCGTATCAAAGCTTTACAATCTTTGACTTCTAAAGGTTACGTCAAGACT
CAATTCTCATGGCAATACTACTACTACCTTGACTGATGAAGGTGTTGAATTTCTTGAGAACCGAA
TTGAACATTTCCAGAAGGTATCTTGCCATTGACCAGATTGAAGAATGCTCCAGCTGAAAGACCAAGA
CCATCAAGAGGCGGTCCAAGAAGAGGTGGTTACAGAGGTAGAGCTAGAGACTAA

YMR230W_homolog 118aa (SEQ ID NO 424)

MLIPKEDRKKIHQYLFQEGVVVAKKDFNQPKHDEIDTRNLFVIKALQSLTSKGYVKTQFSWQYYYY
TLTDEGVEFLRTELNIPEGILPLTRLKNAPAEPRPSRGGPRRGYRGRARD

YNL054W_homolog 2840bp public: 1..2197/2199..2840, PathoSeq: 2198;
CDS: 501..2197 (SEQ ID NO 425)

TGTTGGGAGTATTCTGGCACAACAAATACTTACTTTTTAGGTTACTAACATTATTTTTCTTCAGCTA
ACTAATTATCTAGTTTATATCTATATCCATTATTGTTGAAATCACTATCGTGAGGTAAATAACAAC
TACAGAGTTGTACAGTATCCAAAAAACTTTGTACCTATCAATACATTTTAAAGCAATAGGTCAT
TTATTGCTGTAATCAAGTGTACCAGTATCTCTAGTTAATGTTGAGTTTATACCTAAAAACATGAAC
TATATCAACTTTAAATGCCCTAATCACGTGATACAGCACATGGGAATTTGCTGATCTTGCTTCTCT
TGACGTACACGGCACATGTACACGACTTTTTTTCTAAATATTTTTTTTTTTGTTGTTGTTT
TTAAACAATATTATTTTCATATATATAATTGCTTTAGTTTACTTGCTTCTTACACCCCTTTGCATATT
TTTTTTTTTTTCTTTTTCTGCCAATTGATCAAATTCGATGCTACATCCTAATAATTCAGTAGTCCG
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CAGTGAGGCAACAACAGTTCAAACCTTCCTTCTACCAAGGCTCCGTCAATTTCCAACCTCCATCAGCA
GTTCAAATAATATAGATTCAATACTTAAACGACCTGTACATCTACGTGAGGCATCAACGTATTCCAG
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CGAACAATATTGGTAATGAAATATACCTCAATACCAGAAAACCTAGTAGTGTGCCCCTCAATCA
ATGAAGGATACAATGATGATACATTTTCATATAATGAAGTTGAGGATAATTTAATTGATGAAGATT
CCACGGACGATGGGGATTTGACAAAAAATACCATTACTAATAACAACAATCCACCAACCACGTCGA
GCCAACAGCAACCACAACCGCAACCACAGCCGCAACCACAGCAACCACAACCTACATACTCTGTCTC
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GAAATTACAAAACCTCATCCACTTCTCTCAAATTAAGATCAACTACATCAAAACCTTTTCGATAAAAA
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TCACATCCATTGAGAACCCCATTTGTTAGTAAAGATGAGTTAGTTTTCATGTTGTTTATTGAAGCAT
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GTAATGACACCAACGATAATGACAACCTCAAGAAGTGGGAAATCATATCAAGCAATCCATTGATT
TGATTATAACTGGAGTATTGAAGTATGATTTACCATTTTCAAGAACCTCAAGATCAGTCGTGGTTA
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AG

YNL054W_homolog 779aa (SEQ ID NO 426)

MLHPNNSVVDMSSTGNMNTDAPPKQQTKKKISKQNSTKTDFFAARLASAVDDIESSDSDETFIY
ENNDTELDNANNNNNNNSTNNIINLDNASVNGSMIASSNAMVTGPPGTSIALGSLRSPSILE
GEQLQYFHDVPVRQQQFKLPSTKAPSISSNSSNNIDSILKRPVHLREASTYSVNDNDHRNLVLPN
STERFTASPSNNIGNENIPQYQKTSSVAHSINEGYNDTFSYNEVEDNLIDEDSTDDGDLTKNTIT
NNNNPPTTSSQQQPQPQPQPQPQLHTSSPLNQIQAATSATPSVSTKNASKRNYKTSSTSSKLR
STTSKLFDDKKSQPRYSTIPDDIDIEDFDELIIYDNTARFPANESTSLNQNQRIPHYRSNLN
FPQVKRQSKRYLSTGQPLESSDRGSNKDGTDNNGNSDHNINSPLTANNNNNNVNHNHGDNKKSN
NNNNIANNRAFFFPYQDQHHYYDYDDFDQESQINGPNFDLPDLINRSASRNFNNNNNPKRFGD
SHFFLPRKTDQYSQRTSFLKSCIYTFVCILIVLTIGFVLGFVLATTKDLTDVGITSIENPIVSKDE
LVFNVVIEAFNPWFVSVDINEVELDLFARSGLPDTDNSKISNMGGSQKVETVKLGTILNFESVLN
FKGGFLSREPTIQKGGIRLLYPGKNVTAEAKLVNMADIKIAASNSIAKESTTSNDTNDNDNSKKW
EIISSNPFDLIITGVLYDLFPFSRTSRSVVVRKTGYIDPTLFVIPQGENNIS

YNL075W_homolog 1352bp public: 1..136/138..1352, PathoSeq: 137;
CDS: 501..1349 (SEQ ID NO 427)

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ACCCCGGTTAGCTGTTTGAGTATTGGATAGCAACACTTTCAATTAGTGCAACACAATCAAATTACC
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TATTAATAATAAAACTTATTTATCAGCTGTTGTTAGTAGTCTCGCAAATTTGAAACCATGGATG
AGTAAACTTGTGTGTAGATGAGCTCAAATATCTGGTGGAACAATTGTGTAGTAGCTCTTTGATA
AATATCCAAGAACAGTCGTGCAAGTTTCAAATACCATCGCAAAAATCCTAACAAAAAATAAAT

MIRKQARERREYLYRKALQLQESSLTEKRQQLKAALASGKLSKELAEDEKLQRDFIYDESEQIEI
DDEYSRLSGISDPKVITTSRDPSPVKLLQFSKEIKLMFPNSLKLNRGNYYIISDLVSTCNRVQVSDM
ILLHEHRGVPSLTVSHFPHGPTAIFTLHNVKLRHDLPLNLGNVSESYPHLIFENFQSDLGKRVVKI
LQHLFFPPGVKQDSSRVITVFVNDDYISVRHHVYVKTQDSVELSEIGPRFEMRLYEIRLGLPDNKDA
DVEWOMRRFIRKTANRKNYL

TCTCTTTTGTTTTTATTTTTGTCTGTGTTACTCCAGAAATGTGCATAATAATGATAATAGTAATTTGT
GACTAATATGAGATGATCGTATGTGGGTGGGTGGGGAGGAAGGGACCCGGAATTCTAGGAACAGGA
AAAATAAAAAACGAATAAACAAAAACCCCCAATCGGCATGCATCGGAATTCCTTTAGCCCAATTAC
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TGCAGTCTATTTTATTTTCTCTTTTTTTTTTGGCTGTGGTAAACTTTTTTTTTTTTCGAGGTG
TGAAAAAAAATCATTTTACAGTTTACATTTCTCTAACCTGCAAAAAGCTCTCGTTTTTTTTGTA
GTGAGAGTTACTCGTTCACAATAGTATACTTTACAGGGGAGTTCTTTTCTTTTGAATAGTCAACC
AACAGCAAATAGCCAAGGATCAAGCTTCATCATTAAATCATGTCTCTAAGATCTTATCAGAAAACC
CAACTGAATTAGAATTA AAAAGTTGCTCAAGCTTTCGTTGATTTGGAATCTCAAGCTGATTTAAAAG
CTGAATTGAGACCATTACAATTCAAATCTATCAAAAGAAATTGATGTTAATGGAGGTA AAAAAGCTT
TAGTGTTTTTCGTCCCAACCAAGTTTACAAGCTTACAGAAAAGTTCAAACATAGATTAACTAGAG
AATTAGAAAAAAAATCCCAAGATAGACATGTTGTCTTTTTTAGCTGAAAGAAGAATCTTACAAAAC
CAGCTAGAAAAGCTAGAAAACAACAAAAAGACCAAGATCAAGAAGCTTTGACTGCTGTTTCATGATA
AAATTTTGAAGATTTAGTTTCCCAACTGAAATCATTGCTAAAAGAGTTAGATACTTGGTTGGTG
GTAACAAAATCCAAAAAGTCTGTGGATTCTAAAGATTCAACTGCTGTTGATTACAAATTGGATT
CTTCCAACAATTGTA CTCAAATTGACTGGTAAACAAGTTGTTTTTGAATCCCAGGTGAATCTC
ATTAG

MSSKILSENPTLELEKVAQAFVDLESQADLKAELRPLQFKSIKEIDVNGGKKALAVFVPPPSLQAY
RKVQTRLTRELEKKFPDRHVFLAERRILPKPARKARKQQKRPRSRTLAVHDKILEDLVFPTETI
GKRVRYLVGGNKIQKVL L DSKDSTAVDYKLDSFOOLYSKLTGKOVVFEIPGESH

TGTTTTGTTTTTGCAATCAAACATAATAGAAGACCAAAACAAATAATTTCTATTTTTTTTTTGACTCTCC
CGTAGTTTTTACACTTCTAGCCTCTCTTGTAATATACACCTAATTGACAGTACCATTAGGACCCCA
TCTTATTGTTAAGGATAATACTTCTTCTTCTTCTTCTTCTTGGTTAATCAAATTTGCAATAAATA
AAAAAAAAAAAAAAAACAAAGCCGCACAAGTTTTTCCTAAAATGACTTATTTTTGTGTAACGCATTAC
GTGATCATATAATTTTTTTAAATTCAAAACCTGAACCAAAATCTGCATATTGAGGTTGAAAAATTAAC
AGAAAAAGAAAAATTTTTTCAATCTTGTTTTGAGGAGAGAGAGGTGAAAAATTTTTTCTCTCTCTTT

CTTTCTTTCTATTCTCATATACCATAAACTTAAACAACCTCTTTTACTTTTTCTTTCTTTTCTTTT
CAAACCTCTACAACAGATCCAATTAATTAACAAAAAATGGTTAACGCTATCTTATCTAAGAAAA
AGAAATTAGTAGCTGACGGTGTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTG
AACAAGGTTATGCTGGTGTGAAGTTAGAAAACTCCATCTAAATTGGAAGTTATTGTTAAAGCTT
CTAACACTCAAGGTGTTTTAGGTGAACAAGGTAGAAGAATCCATGAATTAACCTCATTGATTGTTA
AAAGATTCAAATTATCTCCAGAAGGTATTGCCATTTATGCTGAAAGAGTTGAAGAAAGAGGTTTAT
CTGCTGCTGTTCAAGCTGAAGCTTTGAAAGCCAAATTATTGTCTGGTTTACCAATTAGAAGAGCTG
CTTATGGTGTTTTAAGATTTGCTATGGGTGCCGGTGCTAAAGGTGTTGAAGTTGTTATCTCTGGTA
AATTAAGAGCTGCTAGAGCTAAATCTCAAAAATATGCTGATGGTTTATGATTCACTCTGGTCAAC
CAACTAGAGATTTTATTGATATTGCCATTAGACATGTTTAAATGAGACAAGGTGTTTGGGTATCA
AAGTTAAATTATGAAAGATCCAGCTGCTAATAGATTTGGTCCAAGAGCTTTACCAGATGCTGTTA
AAATTGCTGAAGCTAAAGATGAAGATGAAGTTATTCCAGCTCCAAGCTGTTAAATCTTATAAACAAA
CTGCTGAAGATGAAACTGAACTGATGCTCCAGTTGAAGCTGAAGCTGAAGTTGAAGCTACTGCTT
AA

YNL178W_homolog 251aa (SEQ ID NO 432)

MVNAILSKKKLVADGVFYAELNEFFTRELAEQGYAGVEVRKTPSKLEIVIVKASNTQGVLEQGRR
IHELTSLIVKRFKLSPEGIAIYAERVEERGLSAVQAEALKAKLLSGLPIRRAAYGVLRFAMGAGA
KGVEVVISGKLRAARAKSQKYADGFMIHSGQPTRDFIDIAIRHVLMRQVGLIKVKIMKDPANRF
GPRALPDAVKIAEAKDEDEVIPAPTVKSYKQTAEDDETETDAPVEAEAEVEATA

YNL182C_homolog 2105bp public: 1..728, PathoSeq: 729..2105; CDS:
501..2102 (SEQ ID NO 433)

AAACTTTCTGATTGAATAAAGTGAACCTCAATCACATTCTTCGGCATATATCAAACCATTATTAGT
TTTATCACGTAAATCTTCAATATACTCAGCCACCCATTGATCATTGGTCTTCTTAGTAAGTAATAT
TAGTTGTGCTCCTCGTTGTCCCAATTCATATGCTATTTGAGCTCCAATACCAGTGGTCCCACAGT
AATCATAAACACTTTCCCATGCATGTCTCGCTCCCACGTATTGGTGGCACCATTGAAATAAATCTT
GGCTCCAGCAAGAGTTAATAGAATGGGAAGAACGGTAGGTCCATATTCTTTAATTTGGTCCCAATA
TGGAATCACCTCTGGCCCATCAAACACAACACTAGTTAAAAAATTCAGTGGCATAATTGGTATATC
AAGAGTGAAGAAAAATGCTGTATTGGAGGTTGGAATTTGTTTCAAAATTGGTTGCCTTTTTATTCT
TCTTGTCTTTTTTTTTTTCAGTGCTAACATAATTTGGGATGTATGTATTGAAAAAATAAATTTTG
TACAATTTCTTGTTCTTGTTCTCCCACTCATCTCATCGCTCTCTTATAAATTCACAAACATGGATG
AAGTAGTATTTTACATAGCTCAAGGTGATCCAGCTGATAAACACAGTCAAGAATCATATGGATATG
TTACATCAATCCATTCTTCCAAACAATATGCATCTTATCGACAAGCAGACTCGCATATAAACGGTA
CTGCCATAACTGGTATTGGCCCAGGAGAAAGAATTTTCACTGCTGTTCTTAACAAGGCATTAATCA
ATGTATATTTCATGGGGAAAAGAAAGTGTGATCAACGTATACCGATACCAGAAGCATTGACTTGTA
TCACGTTGATAAACCATCCAAATGGCAGTAACAACAACAGCGACAATGATGACAACAGGTTATACA
AATTACCAAATTACCGAGTTCCTTGGTTGTTAGCAGGTGGATCAAAGAGTGGGAAATTGTACATTT
GGGAATTAAGTTTCAAGCAATTTATTATGTGTGAGAGACGCCATTATCAGGGGATCACTACCATCA
AGGGTTCAAGCTGTGGAACATTTTAAATTACTGGAGGAGAGGATGCCAGATGTCTTGATGGAATT
TAGCAGAATTAATTAGTATTTATGACAAATCAGACCATCAAGTGAACCATATTGGCAAATCACTG
ATAACACATTACCACTCACTGATCTTTGTTTAAATGATACTCATAACATTAATGATCTAAAATTAT
ATACAACCTTCAGAAGACAGCACGGTCAGGATTTATGATATAGTCACAAAGAGTTTGTAAACCAT
TTATTTTACCCAGTTCGGCTGAATGTATCACCAGGATCCAGCTAATAGAGCGTTATATGTCGGGT
TGAATAACGGTCTTGTAAGATCAATTCCTTTATATTCTATAAATAGCCATACATCAGTGTGGAAA
GTATTGGCGGCATGAATAAGATAATCACGGTTGATGCTGATCAAAATTTAAAGAGACATTTGTTG
CACATCAACAAAAGACGAAAACAGGAGACGATAAGCCTGTTGTTGTTACGAAATTGACAATTTCTT
TTGATGGTACAAGTATAATATCTGGTGATTCTGAAGGCAGAGTGTGTTGTCTGACATTGTAACGA
AACAAGTTGTGAAATCATTCACACCTTGTAACCTCTCCAATAGCTTATATTGCTGTTGAAACTATCC
CTGATGACTTTGTCAATAACTTAGCTACTAGTACTACCACTAATAAAGCTGACAAGAAACATAGAA
TGATACCTCAATTTAAACGAGTACTAGCAAGCACCAATTTCTGAAGAACATCAGATATTCTTGGACA
TTCTTGGTAAAACACCGCAACCACCAACGCAACCGGCAATATTGACTTTGCAACTTGGTTACAAG
GCAACAATCTGAAGAATTACAATTCAAAAACCTTTCTGGAATAAACTCTATTGTCAAACAAGTTG
GCAACGAGAATGTATCGGATCTCGAAGAGAGATTACAAAGAGTTTCTCAAGCATACACTGAATTA
GAAACAAACATGAAGAATTAATTAAAGAACATGCCAAATTATTAGATAAATTAGAATAG

YNL182C_homolog 534aa (SEQ ID NO 434)

MYVLKKKNFVQFLVLVPLISSLSYKFTNMDEVVFYIAQGD PADKHSQESYGYVTSIHSSKQYASY
RQADSHINGTAITGIGPGERIFTAVPNKALINVYSWGKESVDQRIPIPEALTCITLINHPNGSNNN
SDNDDNQLYKLPNYRVPWLLAGGSKSGKLYIWELSSGNLLCVRDAHYQGITTIGKSSCGTFLITGG
EDARCLVWNLAELISYDKSDHQVKPYWQITDNTLPLTDLCLNDTHNINDLKLYTTSEDSTVRIYD
IVTKSLLTFFILPSSAECITKDPANRALYVGLNNGLVRSIPLYSINSHTSVLESIGGMNKIITVDA
DQNLKETFVAHQKTKTGDDKPVVVTKLTISFDGTSIISGDSEGRVVFVSDIVTKQVVKSFPCNSP
IAYIAVETIPDDFVNMLATSTTTNKADKKHRMIPQFKRVLASTNSEEHQIFLDIPGKTTATTNATG
NIDFATWLQGGKQSEELQFKNLSGINSIVKQVGNENVSDLEERLQRVSQAYTEL RNKHEELIKEHAK
LLDKLE

YNL190W_homolog 896bp public: 1..896; CDS: 501..893 (SEQ ID NO 435)

TTTCTGCAAGTATTGCGTGTGCTGCACAACTTTTTATATCCGAAAATTTTGGCCGGGAACGAAA
CGGCAAGAAAAAACAGAAACAATACCACCAGCACGGACAAAAAGATTATAAGCTTTGTGTAATAAG
GTTATGTCATCGGGTATTACAGATTGCAGGGCCATCTTGTCTTCATCAGTTATAGCATTTCATAATA
AAATAAGCCACATATGTGTACAGCGCTGAGTCTACTCAACATGTGTAAATAGAATAAATCAATTGA
CACAGTCTTTTGAGATCTGTTATTCTGGCCTATAGCGTTTTAGGAAATTGCGGTATTTCTTGTCT
GTTTTCTTTTATCTATTTTCGCACGACTTGGGGTGGTTTGTGTGACTTTTTTAGCAAATTAATTT
TGTCGGTCTTCGCAGTAAAAATAAAAAATTCAAAAAACAATGACTTTTTTTTTTACTTT
CTTTCTTTTCTATCAACAATACTAATCACAAGCCAACCATGAAATTCACTACTGTTGCCACTGTTT
TTGCTATTTCTCATTAGCTGCCGCTAAAGGTGGTGAAAAAGATCACGGTAAAGCTTCTACTGTCA
CCAAATATGTCACTGAACTACCCACAGATACGGTCTGTTTTGACAAAACAGTAGATCTAAAAAGC
CAAAGGAACTGGTACTCACAGATACGGTAAATTCACAAGACTCCACGTCCAGTTACCACAACCTG
TCTTGGTCAAAGAAAGCGACCTTCCAAAGAAAAGAGATGCTGTTGTTGCTAGAGATTCTAAAAACG
CTTCTTCCAACCTTACCACCTCTAGTGGTAACAATGGTGTGCCACTGGTGTGAGCTTGGGTCTTG
CTGGTGTCTTAGCTGTTGGTGCTGCTTTGGTCATCTAA

YNL190W_homolog 131aa (SEQ ID NO 436)

MKFTTVATVFAISSLAAAKGGEKDHGKASTVTKYVTETTHRYGRFDKTSRSKKPKETGTHRYGKFN
KTPRPVTTTTLVKESDLPKKRDAVVARDSSKNASSNSTTSSGNNGVATGVSLLGLAGVLAVGAALVI

YNL208W_homolog 1076bp PathoSeq: 1..1076; CDS: 501..1073 (SEQ ID NO 437)

TTTTTGATCAGGCCTTTTGTGTTTTTTTTTGGGTGGTGCTGTGGTTCGTTGGGTAGTTGGCTCTTG
TTTCGGTCTACTTGTTCCTTTTTTTTATTCTCCTCGTTAATCCTAATTTGTGTAACAAATTAAT
TATAGGGAGTTGGAAATTAAGCTTGAAAAGAAAGAAAGAAATACCAACGTGGAATTTCT
ATTACGTAAGTCACTATAACTTGCATAGAAATTTACGGTTTTCAATTTAAGAAAGTATTAATCAAC
TGAATTAAGCAATTGAAACGAATTGAACCAGCTCAGCATTATTTTTTCGTTTTCTTTTTTTTCAA
GGGGGTGGGTGAAAGAAAAATCTAAAAATATATAATACTCCACTTATCTCCTCTCTCTCTCTT
TCTCTCTCTAACTCAATTTCAATTTTTCCCAAACCAAATTTCTTTCTTTCTTTCTTTCTTTATT
TTTTACTCAATTGAATCAATATTAACAATAAAAGCCATGTCAGCTAACGATTTTTATTTCATCTG
GTGATCAATCCAATTATGATCCAAAAGATCCTCGAATCAAGGATCATCATCAATGATGAAC
AACAAGACAGAGGGTTATTATCTACTGTGCGCGGTGGTGTGCTGGTGGTTATGGTGGTCACAAAT
TAGGTGAAAAGGCACAACATGGTACTTTGGGTACTGTATTAGGTGCCATTGGGGGTGCCATTGGTG
CCAATAAACTAGAAGATGCTTATGAAGACCGTAAAGAACATAAAAAACACGAGCAACAATATGGTG
GTAGTGGTAAACACGAAGCGGAAGACATGAAGGTGGTTTTGGTGGTGGTAGACCAGATGATCGTT
ATGAAGCGGATAGAAGAAATGATAATTACGGTGGTGGTTACAATGATAGAAGAGATGACGGTTATG
GTGGTGGTTACGGTGGTGGCAGACCAGACGATAGAAGACACGAAGGTGGTTTCGGCGGTGGCAGAC
CAGATGACCGTTTTTGGTGGCGGTAGACCAGATGACCGTTTTTGGAGGTGACAGAAGAGATGATAGAA
GAGATGACCGTAGATGGTAA

YNL208W_homolog 191aa (SEQ ID NO 438)

MSANDFYSSGDQSNYDPKRSSNQSSSSNDEQQDRGLLSTVAGGVAGGYGGHKLGEKAQHGLTGLTV
LGAIGGAIGANKLEDAYEDRKEHKKHEQYGGSGKHEGGRHEGGFGGGRPDDRYEGDRRNDNYGGG
YNDRRDDGYGGGYGGGRPDDRRHEGGFGGGRPDDRFGGGRPDDRFGGDRRDDRRDDRRW

YOL031C_homolog 1745bp public: 1..1342, PathoSeq: 1343..1745; CDS: 501..1742 (SEQ ID NO 439)

TTGGTATTGAAGACACCGAAGACTTGTTGAAAGATATTGAACAAGCTTTACAAAAGGCTGCTTCTG
TTTGAGGGGATGTTTCATTAGCAATGTATATAATTATTGTATATTATGACAAAAGAAAGAAAAAGAA
AACCAGAAAAGTGGTTTATACAGGAATATTTTAATAGAAATATCGCTTATATTGTGATAAAAAATT
TGAAAGACAATCCGAATGTAGTGCTTGTCTTATTCTGCTTGGGAATACTGTAGTATTAGCATCAAT
TGAGGAAATTCCAGATAGCTAACGGTTTTCGCGATTACGAATTCGCAACCAAATAAATATGTGACA
AGGAATACACTACTGATCAAGGTTATTCTTAGTACAATGGAAAAAAGGAAGCAAAACAAAA
AAACGAGAAATTAATGAACACGACTTCACCTTCTACAACCTACTGGGAAAAAAGGCAGAGAGTTA
TTGAAAAAGGATCATATCAAGTTCTTATTGTATATTATATGAAGTTTTCTGTTTTAGTATTACTTG
CCAGTTACTTAGTTGGTGTGAATTCTCTGATTGTTGATACTTCAGAGGAATTAATTTGTCCAGATC
CAGAAAACCCCTTTAGATTGTTATCCAAAATTGTTTGTTCACAAACGAGTGGCAAACCATTAAC
CAGGTCAAGATATACCACCTGGGTACACGTTAGATTAAATATAGATACGTTGGAAAAAGAGGCCA
AGCTAATGAGTGCTGACGAAAAAGACGAGCCAGTTCAAGAAGTAGTTGTTGGTGGCGAATTGCAGG
ATCAATTCGAGGGAAGCCATCACTGAGAATCTACAAAAGTTGCATGAGCTGAAACCTCTGAAGTAA
AACAGGAGCAGCTCATCGTACAAAAGTTAGCAGGGAGATTGAGTAATTTTGACGCAAGTTTGTCT
TGGAAATTGAGAGTTTCAAGCCACATGAGAGTGATGTGGAAGGTTGCATTTGGCACTAGATACTT
TAGAGGAATTAAGTCATGATATCGAATTTGGGGTGAAATTGACCTCAGACAAAGCCATATTTTCAGA
GTTTTGTCAACATTGCCAATGGTGCTTCTGATCCAAAAATAACCGAAAAGGTATATCGTGTAATGG
GGTCTAGTTTGAGAAATAATCCTGAAGCGATTAGTAATATCTTGACCAACTTCGACAAGAGCTATG
TGGATAATTTGTTTGAGCAATTAGCGAATGAAAATGATGTTCTACAAAAGAGGATTTTGGGTATAA
TTCAAGCTTTAGTCCAAAATAGCCATTTTGCAAGACAATATTTTTTCATTTGACCACAGTTCCGGGT
TAAATGATTTAATAGCGATTTTCCCAAACCTTGGTCCAACTCAAAGTCCAGGGCAAGTAACATTT
TAGAGGATTTACAATTGTTCCAGTAACAAACGATAGAAGATCACTTGAAGATCAAGATCCTGAAT
CACAGGTTTCAAATTTATTTCAGAAATTCCTTTGTTGGAAATAAACTTGACGAGAAGAATTTCAAGT
CTTATTTTGATCAACTAGTAAATTTGCATCAGCTGAATAAGAGTTTGGCGACCAAGTGGTGACTTTC
TCAATTGGTTAGCTGAAGAAGTGGAGTCGCGTAAAGAGAATAAAAAAAGAGACGATTATTCACAAG
AAGACAAAGACTTTGATGAGTACATGTTGCGAGCACGTCATGAAGTATTTGGCAATCCAATGGGAT
TAAGAAAGGCAATTGCCGACGAGTTGTAG

YOL031C_homolog 414aa (SEQ ID NO 440)

MKFSVLVLLASYLVGVNSSIIVDTSEELICPDNPENPLDCYPKLFVPTNEWQTIKPGQDIPPLHVRL
NIDTLEKEAKLMSADEKDEPVQEVVVGELQDHSREAITENLQKLHESKHPEVKQEHARTKVSQG
DLSNFDAACSEIESFKPHESDVERLHLALDTLEELSHDIEFGVKLTSDKAIFQS FVNIANGASDPK
ITEKVYRVMGSSLRNNPEAISNILTDFDKSYVDNLFQLANENDVLQKRILGIIQALVQNSHFARQ
YFSFDHSSGLNDLIAIFPKLGPNSKSRASNILEDLQLFPVTNDRSLEDQDPESQVSKFIQNSFVG
NKLDEKNFKSYFDQLVNLHQSNKSLRPSGDFLNWLAEVEESRKENKKRDDYSQEDKDFDEYMLRAR
HEVFGNPMGLRKAIADDEL

YOL048C_homolog 1244bp PathoSeq: 1..27/985..993, public: 28..984/994..1244; CDS: 501..1241 (SEQ ID NO 441)

ATGATTTTTTCTTGGATTTTAGAGCTGTTAATTATACCTTTTTTGTTCCTCAAATAAGCGCTAAAAA
TGATTGAAATTAATAATACTAACTATTCAGGTCAAAGTAAACACTATAAAACAATATATTTCAAT
AACAGGAGCAGTAATTAGCTTCAACATCAAGTACTCTTTTATTTTCTACCAAAAACACATCTGA
AGTAGCTCTTATCCATAGATCCAAATATTTTAACCTTTTTTTTTTCTACTCTCATCTACTTTTTT
TTGCAACACTTACTGCTCACAACGCCAATGACCATAACCATTAATTTCAATAATCAAATCAAGAGCT
TATTTGTATCCTCTCAAGGTATGTTAATGTATTAAACAACACCGATTCTATTTACCAACTAACACG
ACAGAAAGGGGTTGTACTATTTTGTAACACATCCCACGTTTGGCCCTTTTACATAACCATATTGA
TACCTCAATTGGTCCTTACACTAGTCATTTACCTGATTATGTTTTCATTTCTTCCACCTCAAG
CTATTGTATATACATTGTTAATGGGACCATTAGGGGTGATTGGTGGTGGTATAGTTTGATCCTGC
AAGCGGACATTTGTCTATATTTGTTGTCACAATATCTTAATGCCTCACATACAACGAGTGGCAT
ATGATGCAATATTGAGTAGAGAGTGTGCAATGATGTGGTACTAATGGGAAAACCTTAGGAGGTATA
GAAAACCTACCCATTAGAGTAAGGGCCAGAGAATACCTTAAGGCCATTCCAGATTTTTCGATCTTTC
CCTTCTCTTTGCTCAAGCTACTTGTGTTTTTCGGTATTTACTTCATACCCTTTGTAGGTCCAATCA

TTGTATTGTTTTTCCAATCTTCCAAGCGTGGACTAAAGGCACATGCAAGATACTTTAAGTTGAAAG
GGTTTTCTGCGTAGTGACATAAGAACAATCCACAAGCTAAACAGACCAGCATATATGGGGTACGGAG
TGGTTGCGCTTTGGCTCGAGCTGTTTCCATTTATCAATATGTTTTTATGTTTACCATACTTTGG
GAGCTGCTTTGTGGGCAGTTGATATTGAACAACAAGAGAAGGCCGTCACAGAGAATGTGGCCGAG
CTACTACCACCGCCACAGATACGAATAGCGTCAATCAACAAGGTCTAGTTATACCCGTACACAATG
AACCAGCAACTAATATACCTGAGGCTACCCCAAAAACCTGCTACAAATACCATCTAA

YOL048C_homolog 247aa (SEQ ID NO 442)

MFSLFPPQAIIVYTLMLGVLGVIGAWYSLISQASTLSIFVVTISLMPHIQVRVAYDAILSRECANDV
VLMGKLRRYRKLPIRVRRAREYLKAI PDFSIFPFSLKLLVFFGIYFI PFVGP IIVLFFQSSKRGLK
AHARYFKLKGFSRSDIRTIHKLNRPAYMGYGVVALWLESFPFINMFMFTNTLGAALWAVDIEQQE
KAVTENVA AATTTATDTNSVNQQGLVIPVHNEPATNIPEATPKTATNTI

YOR027W_homolog 2270bp PathoSeq: 1..947/1781..1828, public:

948..1780/1829..2270; CDS: 501..2267 (SEQ ID NO 443)

GCATTTTACTTATTTAGATATTACTTCATATTGCTTTTATTTAGATTGATTTTGTTTAACAGTGAA
AGTTTTTATTTTTTTTTTGTTTAAAGTTTTTATTTTTTTTTTGTTTAAAGTTTTTGTATTATACAA
TATTTAAATTATAGTAATCATCCTATAAATTTCAAAGTCAAAGACAGATCTTAAGGTCTAATTAA
TAACCTCTCTATGGCCTTCTGTGTCAAATTTGTTGTCGTTTGATAACAAGTTTGGAACGGTAATGGTT
GAAATTAGAAAAGAAAAAATTACACATGGTAGCAGCTGATGTATAGAAC'TTC'TAGCAAAAAAAA
AAAGAAAGAATTTTTTTTCTTCCATTTTTCAAATTTGAGAGATCGAAATAATTTTCTTGAATTTA
TTAAAAGGGGAACCCCTTCCCGAAAAATCCAAAACCAAACCTTCCACCCAAATATCAAATAACTAAC
TTATCATTTCCAACAGATAATATTTCCCACTTCAATAACAATGACAACAGCTGACGAATACAAAGCAG
AAGGTAACAAATATTTTGTGCTAAAGATTTTGAAGAGGCGATTGAAGCATTCACTAAAGCAATTG
AAGCATCACCTGAACCAAACCATGTTCTTTATTCAAATCGTTCTGGATCTTATGCCTCTTTAAAG
ATTTTAACAACGCATTTAAAGATGCTCAAGAATGTGTCAAGATCAATCCTAGTTGGGCCAAAGGGT
ATAATAGAAATTGCTGGGGCTGAATTTGGTTTAGGTAATTTTGATCAAGCCAAATCCAATTATGAAA
AATGTTTGGAGTTGGATCCAAATAATGCCATGGCTAAAGAAGGTTTAAATCAGTTGAATCTGCTT
TATCATCTGGTGGTGGTGTGACAAGGATTTAGGATTTGGTAAATTTTAAATGATCCTAATCTTT
ATACTAAATTGAAAAATAATCCTAAACAAGTGAATTTATGAATGATCCTCAATTTGTTGCTAAAC
TTGAACGTCTTAAACTAATCCACAATTGGGTAATCCTGATATGTTTAGTGATCCAAGATTATTGA
CGGCTTTTGTGCTGCTTTAATGGGTATTGACATGGATTTACCAAATATGGGATTCACTGCTCCAAACG
AATCACAATCCAATGCATCAGAACCAAACCTGGAACCAAATCAGTACCAGAATCTAAACAGAAC
CAAAAGCAGAACAAAGGAAGAAGAATCAACCTCAGGCCAAAGATGAAGACACTCCAATGACTGATG
CCCAAGACGACACTAATGATAATGATGCCAAAACCCAAGCTGACAATGCTAAAGCTGAAGGTAATG
CCTTATACAAGAAACGTCAATTTGATGAAGCAATTGCCGCCTATAATAAGGCTTGGGAATTACATA
AGGATATCACTTATTTAAACAATCGTGCTGCTGCCGAATATGAAAAGGTGATTATGATGCTGCTA
TTGCTACATGTGAAAAGGCCATTGATGAAGGTAGAGACATGAGAGCTGATTATAAATTGATTGCTA
AATCATTTGCTAGATTAGGTAATATTTATTTGAAAAAAGATGAATTACCCGAAGCAGTGAAAAATT
TTGAAAAATCTTTAACTGAACATCGTACCCCTGATGTTTTAAATAAATTAAGATCAACTCAACGTG
AAATTTAAACTAGAGAATTAAATGCTTATATAGATCCAGAAAAGGCTGAAGAAGCAAGATTACAAG
GTAAAGAATATTTACCAAAGGAGATTGGCCAAATGCCGTTAAGGCTTATACTGAAATGATTAAAA
GAGCACCAGAAGATGCTAGAGGATATTCTAATCGTGCTGCTGCATTGGCAAAATTGTTATCATTTT
CTGATGCTATACAAGATTGTAATAAAGCCATTGAAAAAGATCCAAATTTCACTAGAGCTTATATTA
GAAAAGCTAATGCTCAATTGGCAATGAAAGAATATAGTCATGTGATGGATACTTTAACCGAGGCAA
GAACTAAAGATGTTGAATTGGGTGGTAAATCAATTCATGAAATTGATGAATTAATGAATAAAGCTA
CTTATCAAAGATTTCAAGCCATTGAAGGTGAAACTCCTGAACAACTATGGAAGAGTTTCTAAAG
ATCCAGAAATTGTTCAAATTTTACAAGATCCAGTAATGCAAGGAATTTTAGCTCAAGCTAGAGAAA
ATCCTGCTGCTTTACAAGATCATATGAAAAATCCTGAAGTTTATAAAAAAATTAATATGTTGATTG
CTGCTGGTGTATTTCGTACCAGATAA

YOR027W_homolog 589aa (SEQ ID NO 444)

MTTAD EYKAEGNKYFAAKDFEKAIEAFTKAIEASPEPNHVLVYSNRSGSYASLKDFNNALKDAQECV
KINPSWAKGYNRIAGAEFGLGNFDQAKSNYEKCLELDPNNAMAKEGLKSVESALSSGGGDDKDLGF
GKILNDPNLYTKLKNNPKTSEFMNDPQFVAKLERLKTNPQLGNPDMFSDPRLLTAFALMGIDMDL
PNMGFTAPNESQSNASEPKSEPKSVPEKPEPKAEQKEEESTSAKDEDTPMTDAQDDTNDNDAKTQ

ADNAKAEGNALYKKRQFDEAIAAYNKAWELHKDITYLNNRAAAEYEKGDYDAAIATCEKAIDEGRD
MRADYKLIAKSFARLGNIYLLKKDELPEAVKNFEKSLTEHRTPDVLNKLIRSTQREIKTRELNAYIDP
EKAEEARLQGKEYFTKGDWPNVAVKAYTEMIKRAPEDARGYSNRAAALAKLLSFPDAIQDCNKAIEK
DPNFIRAYIRKANAQLAMKEYSHVMDTLTEARTKDVELGGKSIHEIDELMNKATYQRFQAIEGETP
EQTMERVSKDPEIVQILQDPVMQGILAQARENPAALQDHMKNPEVYKKINMLIAAGVIRTR

TCTCGATGATGCAAGTTCTTCACCGTCATCTTCATTAAACTCTGATGGGGGGCTTAAGTTTTTCAG
GAGACGTTCTCTGTGGCATCTACACCATCAACACACGCGTCAACACCTCGAGTGATTTTGAACAA
AAACCCCAATAGGAGAAAAGTACCCATTGAAGAAATATCTGAAGTTCGATTGCGTCGGGTACCTT
TTCTGTTGATAAACTCGAGCAGATCCGCAACAGCAGATTCTTCAAGAAGACCTAAACGAGGTAA
TGTTTTTAATTCACAGGACATCAATGCACCACCTCCAAGACTATGTCTTGGGATTTTCAGTTAATGA
ACCAAATAATAAGATGACGGTAAATCACACAACCATTCCAAATATAGTGATCATGAAATTCGATT
AGCTGAAGATGCTCAACGCCGAGCAATTATTGAAGCAGAAAAACATGCTCAAGAAGCTCATCGACA
AGCCAAAAAGATTGCTCAAGAAGTTTCTGGGTATAGATCACATAGATTTCATATCCATTAAAGAAGG
TGGTAGTGTGGTAATTCTAACACCAACGGCAACGACAATGACGAAGATGATGATGAGGTTGAAGA
AGCAGTTGATAAGAAATTGGCAAATGATGTTTCTGTGGATGGACCGTTGCATGTCCACGAACAACA
TTTCGAAGAAGAAATTGAAAGCAAAACAGGTGAAAAGACCATTTCATTGGAAACAATCTATACAAG
ATGTTGTCAATTTACGAGAAATTTTACCAATCCCAGCAACATTGAAACAATTGAAAAATAAGACAGC
ACCGTTGGAAGTGTTAAAGATGCTCAACCCAAAACCAACTTTAATTGATGTGTTATCTTTTTTCAGA
TTTTATTGCCATTACACCTATTAAACCGGTCATTTTGTATAACGTGACTATGACAACAGAGATGTT
GAAAAACTTTCTTGGATCGTTGACATATAATAAACAATTGGAAAAAGTTATCGTTGAGAAATGTTTC
CATTGATGAGTTGGGATGGAAGTATTTGTGTGAATTTTTGGCAACAAATAAAACAGTTAAGAAATT
GGATATATCACAACAACGTATCAAGCCAGATACCCAGACACAAGCATTTCGTGGTAATATGAACTG
GGACTTATTTATTCGATCATTAATTTTGCCTGGTGAATAGAAGAATTGGTTATCAATGGATGTAA
ACTATCCGATGCAATATTTGAAAAGTTCATCAATCAAGCGGTTAAGAAGTCAACCTATCGATTAGG
TATTGCTGGTATTGATTTGAATGTTAAAAAATCAGAAATGGTCACATCGTGGTTAACTGATGGTAA
TTCTCAATGTGTTGGTGTGATATTGCTTTTAATGATTTGAGCAAGGGACAATTACGTCCATTCAAT
TAATGCGTTTAACTGCGCAAAGTCAACAATTTAGTGTTTTTTTTCATTGAATTCACCAATTTACT
GAACATTGAAGAACTTCTGACTTGATCAAGTCATTAATTAATGTTAAAACATTACGATTTTTAGA
TTTAAGTTCCATACCTAATATCTTCCCGAAAATAATTACCCATTTGGACAAATACTTGCCAGATA
TCCTAATCTTGAAGAATACATTTTGATCTTAATGAATTAACCGCACAAAGCTATTGGGTCATTGGC
GGGGTGTTTACTGAAAATGCCCCAATTAGTTCATGTCTCGTTATTGGGTAATAGAAATTTGTCAAC
TACGTGAGCAGTACATTATACGGAGCAGTTAAACAATCCAAGACCTTGTTTGCTCTTGATTTGGA
CTACGATTTAATACCTGATCAATTATCACAACGTATTGCCTTTTATTTGATGAGAACTTGGAATA
CACTTTGAAGCCATCTCATGGCGGCAATATTGAAAGCAATCCAGAAAAACCAGAGGATTTGATGTA
TGATGGATCGTTATTAATGGAAACAGCTGAAAAATTATTAGTTGAAATAGAAAAGGGTAAGAAAGA
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TATTACAAAACCATTTGATACATTATTGCAACAAGAAATTTAGGTAAATTATCATTTGAAGGTA
AGAGAATTTAGTTTCGATTTTGTTTATTAGATTTCGCTTTTAGAAAAATTGGTTGTTGATTTGGA
ACATGCCAACGGATTATTATTAACACCAACGACCTCCACGGACGATCTCAGAAGTAGAGCCATGTC
GCCATCGGTCACTGTTGATACAATCCATGAAAGTGCAATGAGTTGATTACTGCTGGACCAATTTT
ATCACCACATGTCAATAGGAAAGCAGAACAAAGCTCGTATTTCCAGTGTTTGCCAATAATGATAA
TTTGACCCCTCATCAAGTTGTCTGTTGAGTCAAATGATGAAGGTAGAGATGTTCCAATAGATAAAAT
GACAGGACGACAGTTTGGATTTCGATCAATTAGTCAAACCTTCTGTGCATGCAAAAGAGCAAGAAAT
TGAAGAAGGGGAGCTTCATAAATTTGGATTCTTTATTCAACAAAAAGAGAGACAAAAACAACA
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ACCAGAGTTGAGAGATGCTATAATGGCAGCTAAGGGAGTAGCAATGTTACTGAATTAATGATCG
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AAATTCTGACAAAGTAGTTGAGGATGAAGTTGAAGTTTCTGATAATGCCTCTATTGATCTACTAA
TGGTGACGATTTACATCAACTTGGTGACGGTAAACATAATGGTAATGGTACGGTTGATCCCATGTT
TAGTGAAGTTTATGACAAGTTGTTAAATGATGCTGAACGAGTCAGACTGAATAGAGATATATAA

YPL137C_homolog 1364aa (SEQ ID NO 452)

MTSNSPPLGSTINDQRLPQSGVSSIPTNKLPLPNANEDFATGVSNGDVDWLFGRKSKKLGGKMMANN
NANKDERKNSHGNIKNSEKTTAKPNETKHESNGEKLEFNVPKSVMPKHTSSGNPKAPTNGQISNV
TPSQPSPKQTTSGSTNANDIPPISPKQPEKASKLNKLKIGRSRSSASTVVPSSSTTASTTTNPGDP
KSQPKRRSSSFNFVTPSLTSDLAYDDPALVSQLSNNSNSNSSSPNVRSNSKKGGLFSSLSKFR
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PAGSGIPIKRKPSISGNSIFKDSFLDDASSPSSSLNSDGLKFFRRRSSVASTPSTHASTPRVIL
NKNPNRRKVPIEIEISEVRLRRVTFSVDKLEHDPQQQIPSRPKRGNVLIPODINAPPRLCLGISV

NEPNNKDDGKSHNHSKYSDHEIALAEDAQRRAIIEAEKHAQEAHRQAKKIAQEVSGYRSHRFISIK
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TRCCHLREILPIPATLKQLKNKTAPLEV LKMLNPKPTLIDVLSFSDFIAITPINTVIFDNVTMTTE
MLKNFLGSLTYNKQLEKLSLRNVSIDELGWKYLCEFLATNKT VKKLDISQORIKPDT'PDTSIRGNM
NWDLFIRSLILRGGIEELVINGCKLSDAIFEKFINQAVKKSTYRLGIAGIDLNVKKSEMVTSWLTD

YGR183C_homolog 65 aa (SEQ ID NO 480)

MLTVLGRLLERNISIYVATIFGGAFQFFDVAVNKWWEEHNKAKLWKNVKGKFLEGEGEEDDE*

YDR529C_homolog 457 bp Pathoseq: 1..457, CDS: 1..457 (SEQ ID NO 481)

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GAAAAGGAAGCTTTTGAAGAAAGCTGTATTGGGGAATATTGACGCTAGTGCGATTGTAATTAATACG
ACGAATAAGAAACGGACGAGGAAGAGGAAGAAGATGAGAAGGTCAAACATTGAAATATGAA

YDR529C_homolog 151 aa (SEQ ID NO 482)

MVQSMTSVVKAANFILARPTLSKIITPLAQKFTAYAGYREMGLKFNDLLEETPIMQTAIKRLPSE
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TNKKRTRKRKKMRRSNIEI

YBL003C_YDR225W_homolog 399 bp public: 1..399, CDS: 1..399 (SEQ ID NO 483)

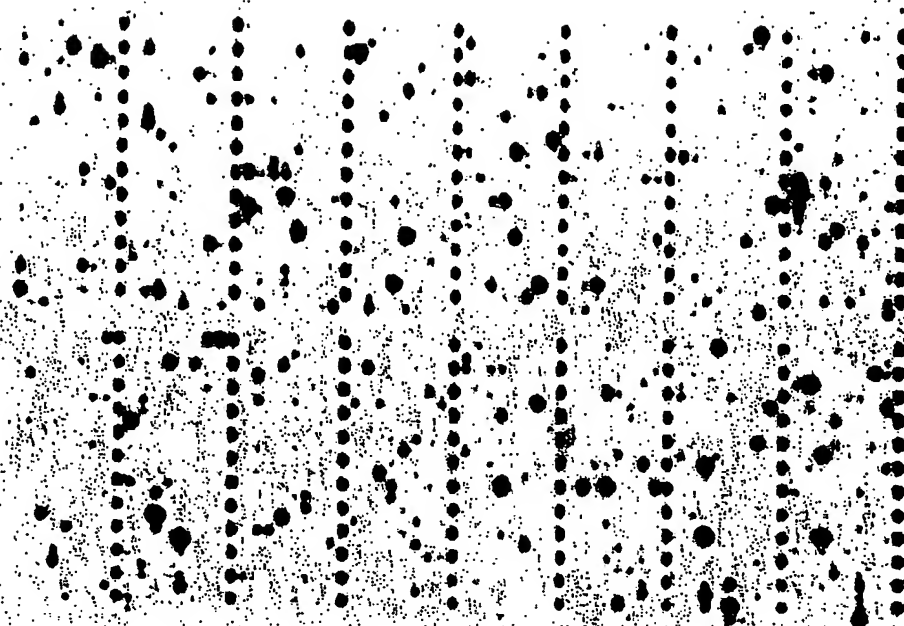
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CAT

YBL003C_YDR225W_homolog 132 aa (SEQ ID NO 484)

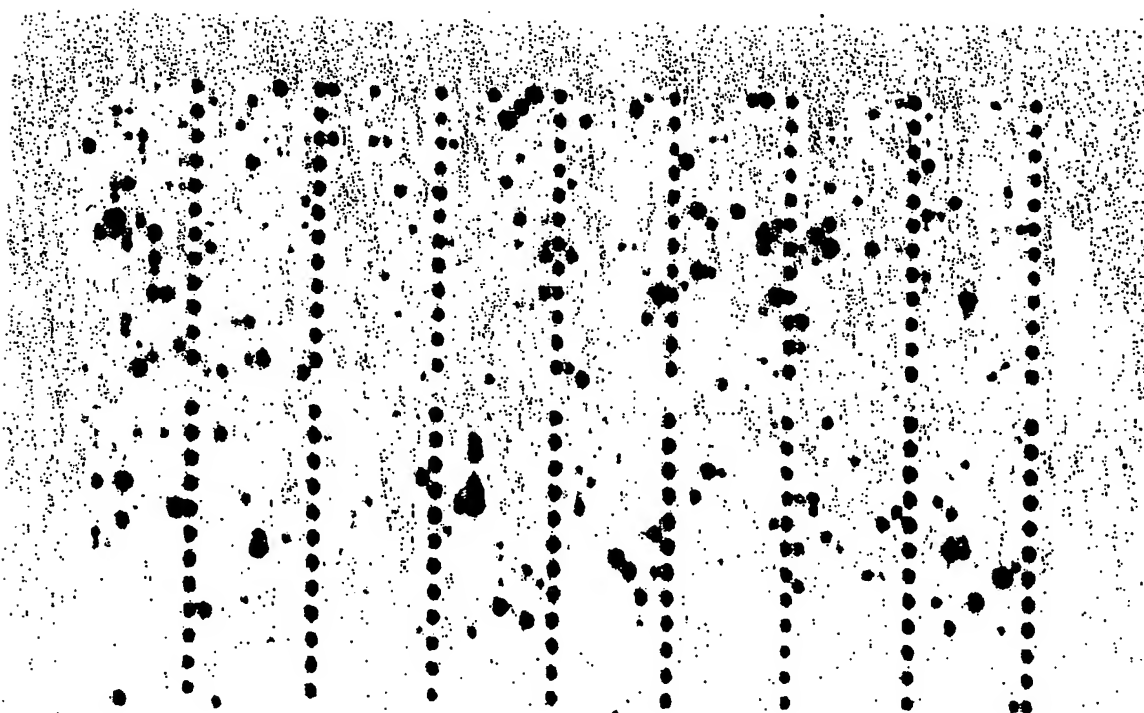
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Filter I



Filter II

FIG. 4A

